



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 153862

TO: Patricia Duffy  
Location: REM/3B05/3C18  
Art Unit: 1645  
Tuesday, May 17, 2005  
  
Case Serial Number: 10/063699

From: Toby Port  
Location: Biotech-Chem Library  
REM1-A59  
Phone: 272-2523  
  
toby.port@uspto.gov

### Search Notes

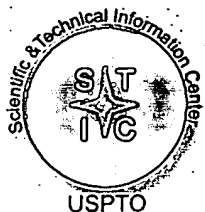
Dear Examiner Duffy,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact **the searcher or contact:**

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg



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STIC-Biotech/ChemLib

153 062

From: Duffy, Patricia  
Sent: Tuesday, May 10, 2005 3:43 PM  
To: STIC-Biotech/ChemLib  
Subject: spdi search  
  
Importance: High

In RE: 10/063,699

Please search SEQ ID NOS: 51 and 52.

Please run the aa seq of SEQ ID NO:52 against the NA database.

Standard SPDI printout.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

STIC  
MAY 19 2005  
153 062

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2005, 18:11:50 ; Search time 5229 Seconds  
(without alignments)  
12622.575 Million cell updates/sec

Title: US-10-063-699-51

Perfect score: 1734

Sequence: 1 gtggactctgagaagccag.....aaaaaaaaaaaaaaaaaaaaa 1734

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	775.8	44.7	868	4	BG680112
2	689.4	39.8	863	4	BG679557
3	673	38.8	792	4	BG681553
4	583	33.6	969	4	BG675558
5	463.4	26.7	634	6	CA446785
6	399.8	23.1	2065	3	AK081753
7	382	22.0	515	7	CN369384
8	372.4	21.5	900	6	CA489311
9	370.8	21.4	843	4	BI822399
10	357.4	20.6	532	2	BF829704
11	333.8	19.3	841	5	BU927828
12	301.8	17.4	415	4	BG676132
13	276.8	16.0	600	7	CO690216
14	275.8	15.9	617	7	CO695910
15	274.8	15.8	538	7	CO680087
16	274.8	15.8	607	7	CO680280
17	274.8	15.8	658	7	CO681303
18	273.8	15.8	520	7	CO688807
19	273.8	15.8	528	7	CO681703
20	273.8	15.8	531	7	CO681087
21	273.8	15.8	611	7	CO680457
22	273.8	15.8	615	7	CO688917
23	272.6	15.7	601	7	CO680520
24	271.8	15.7	514	7	CO716268

c	25	271.6	15.7	626	7	CO682918
	26	264.2	15.2	398	6	CD174603
	27	264.2	15.2	414	6	CD173452
	28	264.2	15.2	430	6	CD173325
	29	263.6	15.2	416	6	CD175306
	30	263.4	15.2	561	4	BM557961
	31	263.2	15.2	454	6	CD388805
c	32	262.6	15.1	502	7	CO691245
	33	261.6	15.1	425	6	CD389076
c	34	261.6	15.1	525	7	CO684145
	35	260	15.0	611	6	CD175431
	36	259.2	14.9	632	1	AV753507
	37	259.2	14.9	778	1	AV752589
c	38	258.6	14.9	528	6	CO684434
	39	255.8	14.8	496	6	CD174636
	40	255.6	14.7	358	7	CN369400
	41	254.4	14.7	748	1	AV751963
	42	252.2	14.5	878	6	CB193179
c	43	249.4	14.4	500	7	CO690072
	44	248.4	14.3	596	7	CO679552
c	45	248.2	14.3	457	7	CO696470
	46	248.2	14.3	633	7	CO690630
c	47	247.6	14.3	441	7	CO685482
	48	247.2	14.3	657	2	BF034006
c	49	245	14.1	439	7	CO684087
	50	241.8	13.9	547	4	BM712887
	51	240.2	13.9	1253	6	CD388578
c	52	237.8	13.7	556	7	CO690415
	53	234.8	13.5	501	7	CO690948
c	54	230	13.3	761	7	CK128355
	55	228.4	13.2	239	5	BQ010428
c	56	226.4	13.1	400	7	CO691099
	57	225.2	13.0	444	7	CO690826
c	58	224.8	13.0	596	1	AU296351
	59	223	12.9	355	1	AA873028
c	60	217	12.5	712	7	CV113267
	61	215	12.4	474	1	AL697958
c	62	213	12.3	394	5	BU784404
	63	213	12.3	803	4	BG741267
c	64	210.2	12.1	440	7	CO681497
	65	209.4	12.1	752	7	CO384272
c	66	209	12.1	342	6	CD172847
	67	205	11.8	239	2	BF834715
c	68	203	11.7	945	6	CD247582
	69	195.4	11.3	412	7	CO680607
c	70	195	11.2	396	4	BG461870
	71	191	11.0	373	5	BU788071
c	72	189.4	10.9	758	4	BG743632
	73	188.4	10.9	488	2	AW786707
c	74	186.8	10.8	503	7	CO695739
	75	186.6	10.8	291	2	BF354727
c	76	186.6	10.8	324	5	BQ308097
	77	185.8	10.7	373	4	BI003515
	78	185.8	10.7	742	2	BB649423
c	79	182.4	10.5	581	5	BF293011
	80	182.4	10.5	746	7	CN369385
	81	182.2	10.5	315	1	CF768508
c	82	181.8	10.5	540	1	A1121206
	83	181.4	10.5	330	7	CO695632
	84	177.6	10.2	546	1	AA756812
c	85	175	10.1	925	5	BQ936377
	86	175	10.1	296	1	BQ935815
	87	171	9.9	953	1	AA336632
c	88	170.4	9.8	274	1	AA337683
	89	168.2	9.7	488	1	AA760019
	90	167.8	9.7	506	1	A1151820
c	91	166.2	9.6	651	2	BES62709
	92	162.2	9.4	737	7	CV126149
	93	157.4	9.1	921	5	BQ935633
c	94	155.2	9.0	289	2	B184234
	95	151.6	8.7	659	7	CF763278
c	96	151.4	8.7	210	7	CO681861
	97	150.4	8.7	537	7	CO679734



244	122.4	7.1	262	7	CR764356	CR764356	DKF2p468D	317	121.8	7.0	822	7	CK796075	CK796075	AGENCOURT
245	122.4	7.1	361	7	CK005157	CK005157	AGENCOURT	318	121.8	7.0	844	2	BE562668	BE562668	601336120
246	122.4	7.1	572	6	CB524812	UI-N-FY0-	AGENCOURT	319	121.8	7.0	853	5	BU927591	BU927591	AGENCOURT
247	122.4	7.1	600	7	CO870977	rt65h10.y	AGENCOURT	320	121.8	7.0	868	7	CO797683	CO797683	AGENCOURT
248	122.4	7.1	690	1	AV681927	AV681927	AGENCOURT	321	121.8	7.0	875	5	BU928010	BU928010	AGENCOURT
249	122.4	7.1	696	7	CK002891	CK002891	AGENCOURT	322	121.8	7.0	889	6	CD249548	CD249548	AGENCOURT
250	122.4	7.1	794	6	CA455515	CA455515	AGENCOURT	323	121.8	7.0	890	5	BU603755	BU603755	AGENCOURT
251	122.4	7.1	805	9	CNS009F8	AL053500	Drosophil	324	121.8	7.0	908	6	CD105753	CD105753	AGENCOURT
252	122.4	7.1	822	5	BU850875	BU850875	AGENCOURT	325	121.8	7.0	949	5	BQ720652	BQ720652	AGENCOURT
253	122.4	7.1	912	6	CD556608	CD556608	AGENCOURT	326	121.8	7.0	955	6	CD513552	CD513552	AGENCOURT
254	122.4	7.1	950	2	BE965060	BE965060	601658845	327	121.8	7.0	956	6	CD051191	CD051191	AGENCOURT
255	122.4	7.1	950	5	BU153588	BU153588	AGENCOURT	328	121.8	7.0	983	6	CD386907	CD386907	AGENCOURT
256	122.4	7.1	1168	4	BM464215	BM464215	AGENCOURT	329	121.8	7.0	1016	5	BM923917	BM923917	AGENCOURT
257	122.2	7.0	233	4	BG880834	1b49h07.y	AGENCOURT	330	121.8	7.0	1041	6	CD051043	CD051043	AGENCOURT
258	122.2	7.0	237	7	CF424418	CF424418	lad30d04.y	331	121.8	7.0	1063	4	BM469499	BM469499	AGENCOURT
259	122.2	7.0	241	6	CA802269	sau33c02.y	AGENCOURT	332	121.8	7.0	1071	6	CD050614	CD050614	AGENCOURT
260	122.2	7.0	290	5	BK486639	BK486639	DKF2p68GM	333	121.8	7.0	1120	4	BM461650	BM461650	AGENCOURT
261	122.2	7.0	304	6	CR802862	CR802862	sau43c08.y	334	121.8	7.0	1327	5	BM9113920	BM9113920	AGENCOURT
262	122.2	7.0	470	7	CF925888	CF925888	lag63b06.y	335	121.6	7.0	198	5	BQ667440	BQ667440	y
263	122.2	7.0	478	7	CK372670	CK372670	lag89g02.y	336	121.6	7.0	310	7	CR630210	CR630210	DKF2p469G
264	122.2	7.0	480	9	CNS01Y58	AL172565	Tetraodon	337	121.6	7.0	319	7	CO195058	CO195058	EC39644.5
265	122.2	7.0	512	6	CA334953	CA334953	NISC lt03	338	121.6	7.0	350	7	CR791224	CR791224	DKF2p468J
266	122.2	7.0	574	6	CB053808	CB053808	NISC gl16	339	121.6	7.0	353	7	CF424463	CF424463	lad31a05.y
267	122.2	7.0	699	6	CD641614	CD641614	AGENCOURT	340	121.6	7.0	397	6	CB570896	CB570896	AGENCOURT
268	122.2	7.0	877	5	BU587984	BU587984	AGENCOURT	341	121.6	7.0	407	1	AV682333	AV682333	AGENCOURT
269	122.2	7.0	901	9	CNS0760F	AL430789	clone XBA	342	121.6	7.0	407	6	CD769076	CD769076	AGENCOURT
270	122	7.0	190	5	BM966075	BM966075	ko21f06.y	343	121.6	7.0	470	4	BG928759	BG928759	HNC36-1-C
271	122	7.0	192	5	BM965779	BM965779	ko17a03.y	344	121.6	7.0	482	6	CD679789	CD679789	lab08b11.y
272	122	7.0	252	5	BU760887	BU760887	sas60a04.y	345	121.6	7.0	568	2	BE909549	BE909549	601502720
273	122	7.0	271	6	CA802849	CA802849	sau38b03.y	346	121.6	7.0	572	5	BQ265428	BQ265428	BP265428
274	122	7.0	275	5	BQ275360	BQ275360	pj44c05.y	347	121.6	7.0	584	4	BG623106	BG623106	602647994
275	122	7.0	275	5	BQ288088	BQ288088	pj53c12.y	348	121.6	7.0	664	6	CD770018	CD770018	AGENCOURT
276	122	7.0	323	6	CB410191	CB410191	NISC nc10	349	121.6	7.0	675	1	AV706520	AV706520	AV706520
277	122	7.0	356	6	CB535894	CB535894	770145.MA	350	121.6	7.0	675	6	CD737352	CD737352	UI-R-GR0-
278	122	7.0	389	5	BQ401026	BQ401026	NISC mp12	351	121.6	7.0	721	7	CN845011	CN845011	EST2961.Z
279	122	7.0	450	5	BQ399241	BQ399241	NISC mp02	352	121.6	7.0	809	6	CD521141	CD521141	AGENCOURT
280	122	7.0	487	6	CD238190	CD238190	FNPAXA08	353	121.6	7.0	833	5	BU529342	BU529342	AGENCOURT
281	122	7.0	533	7	CK1789223	CK1789223	4123655.B	354	121.6	7.0	937	6	CD514598	CD514598	AGENCOURT
282	122	7.0	639	7	CK141621	CK141621	AGENCOURT	355	121.6	7.0	945	5	BU850564	BU850564	AGENCOURT
283	122	7.0	666	7	CO874611	CO874611	BovGen.02	356	121.6	7.0	949	2	BE285783	BE285783	601096386
284	122	7.0	786	5	BU530847	BU530847	AGENCOURT	357	121.6	7.0	1214	4	BG293353	BG293353	602390748
285	122	7.0	834	5	CK198893	CK198893	FGAS007338	358	121.6	7.0	3509	3	EC038795	EC038795	Homo.sapi
286	122	7.0	932	4	BG033403	BG033403	602301577	359	121.4	7.0	275	1	AL043326	AL043326	DKF2p4340
287	122	7.0	1024	5	BU907570	BU907570	AGENCOURT	360	121.4	7.0	275	5	CD288591	CD288591	Pj32f12.y
288	122	7.0	1027	6	CD050242	CD050242	AGENCOURT	361	121.4	7.0	300	7	CN000523	CN000523	1099f03.b
289	121.8	7.0	245	7	CO581347	CO581347	ILLUMIGEN	362	121.4	7.0	403	1	AV682162	AV682162	AGENCOURT
290	121.8	7.0	304	7	CR629112	CR629112	DKF2p468L	363	121.4	7.0	428	6	CB841809	CB841809	M15E-2418
291	121.8	7.0	311	2	AW734023	AW734023	sk79e10.y	364	121.4	7.0	458	6	CB054351	CB054351	NISC.gm03
292	121.8	7.0	317	4	BU702913	BU702913	BU702913	365	121.4	7.0	507	7	CK431107	CK431107	oj58a07.y
293	121.8	7.0	335	5	BP430945	BP430945	BP430945	366	121.4	7.0	677	7	CK468342	CK468342	939726.MA
294	121.8	7.0	336	5	BO783539	BO783539	fab30h11.y	367	121.4	7.0	691	7	CK005554	CK005554	AGENCOURT
295	121.8	7.0	373	6	CB216979	CB216979	NISC.nq11	368	121.4	7.0	802	5	BU960570	BU960570	AGENCOURT
296	121.8	7.0	393	7	CF805242	CF805242	lad55c08.y	369	121.4	7.0	965	6	CD048770	CD048770	AGENCOURT
297	121.8	7.0	400	1	AL361281	AL361281	AGENCOURT	370	121.4	7.0	984	6	CD556844	CD556844	AGENCOURT
298	121.8	7.0	400	5	BK499470	BK499470	DKF2p779M	371	121.4	7.0	990	6	CB201646	CB201646	AGENCOURT
299	121.8	7.0	475	7	CN8433209	CN8433209	AGENCOURT	372	121.4	7.0	1160	3	BC050973	BC050973	Mus.muscu
300	121.8	7.0	515	6	CB139650	CB139650	K-EST0192	373	121.4	7.0	1440	3	BC033555	BC033555	Homo.sapi
301	121.8	7.0	553	7	CB169395	CB169395	170005977	374	121.4	7.0	1474	3	BC032331	BC032331	Homo.sapi
302	121.8	7.0	557	6	CB163124	CB163124	K-EST0223	375	121.2	7.0	173	6	CB084519	CB084519	hg16f08.b
303	121.8	7.0	557	6	CB163124	CB163124	K-EST0223	376	121.2	7.0	184	6	CA935285	CA935285	sau51f03.y
304	121.8	7.0	559	7	CB169398	CB169398	170006001	377	121.2	7.0	268	5	BM889222	BM889222	kb07d03.y
305	121.8	7.0	582	5	BP292786	BP292786	BP292786	378	121.2	7.0	287	5	CK975391	CK975391	4106215.B
306	121.8	7.0	583	5	BP326188	BP326188	BP326188	379	121.2	7.0	287	5	BM899222	BM899222	kb07d03.y
307	121.8	7.0	601	6	CD635038	CD635038	56088965H	380	121.2	7.0	287	5	CK975391	CK975391	4106215.B
308	121.8	7.0	602	6	CD635039	CD635039	56088965H	381	121.2	7.0	287	5	CK975391	CK975391	4106215.B
309	121.8	7.0	632	6	CD770157	CD770157	AGENCOURT	382	121.2	7.0	287	5	CK975391	CK975391	4106215.B
310	121.8	7.0	655	4	BM715676	BM715676	UI-E-EJ0-	383	121.2	7.0	305	6	CD672586	CD672586	Fg13h02.x
311	121.8	7.0	691	2	BF037291	BF037291	601460818	384	121.2	7.0	310	7	CR559169	CR559169	DKF2p468L
312	121.8	7.0	692	7	CB369396	CB369396	170006000	385	121.2	7.0	320	7	CO294973	CO294973	EK208103.y
313	121.8	7.0	713	7	CB369393	CB369393	170005331	386	121.2	7.0	328	7	CO294973	CO294973	DKF2p468L
314	121.8	7.0	738	4	BI912029	BI912029	603066835	387	121.2	7.0	332	6	CB572886	CB572886	AGENCOURT
315	121.8	7.0	795	5	BU963666	BU963666	AGENCOURT	388	121.2	7.0	334	7	CO184694	CO184694	EC28424.5
316	121.8	7.0	822	5	BU953460	BU953460	AGENCOURT	389	121.2	7.0	347	6	CD639672	CD639672	AGENCOURT





536	120.4	6.9	1061	6	CD386766	CD386766 AGENCOURT	609	120.2	6.9	853	5	BU858872	BU858872 AGENCOURT
537	120.4	6.9	1079	6	CD556170	CD556170 AGENCOURT	610	120.2	6.9	865	5	BU842872	BU842872 AGENCOURT
538	120.4	6.9	1467	5	BU509801	BU509801 AGENCOURT	611	120.2	6.9	868	5	BU529631	BU529631 AGENCOURT
539	120.4	6.9	1798	3	BC027967	BC027967 Homo sapi	612	120.2	6.9	878	7	CK790722	CK790722 AGENCOURT
540	120.4	6.9	4471	3	BC040368	BC040368 Mus muscu	613	120.2	6.9	884	6	CD050152	CD050152 AGENCOURT
541	120.2	6.9	162	5	BQ667458	BQ667458 pb61g06.y	614	120.2	6.9	895	7	CN839484	CN839484 AGENCOURT
542	120.2	6.9	167	5	BQ667004	BQ667004 pbs0h12.y	615	120.2	6.9	920	7	CK426359	CK426359 AUF_Ipsdn
543	120.2	6.9	194	5	BA489675	BA489675 DKF2p686K	616	120.2	6.9	937	5	BU532714	BU532714 AGENCOURT
544	120.2	6.9	199	4	BG743745	BG743745 602635232	617	120.2	6.9	944	7	CK403255	CK403255 AUF_lfhdk
545	120.2	6.9	214	7	CO182772	CO182772 EC24004.5	618	120.2	6.9	954	5	BQ278347	BQ278347 AGENCOURT
546	120.2	6.9	220	7	CF424575	CF424575 lad32g04.y	619	120.2	6.9	960	6	CD050329	CD050329 AGENCOURT
547	120.2	6.9	223	7	CR791578	CR791578 DKF2p468D	620	120.2	6.9	966	6	CD0516774	CD0516774 AGENCOURT
548	120.2	6.9	226	5	BA473492	BA473492 DKF2p688E	621	120.2	6.9	991	6	CD050059	CD050059 AGENCOURT
549	120.2	6.9	236	4	BM496455	BM496455 lpcGBR2.1	622	120.2	6.9	993	6	CD244862	CD244862 AGENCOURT
550	120.2	6.9	240	4	BM874548	BM874548 laa05c0.1	623	120.2	6.9	994	6	CD389287	CD389287 AGENCOURT
551	120.2	6.9	256	6	CB060676	CB060676 4010944.B	624	120.2	6.9	996	6	CD050659	CD050659 AGENCOURT
552	120.2	6.9	257	7	CR546572	CR546572 DKF2p470F	625	120.2	6.9	1011	6	CD388386	CD388386 AGENCOURT
553	120.2	6.9	260	4	BM567590	BM567590 kx96a05.y	626	120.2	6.9	1038	6	CD051142	CD051142 AGENCOURT
554	120.2	6.9	260	7	CK377340	CK377340 lai02e06.y	627	120.2	6.9	1040	6	CD047873	CD047873 AGENCOURT
555	120.2	6.9	273	6	CB945895	CB945895 AGENCOURT	628	120.2	6.9	1043	6	CD047944	CD047944 AGENCOURT
556	120.2	6.9	277	7	CR764297	CR764297 DKF2p468J	629	120.2	6.9	1057	6	CD387510	CD387510 AGENCOURT
557	120.2	6.9	278	2	AW274192	AW274192 x87b10.x	630	120.2	6.9	1063	6	CD051032	CD051032 AGENCOURT
558	120.2	6.9	282	2	AW827249	AW827249 xn14h03.y	631	120.2	6.9	1067	6	CD386564	CD386564 AGENCOURT
559	120.2	6.9	288	1	AI538829	AI538829 tp61b10.x	632	120.2	6.9	1120	6	CD048980	CD048980 AGENCOURT
560	120.2	6.9	292	7	CF805143	CF805143 lad63b02.y	633	120.2	6.9	1231	6	CD048493	CD048493 AGENCOURT
561	120.2	6.9	315	7	CN833015	CN833015 AGENCOURT	634	120.2	6.9	2061	3	BC049385	BC049385 Homo sapi
562	120.2	6.9	324	5	BU588095	BU588095 AGENCOURT	635	120.2	6.9	2735	3	HSN806723	HSN806723
563	120.2	6.9	334	4	CF805275	CF805275 lad65h08.y	636	120.2	6.9	3226	3	CR627326	CR627326 Homo sapi
564	120.2	6.9	348	6	CR704555	CR704555 AMGNNUC.N	637	120	6.9	153	4	BI425327	BI425327 aaf28a08.y
565	120.2	6.9	355	1	AI801322	AI801322 t087g03.x	638	120	6.9	181	7	CO322533	CO322533 EK188327.y
566	120.2	6.9	364	7	CR764352	CR764352 DKF2p468K	639	120	6.9	189	4	BM269796	BM269796 bak20d03.y
567	120.2	6.9	365	5	BM966550	BM966550 ko09a03.y	640	120	6.9	199	7	CR788701	CR788701 DKF2p459U
568	120.2	6.9	374	4	BG109221	BG109221 602281245	641	120	6.9	215	5	BM896570	BM896570 ph53a04.y
569	120.2	6.9	378	7	CO882568	CO882568 BovGen.10	642	120	6.9	225	1	AA597154	AA597154 v035g03.1r
570	120.2	6.9	383	7	CR791094	CR791094 DKF2p469C	643	120	6.9	230	7	CO180224	CO180224 EC01250.5
571	120.2	6.9	402	6	CR768940	CR768940 AMGNNUC.N	644	120	6.9	239	1	AL714328	AL714328 AL714328
572	120.2	6.9	405	1	AL048871	AL048871 DKF2p4341	645	120	6.9	239	7	CK376983	CK376983 lah72e12.y
573	120.2	6.9	406	5	BA484065	BA484065 DKF2p686C	646	120	6.9	240	7	CR774358	CR774358 DKF2p459P
574	120.2	6.9	413	7	CK385698	CK385698 lah61a10.y	647	120	6.9	241	5	BX504689	BX504689 DKF2p686B
575	120.2	6.9	442	2	BEG25437	BEG25437 uu18f11.y	648	120	6.9	283	5	BX644833	BX644833 DKF2p781M
576	120.2	6.9	460	6	CD640295	CD640295 AGENCOURT	649	120	6.9	305	4	BG609663	BG609663 323594.MA
577	120.2	6.9	460	7	CO871594	CO871594 BovGen.00	650	120	6.9	311	4	BM154695	BM154695 fv88c02.y
578	120.2	6.9	472	4	BM514120	BM514120 kx96a05.y	651	120	6.9	311	7	CR559327	CR559327 DKF2p468G
579	120.2	6.9	474	2	BF726322	BF726322 by04h07.y	652	120	6.9	319	5	BU764204	BU764204 aaf53h09.y
580	120.2	6.9	474	7	CO873267	CO873267 BovGen.01	653	120	6.9	330	4	BG834096	BG834096 352197.MA
581	120.2	6.9	477	6	CB530084	CB530084 595730.MA	654	120	6.9	335	7	CF381770	CF381770 lab84b07.y
582	120.2	6.9	490	4	BM513549	BM513549 kx96a05.y	655	120	6.9	346	6	CD722422	CD722422 o109e08.y
583	120.2	6.9	512	5	BQ390352	BQ390352 NISC_mq12	656	120	6.9	376	6	CB286466	CB286466 CMD38.B02
584	120.2	6.9	517	6	CA335652	CA335652 NISC_lu02	657	120	6.9	387	7	CF426295	CF426295 lad22503..
585	120.2	6.9	530	7	CK384690	CK384690 lah53a10.y	658	120	6.9	389	7	CK430907	CK430907 o155d10.y
586	120.2	6.9	549	4	BG925940	BG925940 HNC21-1-G	659	120	6.9	398	2	BE048081	BE048081 tz47g03.y
587	120.2	6.9	554	6	CA369262	CA369262 645652.NC	660	120	6.9	421	7	CR764353	CR764353 DKF2p468K
588	120.2	6.9	554	7	CK962071	CK962071 4076522.B	661	120	6.9	437	5	BR953282	BR953282 DKF2p781K
589	120.2	6.9	583	5	BP209684	BP209684 BP209684	662	120	6.9	443	4	BM514199	BM514199 kx97f04.y
590	120.2	6.9	598	4	BM514970	BM514970 kx96a08.y	663	120	6.9	458	7	CR549875	CR549875 DKF2p469M
591	120.2	6.9	611	6	CA378212	CA378212 656969.NC	664	120	6.9	461	7	CO194931	CO194931 EC39483.5
592	120.2	6.9	625	6	CA361597	CA361597 635456.NC	665	120	6.9	470	5	BP376697	BP376697 BP376697
593	120.2	6.9	628	6	CD766420	CD766420 AGENCOURT	666	120	6.9	518	5	BO748115	BO748115 UT-M-PAO-
594	120.2	6.9	634	6	CB127790	CB127790 K-EST0177	667	120	6.9	512	6	CA744558	CA744558 wr1a.pko
595	120.2	6.9	661	1	CK656411	CK656411 AGENCOURT	668	120	6.9	529	1	AV758217	AV758217 AV758217
596	120.2	6.9	680	1	AV733537	AV733537 AV733537	669	120	6.9	534	4	BG781907	BG781907 SEAMUC001
597	120.2	6.9	687	6	CD640205	CD640205 AGENCOURT	670	120	6.9	554	5	BQ394230	BQ394230 NISC_rg08
598	120.2	6.9	724	6	CD239019	CD239019 FNPBJF02	671	120	6.9	562	7	CK997320	CK997320 ip17b02.b
599	120.2	6.9	763	5	BU566497	BU566497 AGENCOURT	672	120	6.9	565	7	CK983884	CK983884 re30e05.y
600	120.2	6.9	768	7	CO802242	CO802242 AGENCOURT	673	120	6.9	589	1	AV714624	AV714624 AV714624
601	120.2	6.9	802	5	BU851163	BU851163 AGENCOURT	674	120	6.9	601	7	CK789624	CK789624 AGENCOURT
602	120.2	6.9	808	6	CB318829	CB318829 AGENCOURT	675	120	6.9	677	7	CK798466	CK798466 AGENCOURT
603	120.2	6.9	831	5	BU530539	BU530539 AGENCOURT	676	120	6.9	679	7	CN843802	CN843802 AGENCOURT
604	120.2	6.9	834	5	BU957897	BU957897 AGENCOURT	677	120	6.9	720	7	CN161903	CN161903 951238.MA
605	120.2	6.9	835	5	BU530772	BU530772 AGENCOURT	678	120	6.9	768	4	BG403695	BG403695 602419523
606	120.2	6.9	837	7	CK398766	CK398766 AGENCOURT	679	120	6.9	778	5	BU533453	BU533453 AGENCOURT
607	120.2	6.9	841	5	BU960741	BU960741 AGENCOURT	680	120	6.9	808	5	BU954956	BU954956 AGENCOURT
608	120.2	6.9	849	7	CK198254	CK198254 FGAS00673	681	120	6.9	812	5	BU958357	BU958357 AGENCOURT

682	120	6.9	814	6	CA465473	AGENCYCOURT	755	119.6	6.9	308	7	CF981057	CF981057	re02c10.y
683	120	6.9	826	5	BU529199	AGENCYCOURT	c 756	119.6	6.9	319	5	AX476602	AX476602	DXFZp686D
684	120	6.9	830	7	KU196984	FGAS00545	757	119.6	6.9	327	1	AL698000	AL698000	DXFZp686M
c 685	120	6.9	837	9	CNS0608L	AL407971 t3 end of	758	119.6	6.9	327	4	BI790851	BI790851	1a07c12.y
686	120	6.9	840	5	BU935967	AGENCYCOURT	759	119.6	6.9	330	5	BQ640108	BQ640108	DC54007.y
687	120	6.9	848	5	BU958202	AGENCYCOURT	760	119.6	6.9	333	7	CF571969	CF571969	MCSA031C0
688	120	6.9	884	5	BU929757	AGENCYCOURT	761	119.6	6.9	346	6	BJ701862	BJ701862	BJ701862
689	120	6.9	903	5	BU861189	AGENCYCOURT	762	119.6	6.9	366	6	CA376389	CA376389	654736 NC
690	120	6.9	943	6	CD106380	AGENCYCOURT	763	119.6	6.9	379	7	CK9317918	CK9317918	CGF100448
691	120	6.9	972	7	KA423944	AUF_IpSpn	764	119.6	6.9	386	6	CB806505	CB806505	AMGNNUC.S
692	120	6.9	975	7	BU851036	AGENCYCOURT	765	119.6	6.9	393	5	BX507033	BX507033	DXFZp779B
693	120	6.9	998	6	CD251032	AGENCYCOURT	766	119.6	6.9	397	1	AL723541	AL723541	AL723541
694	120	6.9	1000	6	BU962341	AGENCYCOURT	767	119.6	6.9	427	7	CN049668	CN049668	V4_P2_G5
695	120	6.9	1214	5	BU167807	AGENCYCOURT	768	119.6	6.9	431	7	CO191531	CO191531	EC31328.5
696	120	6.9	1269	6	CD050402	AGENCYCOURT	c 769	119.6	6.9	444	5	BQ391745	BQ391745	NISC_mq20
697	120	6.9	1438	9	CL078561	AGENCYCOURT	c 770	119.6	6.9	476	5	BQ391769	BQ391769	NISC_mq20
698	120	6.9	1495	3	HSMB03410	CL078561 CH216-151	771	119.6	6.9	479	7	CK386176	CK386176	1ah33a09.
c 699	120	6.9	5201	3	BC063852	AL832103 Homo sapi	772	119.6	6.9	504	6	CA373381	CA373381	647497 NC
700	119.8	6.9	207	6	CB978499	BC063852 Homo sapi	773	119.6	6.9	513	1	AV729334	AV729334	AV729334
701	119.8	6.9	230	6	CB286070	CB978499 CAB40005	774	119.6	6.9	515	7	CN049660	CN049660	V4_P2_G11
702	119.8	6.9	232	7	CR537572	CB286070 CMD30_A04	c 775	119.6	6.9	523	6	CB083179	CB083179	h67f10.b
703	119.8	6.9	278	7	CR545039	CR537572 DXFZp459K	776	119.6	6.9	532	6	CA354283	CA354283	625969 NC
704	119.8	6.9	281	2	AW785969	CR545039 DXFZp470L	777	119.6	6.9	535	1	AV757455	AV757455	AV757455
705	119.8	6.9	289	7	CR559200	AW785969 117506 MA	c 778	119.6	6.9	540	1	AJ655991	AJ655991	AJ655991
706	119.8	6.9	313	4	BI839345	CR559200 DXFZp468F	c 779	119.6	6.9	545	6	CA353983	CA353983	625617 NC
707	119.8	6.9	328	1	AL708249	BI839345 f866d05.y	780	119.6	6.9	549	6	CB523098	CB523098	UT-M-GK0-
708	119.8	6.9	343	7	CV042716	AL708249 DXFZp686A	781	119.6	6.9	576	6	CA364401	CA364401	639298 NC
709	119.8	6.9	349	6	CD679438	CV042716 dba10f02.	782	119.6	6.9	598	3	CR639557	CR639557	Tetradon
710	119.8	6.9	349	7	CV193543	CD679438 hq10902.y	c 783	119.6	6.9	604	5	BQ394396	BQ394396	NISC_ng08
711	119.8	6.9	358	6	CB721263	CV193543 SNEStbabo	784	119.6	6.9	605	2	BH637500	BH637500	BB637500
712	119.8	6.9	386	7	CF211695	CB721263 jnn603C06	785	119.6	6.9	608	4	BG678047	BG678047	602625771
713	119.8	6.9	413	7	CN788655	CF211695 AGF100066	786	119.6	6.9	661	6	CD640938	CD640938	AGENCYCOURT
714	119.8	6.9	413	7	CV223489	CN788655 4123012 B	787	119.6	6.9	679	6	CD46924	CD46924	E04912701
715	119.8	6.9	417	4	BF966050	CV223489 t3i63e05	788	119.6	6.9	706	6	CD641730	CD641730	AGENCYCOURT
716	119.8	6.9	420	4	BM574321	BF966050 602277352	789	119.6	6.9	754	2	BF340104	BF340104	602037263
717	119.8	6.9	425	4	BM574321	CF613102 1a132g12.	c 790	119.6	6.9	784	2	BF534220	BF534220	602047770
718	119.8	6.9	425	4	BM574321	BM574321 fx84h04.y	791	119.6	6.9	806	1	AV757705	AV757705	AV757705
719	119.8	6.9	427	4	BI523504	BM574321 fx84h04.y	792	119.6	6.9	820	5	BU850939	BU850939	AGENCYCOURT
720	119.8	6.9	437	7	CK384228	BI523504 603175314	793	119.6	6.9	830	5	BU958317	BU958317	AGENCYCOURT
721	119.8	6.9	458	9	CNS006FT	CK384228 1ah06h09.	794	119.6	6.9	832	5	BU858775	BU858775	AGENCYCOURT
722	119.8	6.9	463	2	BF727212	AL065671 Drosophila	795	119.6	6.9	834	5	BU842573	BU842573	AGENCYCOURT
723	119.8	6.9	476	6	CB721269	BF727212 by18c08.y	796	119.6	6.9	841	5	BU555504	BU555504	AGENCYCOURT
c 724	119.8	6.9	548	6	CA729868	CB721269 jnn603D03	797	119.6	6.9	847	5	BU954608	BU954608	AGENCYCOURT
725	119.8	6.9	587	5	BQ747159	CA729868 w1p1c.pko	c 798	119.6	6.9	893	6	CD243740	CD243740	AGENCYCOURT
726	119.8	6.9	625	7	CK005086	BQ747159 UT-M-PK0-	c 799	119.6	6.9	905	7	CV069870	CV069870	WPAHx15
727	119.8	6.9	741	7	CK491293	CK005086 AGENCYCOURT	c 800	119.6	6.9	911	5	BU942433	BU942433	AGENCYCOURT
c 728	119.8	6.9	813	7	CK193688	CK491293 AGENCYCOURT	801	119.6	6.9	911	6	CB587843	CB587843	AGENCYCOURT
729	119.8	6.9	815	5	BU537523	CK193688 FGAS00210	802	119.6	6.9	921	5	BU556146	BU556146	AGENCYCOURT
730	119.8	6.9	840	7	CK804852	BU537523 AGENCYCOURT	803	119.6	6.9	922	3	AY106532	AY106532	Zea mayb
731	119.8	6.9	862	7	CA464386	CK804852 AGENCYCOURT	804	119.6	6.9	937	5	BU193300	BU193300	AGENCYCOURT
732	119.8	6.9	927	7	CA426398	CA464386 AGENCYCOURT	805	119.6	6.9	942	5	BU170642	BU170642	AGENCYCOURT
733	119.8	6.9	1002	5	BU940773	CA426398 AUF_IpTes	806	119.6	6.9	943	6	CD388494	CD388494	AGENCYCOURT
734	119.8	6.9	1043	5	BM922786	BU940773 AGENCYCOURT	807	119.6	6.9	951	5	BU554730	BU554730	AGENCYCOURT
735	119.8	6.9	1066	5	BU540067	BM922786 AGENCYCOURT	808	119.6	6.9	978	4	BG284619	BG284619	602408789
736	119.8	6.9	1076	6	CD247055	BU540067 AGENCYCOURT	809	119.6	6.9	1057	6	CA475599	CA475599	AGENCYCOURT
737	119.8	6.9	1164	3	AF113694	CD247055 AGENCYCOURT	810	119.6	6.9	1177	6	BM904746	BM904746	AGENCYCOURT
738	119.8	6.9	1176	5	BM927266	AF113694 Homo sapi	811	119.6	6.9	1193	6	CD556392	CD556392	AGENCYCOURT
739	119.8	6.9	8002	3	CR627249	BM927266 AGENCYCOURT	812	119.6	6.9	1804	3	BC030527	BC030527	Homo sapi
740	119.6	6.9	185	5	BQ077400	CR627249 Homo sapi	813	119.6	6.9	3322	3	BC030457	BC030457	Mus muscu
c 741	119.6	6.9	191	6	CB606695	BQ077400 f216b02.y	814	119.6	6.9	3322	3	BC030457	BC030457	Mus muscu
742	119.6	6.9	200	6	CA676034	CB606695 AMGNNUC.S	815	119.6	6.9	179	1	AU284833	AU284833	AU284833
743	119.6	6.9	206	7	CF329066	CA676034 w1leu2.pko	816	119.4	6.9	182	4	BM155342	BM155342	fW02f02.y
744	119.6	6.9	212	5	BM927266	CF329066 NACL--04-	817	119.4	6.9	197	4	BM308701	BM308701	sak49d05.
745	119.6	6.9	222	4	BQ47503	BM927266 AGENCYCOURT	818	119.4	6.9	199	7	CR630322	CR630322	DXFZp4691
746	119.6	6.9	223	5	BX475604	BQ47503 BU047503	819	119.4	6.9	208	4	BI901084	BI901084	1b84908.y
747	119.6	6.9	233	6	CA692459	BX475604 DXFZp686P	820	119.4	6.9	209	7	CK427762	CK427762	1aJ03e08.
748	119.6	6.9	236	6	CB948928	CA692459 w1m96.pko	821	119.4	6.9	218	6	CB337787	CB337787	1aa29b05.
749	119.6	6.9	245	5	BX951835	CB948928 AGENCYCOURT	822	119.4	6.9	219	5	BX255540	BX255540	AX255540
750	119.6	6.9	267	2	AW619318	BX951835 DXFZp781A	823	119.4	6.9	227	7	CK374613	CK374613	1a180a01.
c 751	119.6	6.9	274	5	BQ385858	AW619318 690 MARC	824	119.4	6.9	237	6	CB083959	CB083959	h606h05.b
752	119.6	6.9	275	7	BI943394	BQ385858 NISC_m14	825	119.4	6.9	265	7	CR559214	CR559214	DXFZp468P
753	119.6	6.9	297	2	BE722549	BI943394 t993H04.y	826	119.4	6.9	266	5	BX504760	BX504760	DXFZp686E
754	119.6	6.9	308	5	BX506616	BE722549 190841 MA	827	119.4	6.9	269	6	CD638413	CD638413	AGENCYCOURT
						BX506616 DXFZp779D								

828	119.4	6.9	269	7	COA16572	COA16572	Mdfr30081	c	901	119.2	6.9	327	1	AI682743	AI682743	wc65f05.x
829	119.4	6.9	276	7	CK430580	CK430580	o51b09.y		902	119.2	6.9	332	7	CO185234	CO185234	EC29979.5
830	119.4	6.9	283	6	CB931364	CB931364	i129a06.y		903	119.2	6.9	351	7	CF949967	CF949967	UI-M-HK0-
831	119.4	6.9	287	7	CO646755	CO646755	ILLUMIGEN		904	119.2	6.9	354	7	CR524605	CR524605	DKFZp470G
832	119.4	6.9	290	5	BA765222	BA765222	DKFZp686K		905	119.2	6.9	360	1	AL714101	AL714101	AL714101
833	119.4	6.9	305	4	BG880350	BG880350	lb69909.y		906	119.2	6.9	371	7	CK377132	CK377132	lan98902.
834	119.4	6.9	305	4	BM570424	BM570424	i101h07.y		907	119.2	6.9	385	6	CB702425	CB702425	ANGNUC:N
835	119.4	6.9	319	5	BU960325	BU960325	AGENCOURT	c	908	119.2	6.9	401	5	BQ524751	BQ524751	NISC.no06
c 836	119.4	6.9	319	5	BA489110	BA489110	DKFZp686J		909	119.2	6.9	411	1	AL120854	AL120854	DKFZp762J
837	119.4	6.9	350	6	CB332172	CB332172	py68609.y		910	119.2	6.9	430	7	CF314838	CF314838	HD--03-11
838	119.4	6.9	374	7	CF353384	CF353384	lab44b12.y		911	119.2	6.9	435	1	AL041573	AL041573	DKFZp434I
839	119.4	6.9	388	6	CB640168	CB640168	AGENCOURT		912	119.2	6.9	435	2	AW187431	AW187431	BNLGH1514
c 840	119.4	6.9	406	5	BQ526114	BQ526114	NISC.no14		913	119.2	6.9	443	7	CK000623	CK000623	AGENCOURT
841	119.4	6.9	417	7	CK384549	CK384549	lah26f05.x		914	119.2	6.9	447	1	AV717299	AV717299	AV717299
c 842	119.4	6.9	426	6	CD678845	CD678845	hq01b11.f		915	119.2	6.9	440	6	CA336955	CA336955	NISC.l07
843	119.4	6.9	446	4	BM513660	BM513660	kx97f04.y		916	119.2	6.9	491	1	AV757797	AV757797	AV757797
c 844	119.4	6.9	447	5	BQ526779	BQ526779	NISC.no18		917	119.2	6.9	528	6	CA385923	CA385923	667420.NC
845	119.4	6.9	454	6	CB843283	CB843283	M1SE-4077		c 918	119.2	6.9	537	5	BQ266461	BQ266461	NISC.ff13
.846	119.4	6.9	466	5	BU705804	BU705804	UI-M-FRO-		919	119.2	6.9	538	7	CO583292	CO583292	ILLUMIGEN
847	119.4	6.9	469	5	BU774122	BU774122	SJEGCH12		920	119.2	6.9	558	5	BQ390915	BQ390915	NISC.mq15
848	119.4	6.9	476	1	AV682082	AV682082	AV682082		c 921	119.2	6.9	558	5	BQ397196	BQ397196	NISC.ng26
849	119.4	6.9	495	6	CD236950	CD236950	FNPAEG11		922	119.2	6.9	571	4	BI860596	BI860596	603387086
850	119.4	6.9	501	7	CK394807	CK394807	EST1314.Z		923	119.2	6.9	580	7	CN194355	CN194355	rg93c12.y
c 851	119.4	6.9	509	6	CA376944	CA376944	655416.NC		924	119.2	6.9	592	7	CK242322	CK242322	rx08603.y
852	119.4	6.9	516	1	AI909666	AI909666	PM-BT219-		925	119.2	6.9	615	7	CK003614	CK003614	AGENCOURT
853	119.4	6.9	536	4	BM155392	BM155392	fW04C02.y		c 926	119.2	6.9	630	6	CB052458	CB052458	NISC.g108
854	119.4	6.9	545	7	CV193434	CV193434	SnESTfab3		927	119.2	6.9	630	7	CO071774	CO071774	GR_Ea30G
855	119.4	6.9	554	5	BP273011	BP273011	BP273011		928	119.2	6.9	634	7	CK120520	CK120520	207g11.pl
856	119.4	6.9	556	7	CK791071	CK791071	AGENCOURT		929	119.2	6.9	685	2	BE905408	BE905408	601499093
c 857	119.4	6.9	578	6	CB051669	CB051669	NISC.g102		930	119.2	6.9	699	6	CD239936	CD239936	FNPCAD07
858	119.4	6.9	579	4	BG925221	BG925221	NHC73-1-B		931	119.2	6.9	753	6	CB599054	CB599054	AGENCOURT
859	119.4	6.9	583	2	BF673434	BF673434	602136211		932	119.2	6.9	771	7	CF519894	CF519894	AGENCOURT
860	119.4	6.9	585	7	CO403863	CO403863	AGENCOURT		933	119.2	6.9	797	6	CA466535	CA466535	AGENCOURT
861	119.4	6.9	609	7	CV199888	CV199888	km22d12.y		934	119.2	6.9	797	6	CB312089	CB312089	AGENCOURT
c 862	119.4	6.9	623	6	CD770235	CD770235	AGENCOURT		935	119.2	6.9	811	7	CK789864	CK789864	AGENCOURT
863	119.4	6.9	633	6	CB051583	CB051583	NISC.g101		936	119.2	6.9	834	6	CA465069	CA465069	AGENCOURT
864	119.4	6.9	640	6	CD639314	CD639314	AGENCOURT		937	119.2	6.9	838	7	CK400797	CK400797	AGENCOURT
865	119.4	6.9	687	6	AD772154	AD772154	AGENCOURT		938	119.2	6.9	843	5	BU555489	BU555489	AGENCOURT
866	119.4	6.9	739	1	CV726951	CV726951	AV726951		939	119.2	6.9	871	5	BU589926	BU589926	AGENCOURT
867	119.4	6.9	779	6	CD356401	CD356401	AGENCOURT		940	119.2	6.9	874	5	BU590078	BU590078	AGENCOURT
868	119.4	6.9	798	7	CK796183	CK796183	AGENCOURT		941	119.2	6.9	875	5	BU962377	BU962377	AGENCOURT
869	119.4	6.9	808	6	CD520988	CD520988	AGENCOURT		942	119.2	6.9	891	4	BM449741	BM449741	AGENCOURT
870	119.4	6.9	829	7	CK794790	CK794790	AGENCOURT		943	119.2	6.9	905	6	CB946345	CB946345	AGENCOURT
871	119.4	6.9	833	5	BU556151	BU556151	AGENCOURT		944	119.2	6.9	906	5	BU529444	BU529444	AGENCOURT
872	119.4	6.9	857	5	BU603693	BU603693	AGENCOURT		945	119.2	6.9	915	7	CK404840	CK404840	AUF.Ifspn
c 873	119.4	6.9	874	7	CF783995	CF783995	AGENCOURT		946	119.2	6.9	935	5	BU842252	BU842252	AGENCOURT
874	119.4	6.9	899	6	CD109103	CD109103	AGENCOURT		947	119.2	6.9	935	5	BU944930	BU944930	AGENCOURT
875	119.4	6.9	905	7	CK403782	CK403782	AUF.IfHCK		948	119.2	6.9	945	9	CL107121	CL107121	ISB1-47N1
876	119.4	6.9	947	6	CD249490	CD249490	AGENCOURT		949	119.2	6.9	965	5	BQ921874	BQ921874	AGENCOURT
c 877	119.4	6.9	957	4	BM415792	BM415792	OP20874.M		950	119.2	6.9	968	6	CD389337	CD389337	AGENCOURT
c 878	119.4	6.9	966	7	CF579148	CF579148	AGENCOURT		c 951	119.2	6.9	972	7	CF594816	CF594816	AGENCOURT
879	119.4	6.9	971	5	BQ950467	BQ950467	AGENCOURT		c 952	119.2	6.9	979	4	BF983875	BF983875	602307421
880	119.4	6.9	971	9	CL120194	CL120194	ISB1-78U1		953	119.2	6.9	1053	4	BG975528	BG975528	602845206
881	119.4	6.9	1002	5	BU509843	BU509843	AGENCOURT		954	119.2	6.9	1054	3	AF130104	AF130104	Homo.sapl
882	119.4	6.9	1006	6	CD388276	CD388276	AGENCOURT		955	119.2	6.9	1073	4	BM544111	BM544111	AGENCOURT
883	119.4	6.9	1010	6	CD050824	CD050824	AGENCOURT		956	119.2	6.9	1077	5	BU560007	BU560007	AGENCOURT
c 884	119.4	6.9	1034	2	BE964486	BE964486	601658194		957	119.2	6.9	1081	6	CB182058	CB182058	AGENCOURT
885	119.4	6.9	1057	4	BM556289	BM556289	AGENCOURT		958	119.2	6.9	1114	5	BM918578	BM918578	AGENCOURT
c 886	119.4	6.9	1086	5	BU960798	BU960798	AGENCOURT		959	119.2	6.9	1147	6	CD050956	CD050956	AGENCOURT
887	119.4	6.9	1090	4	BM456601	BM456601	AGENCOURT		c 960	119.2	6.9	1150	4	BM477385	BM477385	AGENCOURT
888	119.4	6.9	1132	5	BM921564	BM921564	AGENCOURT		961	119.2	6.9	1214	4	BG030837	BG030837	602299535
889	119.4	6.9	4793	3	CR749666	CR749666	Homo.sapl		962	119.2	6.9	1309	4	BM463041	BM463041	AGENCOURT
890	119.4	6.9	7801	3	CR749850	CR749850	Homo.sapl		c 963	119.2	6.9	1450	4	BG297378	BG297378	602395514
891	119.2	6.9	196	6	CB073175	CB073175	taa29d07		964	119.2	6.9	2769	3	BC046986	BC046986	Mus.muscu
892	119.2	6.9	201	5	BA744221	BA744221	DKFZp686D		965	119	6.9	160	4	BI500352	BI500352	rs71a10.y
893	119.2	6.9	205	7	CR771816	CR771816	DKFZp468A		966	119	6.9	170	4	BU701487	BU701487	BZ701487
894	119.2	6.9	211	2	BE013113	BE013113	122910.MA		967	119	6.9	182	5	BM507031	BM507031	DKFZp779A
895	119.2	6.9	224	1	AA606934	AA606934	vm93a11.r		968	119	6.9	188	7	CO649268	CO649268	ILLUMIGEN
c 896	119.2	6.9	230	5	BA481892	BA481892	DKFZp686P		969	119	6.9	192	7	CF645516	CF645516	K37_C12.F
897	119.2	6.9	235	1	AA606938	AA606938	vm93c11.r		970	119	6.9	200	7	CF559013	CF559013	DKFZp468P
898	119.2	6.9	239	7	CK853245	CK853245	13994.Sto		971	119	6.9	206	7	CR766913	CR766913	DKFZp468L
c 899	119.2	6.9	250	1	AI702433	AI702433	tz67f08.x		c 972	119	6.9	207	1	AI433976	AI433976	t112c12.x
c 900	119.2	6.9	317	9	CNS0002C4	AL097486	Drosophila		c 973	119	6.9	207	4	BM579757	BM579757	170006872

974	119	6.9	209	1	AA638753	vm93e12.r	1047	119	6.9	1030	5	BUS90415	BUS90415	AGENCOURT
975	119	6.9	212	5	BU760971	esa61b04.	1048	119	6.9	1091	5	BUS55642	BUS55642	AGENCOURT
976	119	6.9	243	7	CF122509	UI-HF-CHO	1049	119	6.9	3583	3	BC030193	BC030193	Homo sapi
977	119	6.9	248	5	BUS530681	AGENCOURT	c1050	118.8	6.9	158	7	CK615927	ck07f07.y	
978	119	6.9	253	7	CF805040	1ad60905.	c1051	118.8	6.9	159	1	AI539153	AI539153	
979	119	6.9	264	6	CB409641	NISC.nc06.	1052	118.8	6.9	183	5	BA477606	BA477606	DRF2p6860
980	119	6.9	268	1	AI811344	tw38f05.x	c1053	118.8	6.9	193	5	BA472408	BA472408	DRF2p686P
C 981	119	6.9	294	2	AW306843	AW306843 sf49d05.y	1054	118.8	6.9	211	4	BJ680884	BJ680884	BJ680884
982	119	6.9	310	4	BM154701	fv88c10.y	1055	118.8	6.9	233	2	BE030380	BE030380	128430 MA
983	119	6.9	312	7	CR791650	DRF2p468G	c1056	118.8	6.9	233	7	CF308041	ABF--01-L	
984	119	6.9	329	4	BI439343	1c62910.y	c1057	118.8	6.9	234	7	CF333001	JMT--01-L	
985	119	6.9	341	5	BA497023	DRF2p799B	1058	118.8	6.9	240	6	CB020904	PKX2C08.y	
986	119	6.9	345	6	DR272327	0j19f04.y	1059	118.8	6.9	245	5	BA476550	BA476550	DRF2p6860
C 987	119	6.9	353	1	AI801608	to91f06.x	1060	118.8	6.9	258	2	BE057317	8n01e03.y	
988	119	6.9	358	5	BP702622	BP702622	1061	118.8	6.9	263	7	CR558976	DRF2p468H	
989	119	6.9	369	6	CD103137	AGENCOURT	1062	118.8	6.9	273	2	BE013212	123085 MA	
990	119	6.9	371	7	CK372901	1a193d05.	1063	118.8	6.9	277	7	CF370764	CF370764	1953f04.y
C 991	119	6.9	371	7	CO736053	SI1L05b13	1064	118.8	6.9	295	1	AL723228	AL723228	AL723228
992	119	6.9	372	2	BF726001	bx22g06.y	1065	118.8	6.9	295	6	CB701960	CB701960	AMGNNUC:S
993	119	6.9	374	7	CV192962	SnESTbabi	1066	118.8	6.9	297	5	BQ128810	1i23d03.y	
994	119	6.9	413	5	BX953260	DRF2p781H	1067	118.8	6.9	298	7	CM654687	UMC-bend	
995	119	6.9	448	6	CB080134	hp82b02.b	1068	118.8	6.9	298	9	CNS00LHC	AL068218 DrosophiI	
996	119	6.9	453	7	CF124640	UI-HF-CHO	1069	118.8	6.9	301	4	BI790700	BI790700	i408a10.y
997	119	6.9	459	1	AL717109	AL717109	c1070	118.8	6.9	307	6	CB697660	AMGNNUC:S	
998	119	6.9	461	5	BA472677	DRF2p686I	c1071	118.8	6.9	316	4	BI278084	BI278084	UI-R-CZO-
999	119	6.9	461	7	CA334925	NISC.lt03	1072	118.8	6.9	320	2	AW509353	AW509353	8i22a03.y
1000	119	6.9	462	6	CA334925	NISC.lt03	1073	118.8	6.9	333	7	CO184639	CO184639	EC28357.5
1001	119	6.9	494	7	CV525345	Malv4011i	1074	118.8	6.9	341	5	BX953635	BX953635	DRF2p781M
1002	119	6.9	499	5	BM966619	kol0a02.y	1075	118.8	6.9	368	6	CB049872	CB049872	NISC.gj12
1003	119	6.9	515	7	CO183561	EC25962.5	1076	118.8	6.9	374	6	BY769200	BY769200	BY769200
1004	119	6.9	538	7	CF755575	lae43b11.	1077	118.8	6.9	374	7	CR549911	CR549911	DRF2p4690
1005	119	6.9	542	7	CV106846	AGENCOURT	1078	118.8	6.9	380	6	CD243157	CD243157	AGENCOURT
1006	119	6.9	549	7	CK983831	re29g10.y	1079	118.8	6.9	395	6	CA380038	CA380038	659255 NC
1007	119	6.9	569	6	CB080064	hp80g02.b	c1080	118.8	6.9	397	5	BQ527014	NISC.no19	
C 1008	119	6.9	577	6	CB044223	NISC.gc03	1081	118.8	6.9	398	3	AF116644	AF116644	Homo sapi
1009	119	6.9	639	1	AV709517	AV709517	1082	118.8	6.9	399	7	CF380178	CF380178	lac77912.
1010	119	6.9	659	6	CD640691	AGENCOURT	1083	118.8	6.9	400	7	CF424715	lad36e04.	
1011	119	6.9	668	6	CD639484	AGENCOURT	1084	118.8	6.9	416	7	CO880080	CO880080	BovGen.08
1012	119	6.9	682	3	BC050980	Mus.muscu	1085	118.8	6.9	424	6	CB083556	hp99d09.b	
1013	119	6.9	693	7	CD641480	AGENCOURT	1086	118.8	6.9	425	6	CD572556	PBL.4.F01	
C 1014	119	6.9	699	7	CF934631	TEST-B03	1087	118.8	6.9	447	6	CB077035	CB077035	h148a05.g
1015	119	6.9	739	5	BU803666	SJFAXA08	1088	118.8	6.9	465	4	BI377706	BI377706	BF1G3_001
C 1016	119	6.9	742	7	CO000046	1o93b11.b	c1089	118.8	6.9	470	5	CF301032	7LEAF--05	
1017	119	6.9	762	7	CF996513	AGENCOURT	c1090	118.8	6.9	476	5	BQ399811	NISC.mp05	
1018	119	6.9	769	7	CV537893	AGENCOURT	1091	118.8	6.9	482	5	BX506526	DRF2p779K	
1019	119	6.9	769	7	CK363079	AGENCOURT	c1092	118.8	6.9	501	6	CD676475	ho01e11.x	
1020	119	6.9	785	5	BUS50973	AGENCOURT	c1093	118.8	6.9	523	5	BA473088	DRF2p686K	
1021	119	6.9	818	5	BUS30033	AGENCOURT	c1094	118.8	6.9	538	5	BQ397543	BQ397543	NISC.ng28
1022	119	6.9	821	6	CD521674	AGENCOURT	1095	118.8	6.9	550	7	CNI64657	CNI64657	995018 MA
1023	119	6.9	830	5	BUS65577	AGENCOURT	1096	118.8	6.9	558	7	CF370787	CF370787	1953h07.y
1024	119	6.9	833	9	CNS007X3	AGENCOURT	c1097	118.8	6.9	570	6	CB049671	NISC.gj12	
1025	119	6.9	835	5	BUS55891	AGENCOURT	1098	118.8	6.9	577	5	BP343324	BP343324	BP343324
1026	119	6.9	835	5	BUS89129	AGENCOURT	1099	118.8	6.9	577	7	CN477441	rx37f08.y	
C 1027	119	6.9	835	7	CO383530	AGENCOURT	1100	118.8	6.9	578	7	CK963370	CK963370	4078054.B
C 1028	119	6.9	843	7	CK197588	FGAS00606	1101	118.8	6.9	609	7	CF369930	CF369930	rg46b02.y
1029	119	6.9	849	5	BUS89154	AGENCOURT	1102	118.8	6.9	629	7	CF370780	CF370780	1953g09.y
1030	119	6.9	852	5	BUS81013	AGENCOURT	1103	118.8	6.9	637	7	CV059227	BNEL4596	
1031	119	6.9	862	5	BUS601053	AGENCOURT	1104	118.8	6.9	655	7	CF370723	CF370723	1953a02.y
1032	119	6.9	871	5	BUS927659	AGENCOURT	1105	118.8	6.9	660	1	AV704928	AV704928	AV704928
1033	119	6.9	888	5	BUS55466	AGENCOURT	1106	118.8	6.9	665	4	BG436064	BG436064	602508851
1034	119	6.9	889	5	BU963271	AGENCOURT	1107	118.8	6.9	726	6	CD639437	CD639437	AGENCOURT
1035	119	6.9	895	5	BQ441805	AGENCOURT	1108	118.8	6.9	749	1	AV757018	AV757018	AV757018
1036	119	6.9	895	5	BUS52045	AGENCOURT	1109	118.8	6.9	775	5	BUS537865	BUS537865	AGENCOURT
C 1037	119	6.9	901	7	CV069875	WPAEbx15	1110	118.8	6.9	779	7	CV482931	CV482931	AGENCOURT
1038	119	6.9	905	5	BUS959672	AGENCOURT	1111	118.8	6.9	816	7	CNS06612	CNS06612	AGENCOURT
1039	119	6.9	916	5	BUS88527	AGENCOURT	1112	118.8	6.9	819	5	BUS64488	BUS64488	AGENCOURT
C 1040	119	6.9	918	7	CV068637	f2.new.ch	1113	118.8	6.9	828	7	CK400196	CK400196	AGENCOURT
1041	119	6.9	921	5	BU172640	AGENCOURT	1114	118.8	6.9	846	5	BUS936109	BUS936109	AGENCOURT
1042	119	6.9	927	6	CD107993	AGENCOURT	c1115	118.8	6.9	848	8	BH166453	BH166453	ENTSL66TF
1043	119	6.9	929	5	BQ428517	AGENCOURT	c1116	118.8	6.9	856	7	CNS27109	CNS27109	AGENCOURT
1044	119	6.9	932	9	CNS0070E	DrosophiI	1117	118.8	6.9	864	5	BU842866	BU842866	AGENCOURT
1045	119	6.9	1009	5	BUS40024	AGENCOURT	c1118	118.8	6.9	870	7	CK194451	CK194451	FCAS00288
1046	119	6.9	1015	6	CD049657	AGENCOURT	1119	118.8	6.9	889	6	CB844768	CB844768	M2PN-0326

1120	118.8	6.9	890	5	BU190380	AGENCOURT	1193	118.6	6.8	527	6	CA381218	660690 NC
1121	118.8	6.9	894	5	BU588228	AGENCOURT	c1194	118.6	6.8	545	5	BU567126	EX567126
1122	118.8	6.9	895	7	CF595897	AGENCOURT	c1195	118.6	6.8	552	7	CF308547	ABF--02-G
1123	118.8	6.9	911	6	CD757353	AGENCOURT	1196	118.6	6.8	565	7	CV199590	km17a03.Y
1124	118.8	6.9	914	5	BQ222594	AGENCOURT	1197	118.6	6.8	579	4	BG434588	602506652
1125	118.8	6.9	917	5	BU597325	AGENCOURT	1198	118.6	6.8	626	6	CD638762	AGENCOURT
1126	118.8	6.9	984	6	CB205726	AGENCOURT	1199	118.6	6.8	656	7	CV182824	ta186c01.
1127	118.8	6.9	984	7	CK419603	AUF_Ipova	1200	118.6	6.8	671	4	BG029399	AGENCOURT
1128	118.8	6.9	1005	4	BG247707	AGENCOURT	1201	118.6	6.8	683	6	CD638960	602296828
1129	118.8	6.9	1034	6	CD388349	AGENCOURT	1202	118.6	6.8	684	1	AV706164	AV706164
1130	118.8	6.9	1059	5	BQ441757	AGENCOURT	1203	118.6	6.8	699	7	CK655434	AGENCOURT
1131	118.8	6.9	1066	5	BU589860	AGENCOURT	1204	118.6	6.8	712	4	CK739805	602630530
1132	118.8	6.9	1071	5	BQ952288	AGENCOURT	c1205	118.6	6.8	737	7	CO562670	AGENCOURT
1133	118.8	6.9	1174	4	CKM56116	AGENCOURT	c1206	118.6	6.8	738	7	CF285052	AGENCOURT
1134	118.6	6.8	147	7	CK616694	cu24c12.Y	c1207	118.6	6.8	754	7	CO395166	AGENCOURT
1135	118.6	6.8	158	5	BM966384	ko06b03.Y	1208	118.6	6.8	768	7	CK397172	AGENCOURT
1136	118.6	6.8	160	5	BQ667470	pb61b09.Y	1209	118.6	6.8	836	5	BU962400	AGENCOURT
1137	118.6	6.8	165	5	BU966327	kk81d12.Y	1210	118.6	6.8	839	5	BU843286	AGENCOURT
1138	118.6	6.8	182	7	CO736101	SILL05b13	1211	118.6	6.8	846	5	BU927827	AGENCOURT
1139	118.6	6.8	188	4	BM569703	AGENCOURT	1212	118.6	6.8	848	5	BU556067	AGENCOURT
1140	118.6	6.8	189	6	CA935078	AGENCOURT	1213	118.6	6.8	849	5	BU565551	AGENCOURT
1141	118.6	6.8	190	2	AW308312	8au64a10.	1214	118.6	6.8	856	6	CB845333	M2PN--0915
1142	118.6	6.8	191	6	CA684337	AGENCOURT	c1215	118.6	6.8	859	7	CN167905	AGENCOURT
1143	118.6	6.8	204	4	BM129081	AGENCOURT	1216	118.6	6.8	863	5	BU556347	AGENCOURT
1144	118.6	6.8	210	4	BM873785	AGENCOURT	1217	118.6	6.8	863	5	BU963584	AGENCOURT
1145	118.6	6.8	215	6	CA302059	tao09f06.	c1218	118.6	6.8	864	7	CV069405	WPAERuX15
1146	118.6	6.8	224	2	AW201825	AGENCOURT	1219	118.6	6.8	869	5	BU563713	AGENCOURT
1147	118.6	6.8	225	2	AW596529	g113e01.Y	1220	118.6	6.8	870	5	BU589706	AGENCOURT
1148	118.6	6.8	241	5	BQ638790	AGENCOURT	1221	118.6	6.8	871	6	CD519237	AGENCOURT
1149	118.6	6.8	246	6	CA802581	8au38g01.	c1222	118.6	6.8	871	7	CK196891	FGAS00535
1150	118.6	6.8	248	1	AI224992	AGENCOURT	1223	118.6	6.8	888	5	BU955707	AGENCOURT
1151	118.6	6.8	248	7	CF772335	AGENCOURT	1224	118.6	6.8	921	5	BU564012	AGENCOURT
1152	118.6	6.8	266	7	CO184060	EC27021.5	1225	118.6	6.8	930	6	CK194142	AGENCOURT
1153	118.6	6.8	268	4	BG058208	nah22b05.	1226	118.6	6.8	939	7	CK421563	AUF_IpSpn
1154	118.6	6.8	271	6	CB601336	AGENCOURT	1227	118.6	6.8	940	6	CD048305	AGENCOURT
1155	118.6	6.8	272	7	CF124216	UI--HR-CHO	1228	118.6	6.8	963	5	BQ221886	AGENCOURT
1156	118.6	6.8	274	6	CA869173	AGENCOURT	1229	118.6	6.8	973	6	CB203325	AGENCOURT
1157	118.6	6.8	278	5	CO192919	AGENCOURT	1230	118.6	6.8	977	5	BQ933223	AGENCOURT
1158	118.6	6.8	279	5	BQ242916	AGENCOURT	1231	118.6	6.8	979	6	CB588735	AGENCOURT
1159	118.6	6.8	285	7	CF791482	K5ZP468D	c1232	118.6	6.8	1028	2	BF138233	602037846
1160	118.6	6.8	294	2	BE665964	155228.MA	1233	118.6	6.8	1031	6	CD105525	AGENCOURT
1161	118.6	6.8	297	7	CO180424	AGENCOURT	1234	118.6	6.8	1073	5	BQ930284	AGENCOURT
1162	118.6	6.8	311	7	CO182176	EC01537.5	1235	118.6	6.8	1077	5	BM907650	AGENCOURT
1163	118.6	6.8	318	5	BM500893	AGENCOURT	1236	118.6	6.8	1202	5	BM904550	AGENCOURT
1164	118.6	6.8	326	2	BF751288	RC3--BN042	1237	118.6	6.8	1247	3	AF116688	Homo sapi
1165	118.6	6.8	331	7	CF291642	LeukoN6.7	1238	118.6	6.8	1545	4	BM544211	AGENCOURT
1166	118.6	6.8	340	6	CD536439	AGENCOURT	1239	118.6	6.8	2144	3	BC080927	Xenopus t
1167	118.6	6.8	340	7	CN836173	AGENCOURT	1240	118.6	6.8	2224	3	BC058228	Mus muscu
1168	118.6	6.8	347	1	AL715214	AGENCOURT	1241	118.6	6.8	2408	3	BC041123	Homo sapi
1169	118.6	6.8	347	5	BM506028	K5ZP686P	1242	118.6	6.8	2417	3	BC021396	Mus muscu
1170	118.6	6.8	356	6	CA335359	NISC lt09	1243	118.6	6.8	3270	3	BC048799	Homo sapi
1171	118.6	6.8	366	7	CN482259	hw18f08.Y	1244	118.6	6.8	7420	3	CR749364	Homo sapi
1172	118.6	6.8	368	4	BM533156	fx68f01.Y	c1245	118.6	6.8	153	6	CA735721	wp18.pk0
1173	118.6	6.8	383	4	BI500678	ra80b10.Y	1246	118.4	6.8	168	4	BU704039	BU704039
1174	118.6	6.8	398	7	CO748385	AGENCOURT	1247	118.4	6.8	175	4	BM187396	fw17b01.Y
1175	118.6	6.8	401	4	BI941782	ed13e11.Y	1248	118.4	6.8	186	2	BF343172	602015819
1176	118.6	6.8	408	7	CF330129	NACL--05-	1249	118.4	6.8	187	6	CA802526	8au37g01.
1177	118.6	6.8	412	7	CF355011	lab66a03.	1250	118.4	6.8	204	1	AL712721	DKFZp6861
1178	118.6	6.8	424	6	CB796123	AMGNNUC.8	c1251	118.4	6.8	205	7	CF214460	CGF100081
1179	118.6	6.8	431	6	CB410125	NISC nc09	1252	118.4	6.8	210	6	CA819140	21069904.
1180	118.6	6.8	435	6	CO088650	1f03H02.b	1253	118.4	6.8	212	6	CB285329	CMD13_E05
1181	118.6	6.8	436	6	CB856507	NISC na01	1254	118.4	6.8	217	5	BM965905	Ko19a03.Y
1182	118.6	6.8	442	1	AV681872	AV681872	1255	118.4	6.8	223	6	CA819345	8au77a09.
1183	118.6	6.8	448	6	CA337570	NISC lw03	1256	118.4	6.8	227	4	BI839377	8au37g01.Y
1184	118.6	6.8	463	6	CD683277	rj4f01.Y	1257	118.4	6.8	229	5	BQ087771	vt08f06.Y
1185	118.6	6.8	467	6	CA336295	NISC lu11	1258	118.4	6.8	234	1	AA562430	KX8B002.f
1186	118.6	6.8	472	7	CK384864	lah55d08.	1259	118.4	6.8	236	5	CR791654	DKFZp4681
1187	118.6	6.8	482	4	BI858408	603383986	1260	118.4	6.8	248	5	BM507072	DKFZp779G
1188	118.6	6.8	491	7	CF805373	lad67e07.Y	1261	118.4	6.8	253	6	CD241885	AGENCOURT
1189	118.6	6.8	496	7	CF801398	rj65f12.Y	1262	118.4	6.8	253	6	CF124406	UI--HP-CHO
1190	118.6	6.8	512	4	BM063316	KS01054A0	1263	118.4	6.8	260	7	CR772316	DKFZp468L
1191	118.6	6.8	512	6	CB095854	1e95e09.b	1264	118.4	6.8	271	4	BM055713	1d82b01.Y
1192	118.6	6.8	517	1	AV758209	AV758209	1265	118.4	6.8	272	7	CR630337	DKFZp469B

c1266	118.4	6.8	274	4	BI496314	dF124d03.	1339	118.4	6.8	915	6	CD251454	AGENCOURT
1267	118.4	6.8	277	7	CR545739	DXFZp470L	c1340	118.4	6.8	919	4	BM415717	OP20797 M
1268	118.4	6.8	287	2	BE018334	b578911.Y	1341	118.4	6.8	921	5	BQ960309	AGENCOURT
1269	118.4	6.8	317	7	CV248497	W501120.B	1342	118.4	6.8	924	5	BQ953272	AGENCOURT
1270	118.4	6.8	318	7	CA674746	MD1v4005h	1343	118.4	6.8	928	7	CK420921	AUF_Ipspn
1271	118.4	6.8	320	7	CK377242	1a101b06.	1344	118.4	6.8	933	5	BUS23369	AGENCOURT
1272	118.4	6.8	322	6	CA323282	UT-M-PX0-	1345	118.4	6.8	951	6	CA792153	AGENCOURT
1273	118.4	6.8	329	2	AW100906	ed62h09.Y	1346	118.4	6.8	952	6	CD385445	AGENCOURT
1274	118.4	6.8	336	7	CK939285	CGF100443	1347	118.4	6.8	958	6	CD247138	AGENCOURT
1275	118.4	6.8	340	7	CF517848	CAP00005_I	1348	118.4	6.8	963	6	CD385737	AGENCOURT
1276	118.4	6.8	341	7	CF369462	IG60B02.Y	c1349	118.4	6.8	975	5	BU912304	AGENCOURT
1277	118.4	6.8	343	6	CD522366	AGENCOURT	1350	118.4	6.8	975	6	CD517925	AGENCOURT
1278	118.4	6.8	353	7	CO752469	Mdfr3024m	c1351	118.4	6.8	987	4	BM415888	OP20370 M
1279	118.4	6.8	370	6	CB940120	IPcGJx14	1352	118.4	6.8	991	5	BU564447	AGENCOURT
1280	118.4	6.8	371	4	BI747246	rm37902.Y	1353	118.4	6.8	1005	9	CL077409	CH216-145
1281	118.4	6.8	374	7	CO181872	EC15148.5	1354	118.4	6.8	1011	5	BQ954179	AGENCOURT
1282	118.4	6.8	385	6	CB986763	AGENCOURT	1355	118.4	6.8	1016	5	BQ926496	AGENCOURT
1283	118.4	6.8	388	6	CA345950	676724 NC	1356	118.4	6.8	1025	3	BC027804	Mus muscu
1284	118.4	6.8	395	7	CO184785	DKF28572.5	1357	118.4	6.8	1077	5	BU540030	AGENCOURT
1285	118.4	6.8	399	7	CR559450	DXFZp468B	1358	118.4	6.8	1158	4	BM556158	AGENCOURT
c1286	118.4	6.8	402	2	AW190286	x113404.X	1359	118.4	6.8	1186	4	BM557257	AGENCOURT
1287	118.4	6.8	413	7	CO580442	ILLUMIGEN	1360	118.4	6.8	1187	4	BM454843	AGENCOURT
1288	118.4	6.8	415	7	CN193529	F988c02.Y	1361	118.4	6.8	1739	3	CR627053	Homo sapi
1289	118.4	6.8	418	7	CF370429	F965B01.Y	1362	118.4	6.8	1806	3	BC020538	Homo sapi
1290	118.4	6.8	418	7	CF370486	F965h05.Y	1363	118.4	6.8	1836	3	HSN802705	Homo sapi
1291	118.4	6.8	421	6	CB085169	hg28d11.b	1364	118.4	6.8	1839	3	BC006034	Mus muscu
1292	118.4	6.8	434	7	CK351931	hg5fha45D	1365	118.4	6.8	1849	3	HSN804512	Homo sapi
1293	118.4	6.8	437	7	CO649087	ILLUMIGEN	1366	118.2	6.8	1854	4	BM032807	kh59407.Y
1294	118.4	6.8	439	6	CB945953	AGENCOURT	1367	118.2	6.8	166	6	CA935301	EAU5912.
1295	118.4	6.8	439	7	CN194216	F991A07.Y	1368	118.2	6.8	174	4	BI324381	xk77h02.Y
1296	118.4	6.8	455	6	CD679736	lab06f12.	1369	118.2	6.8	193	7	CR763207	DXFZp470F
1297	118.4	6.8	475	7	CR629433	DXFZp469J	1370	118.2	6.8	199	1	AL697905	DKFZp686B
1298	118.4	6.8	480	6	CB483255	ju805_B01	1371	118.2	6.8	201	2	BE057319	en01605.Y
1299	118.4	6.8	485	7	CK430863	oj54h03.Y	1372	118.2	6.8	210	6	CA819349	EAU77B01.
1300	118.4	6.8	491	7	CO866143	CF13020c	1373	118.2	6.8	213	5	BQ927115	EAU995909.
1301	118.4	6.8	494	7	CF124299	UT-HP-CHO	1374	118.2	6.8	229	5	BQ075610	fz06908.Y
1302	118.4	6.8	501	7	CF724239	UT-HP-CHO	c1375	118.2	6.8	242	7	CF329593	NACL--04-
1303	118.4	6.8	504	6	CA335368	NISC Lt10	1376	118.2	6.8	243	6	CD578259	21_H11_21
1304	118.4	6.8	525	1	AV756560	AV756560	c1377	118.2	6.8	245	7	CR542778	DXFZp459H
1305	118.4	6.8	527	7	CV072206	EST4367_Z	1378	118.2	6.8	253	1	AI569616	tc04604.X
1306	118.4	6.8	544	5	BQ398892	NISC mo12	1379	118.2	6.8	254	4	BU683565	BU683565
c1307	118.4	6.8	555	5	BX555180	BX555180	1380	118.2	6.8	255	6	CA335171	NISC Lt07
1308	118.4	6.8	562	4	BM155067	f493a12.Y	1381	118.2	6.8	255	7	CO191613	EC1524.5
1309	118.4	6.8	566	7	BM786219	4120178_B	1382	118.2	6.8	256	1	AL598278	DKFZp3130
1310	118.4	6.8	579	7	CF369512	tg60f11.Y	1383	118.2	6.8	264	4	BG608928	322402_MA
c1311	118.4	6.8	589	9	BZ695387	SP_Ba006	1384	118.2	6.8	270	5	BX503644	DXFZp686N
1312	118.4	6.8	595	9	CN500101	Tetraodon	1385	118.2	6.8	274	1	AL703377	DXFZp686O
1313	118.4	6.8	610	7	CF123208	UT-HP-CHO	1386	118.2	6.8	277	5	BX642023	DKFZp468F
1314	118.4	6.8	613	1	AJ792512	AJ792512	1387	118.2	6.8	296	7	CR772783	DKFZp468F
1315	118.4	6.8	626	6	CD771746	AGENCOURT	1388	118.2	6.8	308	1	AI613017	ty05907.X
1316	118.4	6.8	640	6	CF369332	tg58f12.Y	c1389	118.2	6.8	309	7	CO191484	EC31151.5
1317	118.4	6.8	645	6	CD773631	AGENCOURT	1390	118.2	6.8	310	6	CB094806	h475006.b
1318	118.4	6.8	655	5	BU114940	603129074	c1391	118.2	6.8	330	6	BF968493	602271266
1319	118.4	6.8	685	7	CK462665	933477_MA	1392	118.2	6.8	336	4	BF968493	602271266
1320	118.4	6.8	703	7	CK128716	AGENCOURT	1393	118.2	6.8	346	7	CO183312	EC25434.5
1321	118.4	6.8	713	6	CD638576	AGENCOURT	1394	118.2	6.8	347	7	CV199646	km17909.Y
1322	118.4	6.8	758	6	CB941654	AGENCOURT	1395	118.2	6.8	352	1	AI292655	GH15605.5
1323	118.4	6.8	778	2	BE159188	603385268	1396	118.2	6.8	362	7	CK350334	hg9fha23D
1324	118.4	6.8	782	4	BE612435	601451811	1397	118.2	6.8	364	1	AV681618	AV681618
1325	118.4	6.8	786	1	AV682266	AV682266	1398	118.2	6.8	370	7	CR791282	DKFZp468A
1326	118.4	6.8	798	6	CD520099	AGENCOURT	1399	118.2	6.8	374	6	BY772249	BY772249
1327	118.4	6.8	801	7	CN175692	AGENCOURT	1400	118.2	6.8	380	2	BF449584	ma445b06.
1328	118.4	6.8	801	7	CV485384	AGENCOURT	1401	118.2	6.8	408	7	CF118651	f8806.z1
1329	118.4	6.8	805	6	CB957054	AGENCOURT	1402	118.2	6.8	410	6	CB956616	AGENCOURT
1330	118.4	6.8	816	7	CK789213	AGENCOURT	1403	118.2	6.8	424	7	CK233937	rg21f12.Y
1331	118.4	6.8	825	4	BI088418	602852914	1404	118.2	6.8	431	7	CK626853	mj27f07.Y
1332	118.4	6.8	840	7	CF578759	AGENCOURT	1405	118.2	6.8	434	1	AJ799276	AJ799276
1333	118.4	6.8	847	6	CD522867	AGENCOURT	1406	118.2	6.8	435	7	CK373916	1a165904.
1334	118.4	6.8	859	5	BU941147	AGENCOURT	1407	118.2	6.8	438	1	AV682466	AV682466
1335	118.4	6.8	868	7	CF783583	AGENCOURT	1408	118.2	6.8	448	6	CB348657	CAB25G000
1336	118.4	6.8	872	5	BU587868	AGENCOURT	1409	118.2	6.8	454	4	BG180468	60231364
1337	118.4	6.8	888	5	BU531592	AGENCOURT	1410	118.2	6.8	456	7	CO168152	Mdfr3013a
1338	118.4	6.8	902	6	CB999402	AGENCOURT	1411	118.2	6.8	468	7	CK625977	mj16f05.Y







Db	661	GGGACATCCCGTGGGTCCACGATACCCGGAACTCAGCGAGCGAGCTTTGGCAATTGGAAT	720
Qy	745	CCTCAGGGAGCTCCTCTGGGGTCAAGAGAGGCAA-TGGAGGGCCACCAAACTTTG--GGACC	801
Db	721	CCTCAGGGAGCTCCTCTGGGGTCAAGAGAGGCAA-TGGAGGGCCACCAAACTTTGGCGACGG	780
Qy	802	AACACTCAGGAGCTGTGGCCAGCTGGCTATGTTTCAGTGTAGAGCCAGCAACAGAAAT	861
Db	781	ACATTTCAGGAGCTGTGGCCAGCTGGCTATGTTTCAGTGTAGAGCAAGCAACAGAAAT	840
Qy	862	GAAGGGTGCACGAATCCCCCACC	884
Db	841	GACGGGTGACTAATCCCCCACATC	863
RESULT 3			
LOCUS	BG681553	792 bp	mRNA
DEFINITION	602628038F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752921 5'		
ACCESSION	BG681553		
VERSION	BG681553.1 GI:13912950		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 792)		
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LIAW10611 row: 1 column: 10 High quality sequence stop: 774. Location/Qualifiers 1. .792 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4752921" /tissue_type="squamous cell carcinoma" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NCI CGAP_Skn4" /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
FEATURES			
source			
Query Match 38.8%; Score 673; DB 4; Length 792;			
Best Local Similarity 98.1%; Pred. No. 4.7e-113;			
Matches 776; Conservative 0; Mismatches 5; Indels 10; Gaps 9			
Qy	7	TCTCAGAGCCAGCGACTTCAGAGACGAGAGAGGAGGCGACAGAGCGAGCAAGCGGCG	64
Db	1	TCTGAGAAGCCAGCGACTTCAGAGACGAGAGAGGAGGCGACAGAGCGAGCGAGCG	60
Qy	65	GAGGACAGGGAGTCCGAAAGGAGGAGGACAGAGGAGGCGACAGAGCGAGCAAGCGGCG	124
Db	61	GAGGACAGGGAGTCCGAAAGGAGGAGGACAGAGGAGGCGACAGAGCGAGCAAGCGGCG	120
Qy	125	GCAAGGAGGAGACCTCTGTGGAGGAGACACTCTTG-GAGAGAGAGGGGCTGGGCGAG	183
Db	121	GCAAGGAGGAGACCTCTGTGGAGGAGGAGACACTCTGTGAGAGAGAGGGGCTGGGCGAG	180







Lebkowski, J and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 515 Std Error: 0.00.  
Location/Qualifiers  
1. 515  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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mitogen-treated hES cell line H7"  
/clone\_lib="GRN PRENEU"  
/note="oligo dt primed, full-length enriched cDNA library  
from hES cell line H7 (p29) maintained in feeder-free  
conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic and mitogens."

FEATURES  
source  
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/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cell, retinoic acid and  
mitogen-treated hES cell line H7"  
/clone\_lib="GRN PRENEU"  
/note="oligo dt primed, full-length enriched cDNA library  
from hES cell line H7 (p29) maintained in feeder-free  
conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic and mitogens."

ORIGIN  
Query Match 22.0%; Score 382; DB 7; Length 515;  
Best Local Similarity 89.2%; Pred. No. 9.7e-60;  
Matches 446; Conservative 0; Mismatches 0; Indels 54; Gaps 1;  
1113 GGGATCCAGCAGCGCTCTCTCCGGCAACACCGGTGGAGCGCGGAGGAAATGGACA 1172  
Db  
70 GGGATCCAGCAGCGCTCTCTCCGGCAACACCGGTGGAGCGCGGAGGAAATGGACA 129  
1173 TAAACCCGGTGTAAAGCCAGGAGGAAATGAAGCCCGGAGCGGGATCTGGGATCA 1232  
Db  
130 TAAACCCGGTGTAAAGCCAGGAGGAAATGAAGCCCGGAGCGGGATCTGGGATCA 189  
1233 GGGCTTCAGAGCAGGAGGATTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCG 1292  
Db  
190 GGGCTTCAGAGCAGGAGGATTTCCAGCAACATGA----- 224  
1293 CTTCTTGGAGGCTCTGGAGACAATATATCGGGGCAAGGTCGAGCTGGGGCAGTGGAGG 1352  
Db  
225 -----GGGGCAAGGTCGAGCTGGGGCAGTGGAGG 255  
1353 AGGTACGCTGTGTGGAGTCAATCTGTGAATCTGAGAGCTCTCTGGGATGTTTAA 1412  
Db  
256 AGGTACGCTGTGTGGAGTCAATCTGTGAATCTGAGAGCTCTCTGGGATGTTTAA 315  
1413 CTTTGACACTTTCTGGAAGAAATTTAAATCCAAAGCTGGGTTTTCATCAACTGGGATGCCAT 1472  
Db  
316 CTTTGACACTTTCTGGAAGAAATTTAAATCCAAAGCTGGGTTTTCATCAACTGGGATGCCAT 375  
1473 AAACAAGGACACAGAGAGCTCTCGCATCCGTCGATCCAGCAAGAGGACCCACAGATTG 1532  
Db  
376 AAACAAGGACACAGAGAGCTCTCGCATCCGTCGATCCAGCAAGAGGACCCACAGATTG 435  
1533 GATGGAGGCCCCACATCCCTCTCTTAAACACCAACCCCTCTCATCACTAATCTCAGCCCT 1592  
Db  
436 GATGGAGGCCCCACATCCCTCTCTTAAACACCAACCCCTCTCATCACTAATCTCAGCCCT 495  
1593 TGCCCTTGAATAAAACCTTA 1612  
Db  
496 TGCCCTTGAATAAAACCTTA 515

RESULT 8  
CA489311  
LOCUS  
DEFINITION AGENCOURT\_10810163 MAPcL Homo sapiens cDNA clone IMAGE:6721694 5',  
mRNA sequence.  
CA489311  
ACCESSION

CA489311.1 GI:24952102  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 900)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Kristi A. Egland, Ira Pastan  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM14283 row: d column: 14  
High quality sequence stop: 596.  
Location/Qualifiers  
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/clone\_lib="MAPcL"  
/note="Vector: pCMV-SPORT6; Site1: EcoRV; Site2: Not I;  
Subtracted with brain, liver, lung, kidney and muscle.  
Directionally cloned. Priming method: oligo-dT. Average  
insert size: 1800 bp. Library amplification: 26,000 fold.  
Kristi A. Egland, James J. Vincent, Robert Strausberg,  
Bungkook Lee & Ira Pastan: Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

ORIGIN  
Query Match 21.5%; Score 372.4; DB 6; Length 900;  
Best Local Similarity 96.0%; Pred. No. 5.8e-58;  
Matches 382; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
1113 GGGATCCAGCAGCGCTCTCTCCGGCAACACCGGTGGAGCGCGGAGGAAATGGACA 1172  
Db  
59 GGGATCCAGCAGCGCTCTCTCCGGCAACACCGGTGGAGCGCGGAGGAAATGGACA 118  
1173 TAAACCCGGTGTGAAAAGCCAGGGAATGAAGCCCGGAGCGGGAATCTGGGATTC 1232  
Db  
119 TAAACCCGGTGTGAAAAGCCAGGGAATGAAGCCCGGAGCGGGAATCTGGGATTC 178  
1233 GGGCTTCAGAGCAGGAGGATTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCG 1292  
Db  
179 GGGCTTCAGAGCAGGAGGATTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCG 238  
1293 CCTCTTCGAGGCTCTGGAGACAATATCGGGGCAAGGTCGAGCTGGGGCAGTGGAGG 1352  
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239 CCTCTTCGAGGCTCTGGAGACAATATCGGGGCAAGGTCGAGCTGGGGCAGTGGAGG 298  
1353 AGGTGACGCTGTGTGGTGGAGTCAATCTGTGAATCTCTGAGAGCTCTCTGGGATGTTTAA 1412  
Db  
299 AGGTGACGCTGTGTGGTGGAGTCAATCTGTGAATCTCTGAGAGCTCTCTGGGATGTTTAA 358  
1413 CTTTGACACTTTCTGGAAGAAATTTAAATCCAAAGCTGGGTTTTCATCACTGGGATGCCAT 1472  
Db  
359 CTTTGACACTTTCTGGAAGAAATTTAAATCCAAAGCTGGGTTTTCATCACTGGGATGCCAT 418  
1473 AAACAAGGACACAGAGAGCTCTCGCATCCCGTGACCTC 1510  
419 AAACAAGGACACAGGTCCTCGCCGCCCGCAGCACCCGAGCCC 456

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RESULT 9
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LOCUS
DEFINITION
603037966F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178952 5',
mRNA sequence.
ACCESSION
BI822399
VERSION
BI822399.1 GI:15933949
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 843)
NIH-MGC http://mgs.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
EMAIL: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1446 Row: C Column: 17
High quality sequence stop: 825.
FEATURES
source
1..843
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/clone="IMAGE:5178952"
/lab_host="DH10B"
/clone_lib="NIH MGC 115"
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pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27, 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 21.4%; Score 370.8; DB 4; Length 843;
Best Local Similarity 95.7%; Pred. No. 1.1e-57;
Matches 381; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1113 GGATTCAGACCGGCTCTCTCCGGCAACACCGTGGAGCGCGGAGGAATGGACA 1172
DB 69 GGGATTCAGACCGGCTCTCTCCGGCAACACCGTGGAGCGCGGAGGAATGGACA 128
QY 1173 TAAACCCGGGTGTAAGCCAGGGAATGAGCCCGCGGAGCGGGGAATCTGGGATCCA 1232
DB 129 TAAACCCGGGTGTAAGCCAGGGAATGAGCCCGCGGAGCGGGGAATCTGGGATCCA 188
QY 1233 GGGCTTCAGAGGACAGGGATTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCG 1292
DB 189 GGGCTTCAGAGGACAGGGATTTCCAGCAACATGAGGGAATAAGCAAGAGGGCAATCG 248
QY 1293 CCTCTTGGAGGCTCTGGAGACAATTTATCGGGGCAAGGGTTCAGTGGGGCAGTGGAGG 1352
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QY 1353 AGGTGACGCTGTGGTGGAGTCAATACTGTGAACTCTGAGACTCTCCCTGGGATGTTTAA 1412
DB 309 AGGTGACGCTGTGGTGGAGTCAATACTGTGAACTCTGAGACTCTCCCTGGGATGTTTAA 368
QY 1413 CTTTGACACTTTTCTGGAAGAAATTTTAAATCCAGAGCTGGGTTTTCATCAACTGGGATGCCAT 1472
Db 369 CTTTGACACTTTTCTGGAAGAAATTTTAAATCCAGAGCTGGGTTTTCATCAACTGGGATGCCAT 428
QY 1473 AAACAGGACCAAGAGAGCTCTCGCATCCGCTGACCTC 1510
Db 429 AAACAGGACCAAGAGAGCTCTCGCATCCGCTGACCTC 466
RESULT 10
BF829704/c
LOCUS
DEFINITION
MR2-HN0035-221200-019-h09 HN0035 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF829704
VERSION
BF829704.1 GI:12175544
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 532)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=MR2&t2=MR2-HN0035-
221200-019-h09&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 462.
FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0035"
/note="Organ: head normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 20.6%; Score 357.4; DB 2; Length 532;
Best Local Similarity 92.9%; Pred. No. 3.1e-55;
Matches 494; Conservative 0; Mismatches 27; Indels 11; Gaps 11;
QY 494 ATGCTCTGGGAAACACTGGGCAAGAGATTGGCAGACAGCAGAGATGTCATTCGACAG 553
DB 532 ATGCTCTGGGAAACCTGGCCACGAGATTGCCACAGCAGCAGAGATGTCATTCGACAG 473
QY 554 GAGCA-GATGCTGTCCGGGCTCTCGGCA-GGGGGTGGCTGGCCACAGTGGTGTGGGA 611
DB 472 GAGCAGATGCTGTCCGGGCTCTCGACACGGGGGTGGCTGCCACATGTTGCTTGGGA 413
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QY 612 AAC-TTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGGCCCTTGGAGGCCAGGGCCAGG 670  
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 Db 412 AACATTTCTGGAGTCCCTGGCATCTTTGGCTCTCAAGATGNCCTTGGAGGCCAGGGCCAGG 353  
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 QY 671 GCAA-TCCTGGAGGCTCTGGG-GACTCCGNGGTTCACAGCATACCCCGGAACTCAGCAGG 728  
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 Db 352 CCAACTCTCTGGAGGCTCTGGGCACTCCGTGGTTCACAGATACCCCGGAACTCAGCAGG 293  
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 QY 729 CAGCTTTGGAATGAATCTCTCAGGGAGCTCCCTGGGTCAGGAGG-CAATGAGGGGCCAC 787  
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 Db 292 CAGCTTTGGAATGAATCTCTCAGGGAGCTCCCTGGGTCAGGAGGCCACTGGAGGGCCAC 233  
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 QY 788 CAAACTTTGGAGCAACACTCAGGGA-GCTGTGGCCCGACCTGGCTATGTTCACTGAGCA 846  
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 Db 232 CAAACTTTGGAGCAACACTCAGGGAGCTGTGGCCAGCTGTGGCCAGCTGGCTATGTTCACTGAGCA 173  
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 QY 847 GCAGCAACAGCAATGAAGGGTGCAGAAATCCCAACCACTCTGGCTCA-GGTGGAGGCTC 905  
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 Db 172 GCAGCAACAGCAATGAAGGGTGTCTCGAATCCCAACCACTCTGGCTCACTGTGTGGAGGCTC 113  
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 QY 906 CA-GCAACTCTCTGGGAGGCGAGCGGCTCACAGTCTGGGCGAGCAGTGGCAGTGGCAGCAATG 964  
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 Db 112 CACGCAACTCTCTGGGAGGCGAGCGGCTCACCGTCTACCGTCTGGGCGAGTGGCAGTGGCAGCAATG 53  
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 QY 965 GTGACACAACTGCGCAGCAGTGTGGTGGCAGCAGCAGTGGCAGCAGCAG 1016  
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 Db 52 GTGACAAACCCCTAT-GCAGCAGC-GTGGTGGCAGTAGTAGTAGCGGCGAGCGG 3

## RESULT 11

BU927828  
 LOCUS  
 DEFINITION BU927828 841 bp mRNA linear EST 18-OCT-2002  
 AGENCOURT 10434243 NIH MGC 126 Homo sapiens cDNA clone  
 IMAGE:6653313 5', mRNA sequence.  
 ACCESSION BU927828  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 841)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: NCI  
 cDNA Library Preparation: Michael Brownstein Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2903 row: c column: 09  
 High quality sequence stop: 444.

## FEATURES

1. 841  
 /organism="Homo sapiens"  
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 /clone="IMAGE:6653313"  
 /tissue\_type="mixed (pool of 40 RNAs)"  
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 /clone\_lib="NIH\_MGC\_126"  
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc);  
 Site 2: SfiI (ggcgctccggcc); Double-stranded cDNA was  
 prepared from a pool of 40 cell line polyA+ RNAs (bladder  
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -  
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,  
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -  
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,  
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'

adaptors were used in cloning as follows:  
 5'-AATCTAGTGTATCAACGAGATGGCCATTAGCGCGG-3' and  
 5'-ATCTAGAGCGGAGCGCGGACATG-DT(30)NN-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.5-1  
 kb size fraction (other fractions present in NIH\_MGC\_127  
 and NIH\_MGC\_128). Library created in the laboratory of T.  
 Uedlin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
 Library."

## ORIGIN

Query Match 19.3%; Score 333.8; DB 5; Length 841;  
 Best Local Similarity 84.3%; Pred.No.6.8e-51;  
 Matches 371; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
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 Db 76 CCACGGTGGAGCGCGGAGGAATGGACATAAACCCGGTGTGAAAGCCAGGGAATCA 135  
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 QY 1353 AGGTGACGCTGTGTGGAGTCAATCTGTGAACCTCTGAGAGCTCTCTGGGATGTTTAA 1412  
 |||  
 Db 136 AGCCCGCGGAGCGGGAATCTGGGATTCAGAACTCTGAGAGCTCTCTGGGATGTTTAA 195  
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 QY 1413 CTTTCACACTTTCTCGAAGAAATTTAAATCCAGCTGGGTTTCATCACTGGGATGCCAT 1472  
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 Db 196 CTTTCACACTTTCTCGAAGAAATTTAAATCCAGCTGGGTTTCATCACTGGGATGCCAT 255  
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 QY 1473 AAACAAGGACAGAGAAGCTCTCGCATCCGTCGACTCCAGACAAGGAGCCACAGATTG 1532  
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 Db 256 AAACAAGGACAGAGAAGCTCTCGCATCCGTCGACTCCAGACAAGGAGCCACAGATTG 315  
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 QY 1533 GATGGAGCCCCACACATCCCTCTTTAAACACACCTCTCATCTCACTAATCTCAGCCCT 1592  
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 Db 316 GATGGAGCCCCACACATCCCTCTTTAAACACACCTCTCATCTCACTAATCTCAGCCCT 375  
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 QY 1593 TGCCCTTGAATAAACCTTAGCTGCCCAACAAAAAANANANANANANANANANANANANAN 1652  
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 Db 376 TGCCCTTGAATAAACCTTAGCTGCCCAACAAAAAANANANANANANANANANANANANAN 435  
 |||  
 QY 1653 AAAAAAAN 1712  
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 Db 436 AAAAAAAN 495  
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 QY 1713 AAAAAAAN 1732  
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 Db 496 AAAAAAAN 515  
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## RESULT 12

BU927828  
 LOCUS  
 DEFINITION BU927828 415 bp mRNA linear EST 01-MAY-2001  
 602622528F1 NCI CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4747446 5',  
 mRNA sequence.  
 ACCESSION BU927828  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 415)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
1 (bases 1 to 600)
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LiON Bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
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Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
1 (bases 1 to 617)
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LiON Bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
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Email: Thomas.Schluter@lionbioscience.com.

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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 123	104.8	6.0	6671	5	PCT-US95-02275-1	Sequence 1, Appli	196	94.2	5.4	477	3	US-09-135-994-1	Sequence 1, Appli
c 124	103.8	6.0	1273	4	US-09-270-767-14731	Sequence 14731, A	197	93.8	5.4	477	4	US-09-684-843A-1	Sequence 1, Appli
c 125	103.6	6.0	708	4	US-09-270-767-13081	Sequence 13081, A	198	93.8	5.4	711	4	US-09-621-976-17854	Sequence 17854, A
c 126	103	5.9	140	1	US-08-628-417-5	Sequence 5, Appli	199	93.8	5.4	3715	4	US-09-234-245-1	Sequence 1, Appli
c 127	102.6	5.9	949	4	US-09-489-847-35	Sequence 35, Appl	200	93.6	5.4	2665	3	US-08-971-089-5	Sequence 5, Appli
c 128	102.4	5.9	1454	3	US-09-372-422A-19	Sequence 19, Appl	201	93.4	5.4	242	4	US-09-621-976-16320	Sequence 16320, A
c 129	102	5.9	102	4	US-09-621-976-14804	Sequence 14804, A	202	93	5.4	1414	4	US-09-501-115-5	Sequence 5, Appli
c 130	102	5.9	371	4	US-09-621-976-16048	Sequence 16048, A	203	93	5.4	1445	3	US-09-814-951A-1	Sequence 1, Appli
c 131	102	5.9	1545	4	US-09-559-023-1	Sequence 1, Appli	204	93	5.4	2323	3	US-09-149-476-24	Sequence 24, Appl
c 132	102	5.9	1882	3	US-09-370-253-1	Sequence 1, Appli	205	93	5.4	2625	4	US-09-270-767-10080	Sequence 10080, A
c 133	101.8	5.9	1474	3	US-08-821-994-64	Sequence 64, Appl	206	93	5.4	1091	4	US-09-328-965-1	Sequence 1, Appli
c 134	101.2	5.8	558	4	US-09-043-861-3	Sequence 3, Appli	207	92.8	5.4	1411	3	US-08-964-127-5	Sequence 5, Appli
c 135	100.8	5.8	240	4	US-09-621-976-1324	Sequence 1324, Ap	208	92.8	5.4	1411	3	US-09-496-692-5	Sequence 5, Appli
c 136	99.8	5.8	2434	4	US-09-489-847-67	Sequence 67, Appl	209	92.8	5.4	1411	3	US-10-000-273-5	Sequence 5, Appli
c 137	99.6	5.7	147	4	US-09-621-976-10254	Sequence 10254, A	210	92.8	5.4	251672	4	US-09-949-016-17296	Sequence 17296, A
c 138	98.8	5.7	123	4	US-09-621-976-12330	Sequence 12330, A	c 211	92.8	5.4	251682	4	US-09-949-016-11973	Sequence 11973, A
c 139	98.8	5.7	147	4	US-09-621-976-10383	Sequence 10383, A	c 212	92.8	5.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 140	98.8	5.7	2806	3	US-09-653-839-9	Sequence 9, Appli	213	92.4	5.3	1248	4	US-09-489-847-101	Sequence 101, App
c 141	98.8	5.7	2806	4	US-10-202-619-9	Sequence 9, Appli	214	92.2	5.3	1582	3	US-08-545-196B-10	Sequence 10, Appl
c 142	98.6	5.7	1037	4	US-09-181-585-3	Sequence 3, Appli	215	92.2	5.3	1582	3	US-08-545-196B-12	Sequence 12, Appl
c 143	98.6	5.7	1159	4	US-09-181-585-1	Sequence 1, Appli	216	92.2	5.3	3334	4	US-09-668-119-2	Sequence 2, Appli
c 144	98.6	5.7	1471	4	US-09-181-585-2	Sequence 2, Appli	217	92.2	5.3	92	4	US-09-621-976-13620	Sequence 13620, A
c 145	98.6	5.7	4086	4	US-09-702-705-1801	Sequence 1801, Ap	218	92	5.3	92	4	US-09-621-976-14689	Sequence 14689, A
c 146	98.6	5.7	4086	4	US-09-736-457-1801	Sequence 1801, Ap	219	92	5.3	193	4	US-09-621-976-10543	Sequence 10543, A
c 147	98.6	5.7	4086	4	US-09-671-325-1801	Sequence 1801, Ap	c 220	92	5.3	260	2	US-08-520-678A-29	Sequence 29, Appl
c 148	98.2	5.7	550	4	US-09-010-147B-5	Sequence 5, Appli	c 221	92	5.3	260	3	US-08-897-126-29	Sequence 29, Appl
c 149	98	5.7	98	1	US-08-088-658-42	Sequence 42, Appl	c 222	92	5.3	359	4	US-09-621-976-16019	Sequence 16019, A
c 150	98	5.7	98	2	US-08-471-907A-42	Sequence 42, Appl	223	92	5.3	1406	4	US-10-000-489-81	Sequence 81, Appl
c 151	98	5.7	98	4	US-09-621-976-12160	Sequence 12160, A	c 224	92	5.3	270	2	US-08-520-678A-30	Sequence 30, Appl
c 152	98	5.7	98	4	US-09-621-976-15091	Sequence 15091, A	c 225	91.8	5.3	270	3	US-08-897-126-30	Sequence 30, Appl
c 153	98	5.7	196	4	US-09-442-054A-42	Sequence 42, Appl	c 226	91.6	5.3	359	4	US-09-621-976-16008	Sequence 35, Appl
c 154	98	5.7	196	4	US-09-442-054A-42	Sequence 42, Appl	c 227	91.6	5.3	1098	3	US-09-485-529-57	Sequence 57, Appl
c 155	98	5.7	790	3	US-09-363-970-4	Sequence 1, Appli	228	91.4	5.3	1746	4	US-09-485-529-13	Sequence 13, Appl
c 156	98	5.7	1308	4	US-10-151-832-1	Sequence 1, Appli	229	91.4	5.3	1768	4	US-09-621-976-9575	Sequence 9575, Ap
c 157	98	5.7	2327	4	US-10-066-130-20	Sequence 20, Appl	230	91.2	5.3	179	4	US-09-621-976-9575	Sequence 79, Appl
c 158	98	5.7	2674	4	US-10-066-130-19	Sequence 19, Appl	231	90.8	5.2	990	4	US-09-800-729-79	Sequence 484, App
c 159	98	5.7	2771	4	US-10-066-130-18	Sequence 18, Appl	232	90.8	5.2	244	4	US-09-621-976-484	Sequence 29, Appl
c 160	98	5.7	5860	4	US-10-066-130-17	Sequence 17, Appl	233	90.6	5.2	1134	3	US-09-248-335-29	Sequence 29, Appl
c 161	98	5.7	12980	3	US-08-811-566-5	Sequence 5, Appli	234	90.6	5.2	1662	4	US-09-668-097A-13	Sequence 13, Appl
c 162	98	5.7	12980	3	US-09-034-756-5	Sequence 5, Appli	235	90.6	5.2	195	4	US-09-621-976-18062	Sequence 18062, A
c 163	97.8	5.6	194	4	US-09-621-976-801	Sequence 801, App	236	90.4	5.2	1190	4	US-09-390-207-1	Sequence 1, Appli
c 164	97.8	5.6	365	4	US-09-621-976-16042	Sequence 16042, A	237	90.4	5.2	6243	2	US-09-056-075-1	Sequence 1, Appli
c 165	97.8	5.6	397	3	US-09-253-691-3	Sequence 3, Appli	238	90.4	5.2	242	4	US-09-621-976-16324	Sequence 16324, A
c 166	97.6	5.6	3438	4	US-10-164-595-29	Sequence 29, Appl	239	90.2	5.2	1342	4	US-09-489-847-89	Sequence 89, Appl
c 167	97.4	5.6	1141	4	US-09-800-729-78	Sequence 78, Appl	240	90.2	5.2	1878	3	US-09-465-558-39	Sequence 39, Appl
c 168	97.2	5.6	1039	4	US-09-802-540-1280	Sequence 1280, Ap	241	90.2	5.2	357	4	US-09-621-976-16058	Sequence 16058, A
c 169	97	5.6	97	4	US-09-621-976-12430	Sequence 12430, A	242	90	5.2	1361	4	US-09-489-847-64	Sequence 64, Appl
c 170	97	5.6	356	2	US-08-520-678A-22	Sequence 22, Appl	243	90	5.2	1636	4	US-09-578-194-6	Sequence 6, Appli
c 171	97	5.6	356	3	US-08-897-126-22	Sequence 22, Appl	244	89.8	5.2	1508	4	US-09-039-046-1	Sequence 1, Appli
c 172	97	5.6	9646	3	US-08-811-566-1	Sequence 1, Appli	245	89.6	5.2	163	4	US-09-621-976-9608	Sequence 9608, Ap
c 173	97	5.6	9646	3	US-09-034-756-1	Sequence 1, Appli	246	89.6	5.2				

247	89.4	5.2	41736	4	US-09-949-016-17091	Sequence 17091, A	320	85.6	4.9	1133	4	US-10-282-048-1	Sequence 1, Appl1
248	89.2	5.1	582	4	US-09-787-292-3	Sequence 3, Appl1	321	85.4	4.9	190	4	US-09-621-976-16784	Sequence 16784, A
249	89.2	5.1	635	1	US-08-455-633A-35	Sequence 35, Appl1	322	85.4	4.9	1602	1	US-08-530-950-3	Sequence 3, Appl1
250	89.2	5.1	635	1	US-08-416-336-5	Sequence 5, Appl1	323	85.4	4.9	1602	3	US-08-888-429A-3	Sequence 3, Appl1
251	89.2	5.1	635	2	US-08-456-460C-35	Sequence 35, Appl1	324	85.4	4.9	1602	3	US-09-149-879-3	Sequence 3, Appl1
252	89.2	5.1	635	5	PCT-US94-05354-35	Sequence 35, Appl1	325	85.4	4.9	1602	4	US-09-057-009-3	Sequence 3, Appl1
253	89.2	5.1	1198	3	US-09-248-333-27	Sequence 27, Appl1	326	85.4	4.9	1602	4	US-09-593-653-3	Sequence 3, Appl1
254	89	5.1	89	4	US-09-621-976-14749	Sequence 14749, A	327	85.4	4.9	3124	3	US-09-734-030-1	Sequence 1, Appl1
255	89	5.1	89	1	US-08-469-802B-2	Sequence 2, Appl1	328	85.4	4.9	3124	4	US-10-153-921-1	Sequence 1, Appl1
256	89	5.1	195	1	US-08-469-802B-2	Sequence 2, Appl1	329	85.4	4.9	3124	4	US-10-669-689-1	Sequence 1, Appl1
257	89	5.1	195	2	US-08-267-803B-2	Sequence 2, Appl1	330	85.2	4.9	347	4	US-09-621-976-16026	Sequence 16026, A
258	89	5.1	997	4	US-09-907-794A-376	Sequence 376, App	331	85.2	4.9	795	4	US-09-270-767-14068	Sequence 14068, A
259	89	5.1	997	4	US-09-905-125A-376	Sequence 376, App	332	85	4.9	85	4	US-09-621-976-13395	Sequence 13395, A
260	89	5.1	997	4	US-09-902-775A-376	Sequence 376, App	333	85	4.9	85	4	US-09-621-976-13395	Sequence 13395, A
261	89	5.1	997	4	US-09-906-700-376	Sequence 376, App	334	85	4.9	2045	3	US-09-152-060-22	Sequence 22, Appl1
262	89	5.1	997	4	US-09-903-603A-376	Sequence 376, App	335	85	4.9	19557	5	PCT-US92-06300-1	Sequence 1, Appl1
263	89	5.1	997	4	US-09-904-920A-376	Sequence 376, App	336	85	4.9	19557	5	PCT-US92-06300-1	Sequence 1, Appl1
264	89	5.1	997	4	US-09-909-064-376	Sequence 376, App	337	84.8	4.9	124	6	5185243-1	Patent No. 5185243
265	89	5.1	997	4	US-09-905-381A-376	Sequence 376, App	338	84.8	4.9	124	6	5185243-1	Patent No. 5185243
266	89	5.1	997	4	US-09-906-618-376	Sequence 376, App	339	84.8	4.9	127	4	US-09-621-976-13933	Sequence 13933, A
267	89	5.1	1249	4	US-09-461-325-128	Sequence 376, App	340	84.8	4.9	1069	3	US-09-372-422A-7	Sequence 7, Appl1
268	89	5.1	1249	4	US-10-012-542-128	Sequence 128, App	341	84.8	4.9	2239	3	US-09-196-390-1	Sequence 1, Appl1
269	89	5.1	1249	4	US-10-115-123-128	Sequence 128, App	342	84.6	4.9	2239	4	US-09-952-677-1	Sequence 1, Appl1
270	89	5.1	1683	3	US-09-347-803-11	Sequence 11, Appl1	343	84.6	4.9	299	4	US-09-621-976-16226	Sequence 26, Appl1
271	89	5.1	7218	1	US-08-232-463-14	Sequence 14, Appl1	344	84.4	4.9	700	3	US-09-152-060-41	Sequence 41, Appl1
272	88.8	5.1	812	3	US-09-091-097-7	Sequence 7, Appl1	345	84.4	4.9	1114	3	US-09-152-060-41	Sequence 9, Appl1
273	88.8	5.1	2010	2	US-07-864-475A-4	Sequence 4, Appl1	346	84.4	4.9	1172	1	US-08-463-831-9	Sequence 9, Appl1
274	88.8	5.1	2010	2	US-08-468-249A-4	Sequence 4, Appl1	347	84.4	4.9	1172	1	US-08-463-831-9	Sequence 9, Appl1
275	88.8	5.1	2852	3	US-09-027-137-2	Sequence 2, Appl1	348	84.4	4.9	1172	1	US-08-461-809-9	Sequence 9, Appl1
276	88.8	5.1	2852	3	US-09-344-441-2	Sequence 2, Appl1	349	84.4	4.9	1172	1	US-08-461-809-9	Sequence 9, Appl1
277	88.6	5.1	160	4	US-09-621-976-10335	Sequence 10335, A	350	84.4	4.9	154605	4	PCT-US93-08518-9	Sequence 9, Appl1
278	88.6	5.1	351	4	US-09-621-976-10335	Sequence 10335, A	351	84.2	4.9	154605	4	PCT-US93-08518-9	Sequence 9, Appl1
279	88.6	5.1	1493	1	US-08-340-820-24	Sequence 24, Appl1	352	84.2	4.9	3410	3	US-09-020-956-110	Sequence 110, App
280	88.6	5.1	1493	1	US-08-593-535-24	Sequence 24, Appl1	353	84.2	4.9	3410	3	US-09-030-607-110	Sequence 110, App
281	88.4	5.1	318	4	US-09-621-976-10247	Sequence 10247, A	354	84.2	4.9	3410	3	US-09-439-313-110	Sequence 110, App
282	88	5.1	1260	4	US-09-461-325-93	Sequence 93, Appl1	355	84.2	4.9	3410	3	US-09-352-616A-110	Sequence 110, App
283	88	5.1	1260	4	US-10-012-542-93	Sequence 93, Appl1	356	84.2	4.9	3410	3	US-09-602-877A-100	Sequence 100, App
284	88	5.1	1260	4	US-10-115-123-93	Sequence 93, Appl1	357	84.2	4.9	3410	3	US-09-232-149A-110	Sequence 110, App
285	88	5.1	1507	3	US-09-453-323-1	Sequence 1, Appl1	358	84.2	4.9	3410	4	US-09-159-812-110	Sequence 110, App
286	88	5.1	1781	4	US-09-818-512-1	Sequence 1, Appl1	359	84.2	4.9	3410	4	US-09-636-215-110	Sequence 110, App
287	88	5.1	2628	1	US-08-143-219-1	Sequence 1, Appl1	360	84.2	4.9	3410	4	US-09-685-166A-110	Sequence 110, App
288	87.6	5.1	1013	4	US-09-322-409-6	Sequence 6, Appl1	361	84.2	4.9	3410	4	US-09-115-453-110	Sequence 110, App
289	87.6	5.1	1013	4	US-09-322-409-8	Sequence 8, Appl1	362	84.2	4.9	3410	4	US-09-688-489-110	Sequence 110, App
290	87.6	5.1	1013	4	US-09-451-527-6	Sequence 6, Appl1	363	84.2	4.9	3410	4	US-09-679-426-110	Sequence 110, App
291	87.6	5.1	1013	4	US-09-451-527-6	Sequence 6, Appl1	364	84.2	4.9	3410	4	US-09-759-143-110	Sequence 110, App
292	87.2	5.0	147	4	US-09-621-976-8551	Sequence 8551, Ap	365	84.2	4.9	5096	4	US-09-651-236-110	Sequence 110, App
293	87.2	5.0	271	4	US-09-621-976-10380	Sequence 10380, A	366	84.2	4.9	5096	4	US-09-949-016-15105	Sequence 15105, A
294	87.2	5.0	331	4	US-09-621-976-10380	Sequence 10380, A	367	84	4.8	1725	4	US-09-668-097A-21	Sequence 21, Appl1
295	87.2	5.0	2406	4	US-09-594-506-37	Sequence 37, Appl1	368	83.8	4.8	2202	3	US-09-465-558-59	Sequence 59, Appl1
296	86.8	5.0	630	1	US-08-185-414B-1	Sequence 1, Appl1	369	83.8	4.8	2320	3	US-09-202-904A-13	Sequence 13, Appl1
297	86.6	5.0	146	4	US-09-621-976-8550	Sequence 8550, Ap	370	83.6	4.8	5021	4	US-09-949-016-786	Sequence 786, App
298	86.6	5.0	554	4	US-09-696-169A-14	Sequence 14, Appl1	371	83.6	4.8	84	4	US-09-621-976-14577	Sequence 14577, A
299	86.4	5.0	165	3	US-09-043-303-17	Sequence 17, Appl1	372	83.4	4.8	639	4	US-09-482-273-49	Sequence 49, Appl1
300	86.4	5.0	203	3	US-09-043-303-7	Sequence 7, Appl1	373	83.2	4.8	1297	4	US-09-800-729-80	Sequence 80, Appl1
301	86.4	5.0	1895	3	US-09-444-336-7	Sequence 7, Appl1	374	83.2	4.8	253	2	US-08-520-678A-25	Sequence 25, Appl1
302	86.2	5.0	196	4	US-09-644-460-40	Sequence 40, Appl1	375	83.2	4.8	253	3	US-08-897-126-23	Sequence 23, Appl1
303	86.2	5.0	1700	2	US-08-897-340-4	Sequence 4, Appl1	376	83.2	4.8	763	4	US-09-743-207-3	Sequence 3, Appl1
304	86.2	5.0	1700	2	US-09-252-329-4	Sequence 4, Appl1	377	83	4.8	1835	3	US-09-485-549-1	Sequence 3, Appl1
305	86	5.0	141	4	US-09-621-976-13435	Sequence 13435, A	378	83	4.8	83	4	US-09-621-976-14751	Sequence 14751, A
306	86	5.0	333	3	US-09-018-584A-27	Sequence 27, Appl1	379	83	4.8	83	4	US-09-621-976-14959	Sequence 14959, A
307	86	5.0	333	4	US-09-074-423-27	Sequence 27, Appl1	380	83	4.8	323	4	US-09-621-976-10374	Sequence 10374, A
308	86	5.0	8638	4	US-10-029-907-6	Sequence 6, Appl1	381	82.8	4.8	1512	2	US-08-909-965C-8	Sequence 8, Appl1
309	86	5.0	1736	3	US-09-489-847-112	Sequence 112, App	382	82.8	4.8	215	4	US-09-621-976-15321	Sequence 15321, A
310	85.8	4.9	1736	3	US-09-182-816-22	Sequence 22, Appl1	383	82.6	4.8	486	4	US-09-621-976-16227	Sequence 16227, A
311	85.8	4.9	1736	3	US-09-182-816-22	Sequence 22, Appl1	384	82.6	4.8	486	4	US-09-639-207-13	Sequence 13, Appl1
312	85.8	4.9	1736	3	US-09-471-528-22	Sequence 22, Appl1	385	82.6	4.8	688	6	5498694-3	Patent No. 5498694
313	85.8	4.9	1736	3	US-09-471-528-22	Sequence 22, Appl1	386	82.6	4.8	688	6	5498694-3	Patent No. 5498694
314	85.8	4.9	1736	3	US-09-634-530-24	Sequence 24, Appl1	387	82.6	4.8	1307	2	US-08-960-022-17	Sequence 17, Appl1
315	85.8	4.9	1736	3	US-09-634-530-24	Sequence 24, Appl1	388	82.6	4.8	1325	1	US-08-306-691B-51	Sequence 51, Appl1
316	85.8	4.9	2280	3	US-08-813-150-1	Sequence 1, Appl1	389	82.6	4.8	1461	5	PCT-US95-04258-4	Sequence 4, Appl1
317	85.8	4.9	2280	4	US-09-546-553-1	Sequence 1, Appl1	390	82.6	4.8	1461	5	PCT-US95-04258-4	Sequence 4, Appl1
318	85.8	4.9	2311	4	US-09-800-729-66	Sequence 66, Appl1	391	82.4	4.8	1492	4	US-09-369-247-23	Sequence 23, Appl1
319	85.6	4.9	1133	4	US-09-916-204-1	Sequence 1, Appl1	392	82.4	4.8	84	4	US-09-621-976-14571	Sequence 14571, A
										1378	3	US-09-149-476-208	Sequence 208, App

393	82.4	4.8	1925	4	US-09-148-545-128	Sequence 128, App	466	79.4	4.6	339	4	US-09-621-976-16015	Sequence 16015, A
394	82.4	4.8	2744	3	US-09-071-101-1	Sequence 1, Appli	467	79.2	4.6	3366	4	US-09-596-141C-6	Sequence 6, Appli
395	82.4	4.8	2744	3	US-09-369-618-1	Sequence 1, Appli	468	79.2	4.6	3366	4	US-09-595-526C-6	Sequence 6, Appli
396	82.4	4.8	2744	3	US-09-369-617-1	Sequence 1, Appli	469	79.2	4.6	10442	4	US-09-596-141C-1	Sequence 1, Appli
397	82.2	4.7	3080	3	US-09-099-041A-25	Sequence 25, Appl	470	79.2	4.6	10442	4	US-09-595-526C-1	Sequence 1, Appli
398	82.2	4.7	3080	3	US-09-245-281-25	Sequence 25, Appl	471	79.2	4.6	10474	4	US-09-596-141C-7	Sequence 7, Appli
399	82.2	4.7	3080	3	US-09-207-359B-25	Sequence 25, Appl	472	79.2	4.6	10474	4	US-09-596-141C-9	Sequence 9, Appli
400	82.2	4.7	3080	4	US-09-340-620A-25	Sequence 25, Appl	473	79.2	4.6	10474	4	US-09-595-526C-7	Sequence 7, Appli
401	82.2	4.7	3080	4	US-09-865-364-25	Sequence 25, Appl	474	79.2	4.6	10474	4	US-09-595-526C-9	Sequence 9, Appli
402	82.2	4.7	7724	4	US-08-486-049-1	Sequence 1, Appli	475	79	4.6	168	1	US-08-469-802B-4	Sequence 4, Appli
403	82.2	4.7	118868	4	US-09-949-016-15746	Sequence 15746, A	476	79	4.6	168	2	US-08-267-803B-4	Sequence 4, Appli
404	82	4.7	118143	4	US-09-949-016-17196	Sequence 17196, A	477	79	4.6	332	4	US-09-621-976-16050	Sequence 16050, A
405	81.8	4.7	188	4	US-09-621-976-10364	Sequence 10364, A	478	79	4.6	601	4	US-09-949-016-195763	Sequence 195763, A
406	81.8	4.7	293	4	US-09-621-976-16965	Sequence 16965, A	479	79	4.6	1147	1	US-08-665-716-1	Sequence 1, Appli
407	81.8	4.7	1927	3	US-09-336-536-66	Sequence 66, Appl	480	79	4.6	2216	4	US-09-426-783-5	Sequence 5, Appli
408	81.6	4.7	132	4	US-09-621-976-13468	Sequence 13468, A	481	79	4.6	2621	2	US-08-553-619B-8	Sequence 8, Appli
409	81.6	4.7	6794	4	US-09-491-356C-2	Sequence 2, Appli	482	79	4.6	9636	1	US-08-323-170B-1	Sequence 1, Appli
410	81.4	4.7	154	1	US-08-469-802B-6	Sequence 6, Appli	483	79	4.6	9636	3	US-08-954-441-1	Sequence 1, Appli
411	81.4	4.7	154	2	US-08-267-803B-6	Sequence 6, Appli	484	78.8	4.5	185	4	US-09-621-976-16779	Sequence 16779, A
412	81.4	4.7	1210	3	US-09-443-041A-29	Sequence 29, Appl	485	78.8	4.5	1277	4	US-09-270-767-25838	Sequence 25838, A
413	81.4	4.7	2989	6	5378464-1	Patent No. 5378464	486	78.8	4.5	2271	4	US-09-205-258-243	Sequence 243, App
414	81.4	4.7	2989	6	5378464-1	Patent No. 5378464	487	78.8	4.5	3556	4	US-09-270-767-10439	Sequence 10439, A
415	81.4	4.7	8643	4	US-10-029-907-4	Sequence 4, Appli	488	78.8	4.5	4239	4	US-09-815-048-1	Sequence 1, Appli
416	81.2	4.7	224	2	US-08-731-272A-26	Sequence 26, Appl	489	78.8	4.5	79	4	US-09-621-976-15090	Sequence 15090, A
417	81.2	4.7	1325	2	US-08-464-517-1	Sequence 1, Appli	490	78.6	4.5	165	4	US-09-621-976-8127	Sequence 8127, Ap
418	81.2	4.7	1325	3	US-08-246-361A-1	Sequence 1, Appli	491	78.6	4.5	231	4	US-09-621-976-16317	Sequence 16317, A
419	81.2	4.7	1325	3	US-08-463-772-1	Sequence 1, Appli	492	78.6	4.5	601	4	US-09-949-016-84943	Sequence 84943, A
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421	81.2	4.7	1332	2	US-09-057-762-1	Sequence 1, Appli	494	78.6	4.5	601	4	US-09-949-016-155437	Sequence 155437, A
422	81.2	4.7	1332	3	US-08-326-119A-1	Sequence 1, Appli	495	78.6	4.5	601	4	US-09-949-016-155438	Sequence 155438, A
423	81.2	4.7	1558	1	US-08-467-607-2	Sequence 2, Appli	496	78.6	4.5	601	4	US-09-949-016-155439	Sequence 155439, A
424	81.2	4.7	1558	2	US-08-469-362-2	Sequence 2, Appli	497	78.6	4.5	601	4	US-09-949-016-155441	Sequence 155441, A
425	81.2	4.7	1558	2	US-08-850-392-2	Sequence 2, Appli	498	78.6	4.5	601	4	US-09-949-016-155442	Sequence 155442, A
426	81	4.7	81	4	US-09-621-976-13152	Sequence 13152, A	499	78.6	4.5	601	4	US-09-949-016-155445	Sequence 155445, A
427	81	4.7	1212	3	US-09-182-145-34	Sequence 34, Appl	500	78.6	4.5	601	4	US-09-949-016-155450	Sequence 155450, A
428	81	4.7	1212	3	US-09-182-145-35	Sequence 35, Appl	501	78.6	4.5	26115	4	US-09-949-016-15959	Sequence 15959, A
429	81	4.7	1921	2	US-08-557-128-11	Sequence 11, Appl	502	78.6	4.5	53768	4	US-09-949-016-17527	Sequence 17527, A
430	80.8	4.7	179	4	US-09-621-976-18054	Sequence 18054, A	503	78.6	4.5	93398	4	US-09-949-016-17527	Sequence 17527, A
431	80.6	4.6	169	4	US-09-621-976-11249	Sequence 11249, A	504	78.6	4.5	93398	4	US-09-949-016-14167	Sequence 14167, A
432	80.6	4.6	273	4	US-09-809-545A-31	Sequence 31, Appl	505	78.6	4.5	93276	4	US-09-949-016-15093	Sequence 16093, A
433	80.6	4.6	601	4	US-09-949-016-182221	Sequence 182221, A	506	78.4	4.5	3527	2	US-08-909-965C-7	Sequence 7, Appli
434	80.6	4.6	1692	4	US-09-821-803A-5	Sequence 5, Appli	507	78.4	4.5	57139	4	US-09-949-016-11771	Sequence 11771, A
435	80.6	4.6	2445	4	US-09-949-016-781	Sequence 781, App	508	78.4	4.5	57150	4	US-09-949-016-16233	Sequence 16233, A
436	80.6	4.6	2539	4	US-10-144-198-21	Sequence 21, Appl	509	78.4	4.5	462589	4	US-09-949-016-12900	Sequence 12900, A
437	80.6	4.6	133358	4	US-09-949-016-16964	Sequence 16964, A	510	78.4	4.5	476044	4	US-09-949-016-12412	Sequence 12412, A
438	80.6	4.6	133360	4	US-09-949-016-12651	Sequence 12651, A	511	78.2	4.5	601	4	US-09-949-016-155444	Sequence 155444, A
439	80.4	4.6	332	4	US-09-621-976-16031	Sequence 16031, A	512	78.2	4.5	1606	4	US-09-820-004-1	Sequence 1, Appli
440	80.4	4.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli	513	78.2	4.5	2223	1	US-08-257-073-4	Sequence 1, Appli
441	80.2	4.6	316	4	US-09-513-999C-838	Sequence 838, App	514	78.2	4.5	5173	1	US-08-242-677-1	Sequence 1, Appli
442	80.2	4.6	593	3	US-09-385-982-262	Sequence 262, App	515	78	4.5	78	4	US-09-621-976-14824	Sequence 14824, A
443	80.2	4.6	601	4	US-09-949-016-150084	Sequence 150084, A	516	78	4.5	1441	3	US-09-621-976-15092	Sequence 15092, A
444	80.2	4.6	601	4	US-09-949-016-155436	Sequence 155436, A	517	78	4.5	189	4	US-09-621-976-14761	Sequence 14761, A
445	80	4.6	171	1	US-08-469-802B-5	Sequence 5, Appli	518	78	4.5	332	4	US-09-621-976-16053	Sequence 16053, A
446	80	4.6	171	2	US-08-267-803B-5	Sequence 5, Appli	519	78	4.5	333	4	US-09-621-976-16032	Sequence 16032, A
447	80	4.6	1008	4	US-09-780-641-1	Sequence 1, Appli	520	78	4.5	333	4	US-09-621-976-16045	Sequence 16045, A
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450	80	4.6	2218	4	US-10-329-668-7	Sequence 7, Appli	523	78	4.5	543	6	5273901-6	Patent No. 5273901
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452	80	4.6	2407	3	US-09-370-807-7	Sequence 7, Appli	525	78	4.5	601	4	US-09-949-016-102738	Sequence 102738, A
453	80	4.6	2407	3	US-09-921-259-7	Sequence 7, Appli	526	78	4.5	1441	3	US-08-821-994-63	Sequence 63, Appl
454	80	4.6	2550	6	5258287-23	Patent No. 5258287	527	78	4.5	678533	4	US-09-949-016-14577	Sequence 14577, A
455	80	4.6	2550	6	5258287-23	Patent No. 5258287	528	78	4.5	678533	4	US-09-949-016-14578	Sequence 14578, A
456	80	4.6	2550	6	5258287-23	Sequence 150085, A	529	77.8	4.5	173	4	US-09-621-976-9851	Sequence 9851, Ap
457	79.8	4.6	2276	4	US-09-205-258-183	Sequence 183, App	530	77.8	4.5	336	4	US-09-621-976-16051	Sequence 16051, A
458	79.8	4.6	9558	4	US-09-949-016-13026	Sequence 13026, A	531	77.8	4.5	675	4	US-09-621-976-2461	Sequence 2461, Ap
459	79.8	4.6	10451	4	US-09-949-016-12192	Sequence 12192, A	532	77.8	4.5	144922	4	US-09-949-016-15890	Sequence 15890, A
460	79.6	4.6	335	4	US-09-621-976-16061	Sequence 16061, A	533	77.6	4.5	329	4	US-09-621-976-16012	Sequence 16012, A
461	79.6	4.6	338	4	US-09-621-976-16041	Sequence 16041, A	534	77.6	4.5	454	2	US-08-623-906A-5	Sequence 6, Appli
462	79.6	4.6	601	4	US-09-949-016-160412	Sequence 160412, A	535	77.6	4.5	1074	3	US-09-248-335-67	Sequence 67, Appl
463	79.6	4.6	601	4	US-09-949-016-160413	Sequence 160413, A	536	77.6	4.5	1709	4	US-09-426-783-9	Sequence 6, Appli
464	79.6	4.6	1027	3	US-09-465-558-57	Sequence 57, Appl	537	77.6	4.5	2028	4	US-09-426-783-9	Sequence 9, Appli
465	79.4	4.6	336	4	US-09-621-976-16013	Sequence 16013, A	538	77.6	4.5	130724	4	US-09-949-016-13753	Sequence 13753, A

c 539	77.6	4.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli	612	75.8	4.4	642	1	US-08-764-100-13	Sequence 13, Appli
c 540	77.4	4.5	336	2	US-07-814-220-3	Sequence 3, Appli	c 613	75.8	4.4	643	1	US-08-764-100-7	Sequence 7, Appli
c 541	77.4	4.5	336	2	US-07-814-220-4	Sequence 4, Appli	c 614	75.8	4.4	960	3	US-09-248-335-57	Sequence 57, Appli
c 542	77.4	4.5	336	2	US-07-812-421-3	Sequence 3, Appli	c 615	75.8	4.4	1559	4	US-09-489-847-42	Sequence 42, Appli
c 543	77.4	4.5	336	2	US-07-812-421-4	Sequence 4, Appli	c 616	75.8	4.4	2993	1	US-08-764-100-2	Sequence 2, Appli
c 544	77.4	4.5	467	2	US-08-841-349-18	Sequence 18, Appli	c 617	75.8	4.4	2993	1	US-08-764-100-10	Sequence 10, Appli
c 545	77.4	4.5	467	2	US-09-431-184A-18	Sequence 18, Appli	c 618	75.8	4.4	3000	1	US-08-764-100-9	Sequence 9, Appli
c 546	77.4	4.5	593	4	US-09-904-615-59	Sequence 59, Appli	c 619	75.8	4.4	3001	1	US-08-764-100-1	Sequence 1, Appli
c 547	77.4	4.5	601	4	US-09-904-615-48520	Sequence 48520, A	c 620	75.8	4.4	131332	4	US-09-949-016-15535	Sequence 15535, A
c 548	77.4	4.5	664	4	US-09-904-615-66	Sequence 66, Appli	c 621	75.6	4.4	98	4	US-09-621-976-11744	Sequence 11744, A
c 549	77.2	4.5	166	4	US-09-621-976-18390	Sequence 18390, A	c 622	75.6	4.4	257	2	US-08-520-678A-24	Sequence 24, Appli
c 550	77.2	4.5	443	4	US-09-621-976-17631	Sequence 17631, A	c 623	75.6	4.4	257	3	US-08-897-126-24	Sequence 24, Appli
c 551	77.2	4.5	658	3	US-08-998-416-595	Sequence 595, App	c 624	75.6	4.4	601	4	US-09-949-016-40844	Sequence 40844, A
c 552	77.2	4.5	1023	1	US-08-252-966B-16	Sequence 16, Appli	c 625	75.6	4.4	601	4	US-09-949-016-40845	Sequence 40845, A
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c 554	77.2	4.5	8642	4	US-10-029-907-2	Sequence 2, Appli	c 627	75.6	4.4	601	4	US-09-949-016-175160	Sequence 175160, A
c 555	77	4.4	77	4	US-08-956-171E-2883	Sequence 2883, Ap	c 628	75.6	4.4	1279	3	US-09-248-335-25	Sequence 25, Appli
c 556	77	4.4	77	4	US-08-781-986A-2883	Sequence 2883, Ap	c 629	75.6	4.4	46589	4	US-09-949-016-12900	Sequence 12900, A
c 557	77	4.4	159	4	US-09-621-976-17448	Sequence 17448, A	c 630	75.6	4.4	47604	4	US-09-949-016-12412	Sequence 12412, A
c 558	77	4.4	250	4	US-09-621-976-18893	Sequence 18893, A	c 631	75.4	4.3	164	4	US-09-621-976-16692	Sequence 16692, A
c 559	77	4.4	601	4	US-09-949-016-155440	Sequence 155440, A	c 632	75.4	4.3	196	4	US-09-270-767-29394	Sequence 29394, A
c 560	77	4.4	601	4	US-09-949-016-155443	Sequence 155443, A	c 633	75.4	4.3	601	4	US-09-949-016-80450	Sequence 80450, A
c 561	77	4.4	1129	3	US-09-227-357-40	Sequence 40, Appli	c 634	75.4	4.3	624	4	US-09-270-767-13424	Sequence 13424, A
c 562	77	4.4	2350	4	US-09-949-016-2281	Sequence 2281, Ap	c 635	75.4	4.3	1844	4	US-10-003-352-7	Sequence 7, Appli
c 563	77	4.4	9571	4	US-09-949-016-14023	Sequence 14023, A	c 636	75.4	4.3	3376	1	US-08-320-559-29	Sequence 29, Appli
c 564	77	4.4	10747	2	US-08-147-777-1	Sequence 1, Appli	c 637	75.4	4.3	3376	3	US-08-545-860D-29	Sequence 29, Appli
c 565	77	4.4	10747	3	US-08-452-872-1	Sequence 1, Appli	c 638	75.4	4.3	3376	5	PCT-US94-04496-29	Sequence 29, Appli
c 566	77	4.4	10747	5	PCT-US93-03985-1	Sequence 1, Appli	c 639	75.4	4.3	11338	4	US-09-949-016-16583	Sequence 16583, A
c 567	77	4.4	24979	2	US-08-147-777-3	Sequence 3, Appli	c 640	75.4	4.3	13124	2	US-08-487-826B-13	Sequence 13, Appli
c 568	77	4.4	24979	5	PCT-US93-03985-3	Sequence 3, Appli	c 641	75.4	4.3	89689	4	US-09-949-016-13089	Sequence 13089, A
c 569	77	4.4	140224	4	US-09-949-016-17002	Sequence 17002, A	c 642	75.2	4.3	552	4	US-10-012-542-111	Sequence 111, App
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c 571	76.8	4.4	1509	3	US-09-149-476-179	Sequence 179, App	c 644	75.2	4.3	558	4	US-09-205-258-64	Sequence 64, Appli
c 572	76.8	4.4	601	4	US-09-949-016-152093	Sequence 152093, A	c 645	75.2	4.3	792	4	US-09-902-540-8438	Sequence 8438, Ap
c 573	76.6	4.4	601	4	US-09-949-016-152166	Sequence 152166, A	c 646	75.2	4.3	1296	4	US-09-461-325-29	Sequence 29, Appli
c 574	76.6	4.4	601	4	US-09-949-016-152239	Sequence 152239, A	c 647	75.2	4.3	1296	4	US-10-012-542-29	Sequence 29, Appli
c 575	76.6	4.4	601	4	US-09-949-016-152312	Sequence 152312, A	c 648	75.2	4.3	1296	4	US-10-115-123-29	Sequence 29, Appli
c 576	76.6	4.4	601	4	US-09-949-016-159398	Sequence 159398, A	c 649	75.2	4.3	8917	4	US-09-902-540-887	Sequence 887, App
c 577	76.6	4.4	601	4	US-09-949-016-159471	Sequence 159471, A	c 650	75.2	4.3	75	4	US-09-621-976-14892	Sequence 14892, A
c 578	76.6	4.4	601	4	US-09-949-016-159544	Sequence 159544, A	c 651	75	4.3	77	4	US-09-621-976-14176	Sequence 14176, A
c 579	76.6	4.4	601	4	US-09-621-976-1894	Sequence 1894, Ap	c 652	75	4.3	258	4	US-09-621-976-15353	Sequence 15353, A
c 580	76.6	4.4	78846	4	US-09-949-016-12396	Sequence 12396, A	c 653	75	4.3	259	4	US-09-621-976-16294	Sequence 16294, A
c 581	76.6	4.4	78846	4	US-09-949-016-12791	Sequence 12791, A	c 654	75	4.3	55841	4	US-09-949-016-16602	Sequence 16602, A
c 582	76.6	4.4	78846	4	US-09-949-016-12792	Sequence 12792, A	c 655	75	4.3	124264	4	US-09-949-016-16396	Sequence 16396, A
c 583	76.6	4.4	78846	4	US-09-949-016-12793	Sequence 12793, A	c 656	75	4.3	423592	4	US-09-949-016-14182	Sequence 14182, A
c 584	76.6	4.4	78846	4	US-09-949-016-16013	Sequence 16013, A	c 657	75	4.3	327	4	US-09-621-976-16018	Sequence 16018, A
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c 586	76.6	4.4	78850	4	US-09-949-016-16015	Sequence 16015, A	c 659	74.8	4.3	601	4	US-09-949-016-47327	Sequence 47327, A
c 587	76.6	4.4	78850	4	US-09-949-016-16016	Sequence 16016, A	c 660	74.8	4.3	7989	4	US-09-539-601-10	Sequence 10, Appli
c 588	76.6	4.4	78850	4	US-09-949-016-16017	Sequence 16017, A	c 661	74.8	4.3	8001	4	US-09-539-601-7	Sequence 7, Appli
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c 591	76.6	4.4	78850	4	US-09-949-016-16020	Sequence 16020, A	c 664	74.8	4.3	8001	4	US-09-539-601-28	Sequence 28, Appli
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c 593	76.6	4.4	78850	4	US-09-342-653-5	Sequence 5, Appli	c 666	74.8	4.3	8638	4	US-10-029-907-7	Sequence 7, Appli
c 594	76.4	4.4	572	3	US-09-690-942-3	Sequence 3, Appli	c 667	74.8	4.3	8638	4	US-10-029-907-24	Sequence 24, Appli
c 595	76.4	4.4	360470	4	US-09-949-016-13173	Sequence 13173, A	c 668	74.8	4.3	8638	4	US-10-029-907-25	Sequence 25, Appli
c 596	76.4	4.4	601	4	US-09-949-016-48516	Sequence 48516, A	c 669	74.8	4.3	8639	4	US-10-029-907-1	Sequence 1, Appli
c 597	76.2	4.4	601	4	US-09-949-016-48517	Sequence 48517, A	c 670	74.8	4.3	8639	4	US-09-539-601-13	Sequence 13, Appli
c 598	76.2	4.4	58768	4	US-09-949-016-13175	Sequence 13175, A	c 671	74.8	4.3	11076	4	US-09-539-601-1	Sequence 1, Appli
c 599	76.2	4.4	76	4	US-09-621-976-14831	Sequence 14831, A	c 672	74.8	4.3	11076	4	US-09-539-601-19	Sequence 19, Appli
c 600	76	4.4	76	4	US-09-621-976-14915	Sequence 14915, A	c 673	74.8	4.3	11076	4	US-09-539-601-25	Sequence 25, Appli
c 601	76	4.4	84	1	US-08-664-598B-3	Sequence 3, Appli	c 674	74.8	4.3	11076	4	US-09-539-601-31	Sequence 31, Appli
c 602	76	4.4	84	1	US-08-738-367-3	Sequence 3, Appli	c 675	74.8	4.3	11076	4	US-09-621-976-18363	Sequence 18363, A
c 603	76	4.4	1663	4	US-09-464-535-43	Sequence 43, Appli	c 676	74.6	4.3	326	4	US-09-621-976-16024	Sequence 16024, A
c 604	76	4.4	3975	4	US-09-270-767-3	Sequence 3, Appli	c 677	74.6	4.3	376	2	US-08-623-906A-18	Sequence 18, Appli
c 605	76	4.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli	c 678	74.6	4.3	3581	2	US-08-738-349-1	Sequence 1, Appli
c 606	76	4.4	212	4	US-09-621-976-1325	Sequence 1325, Ap	c 679	74.6	4.3	321	2	US-08-520-678A-23	Sequence 23, Appli
c 607	75.8	4.4	601	4	US-09-949-016-48517	Sequence 48517, A	c 680	74.4	4.3	321	3	US-08-897-126-23	Sequence 23, Appli
c 608	75.8	4.4	601	4	US-09-949-016-48518	Sequence 48518, A	c 681	74.4	4.3	601	4	US-09-949-016-204598	Sequence 204598, A
c 609	75.8	4.4	601	4	US-09-949-016-48519	Sequence 48519, A	c 682	74.4	4.3	601	4	US-09-949-016-204599	Sequence 204599, A
c 610	75.8	4.4	601	4	US-08-764-100-8	Sequence 8, Appli	c 683	74.4	4.3	601	4	US-09-949-016-204600	Sequence 204600, A
c 611	75.8	4.4	602	1			c 684	74.4	4.3	601	4		

685	74.4	4.3	601	4	US-09-949-016-204601	Sequence 204601,	758	73.6	4.2	524032	4	US-09-949-016-16931	Sequence 16931, A
686	74.4	4.3	601	4	US-09-949-016-204602	Sequence 204602,	759	73.6	4.2	529885	4	US-09-949-016-14340	Sequence 14340, A
687	74.4	4.3	601	4	US-09-949-016-204603	Sequence 204603,	760	73.6	4.2	529885	4	US-09-949-016-14341	Sequence 14341, A
688	74.4	4.3	601	4	US-09-949-016-204604	Sequence 204604,	761	73.6	4.2	529885	4	US-09-949-016-14342	Sequence 14342, A
689	74.4	4.3	601	4	US-09-949-016-204605	Sequence 204605,	762	73.6	4.2	529885	4	US-09-949-016-14343	Sequence 14343, A
690	74.4	4.3	601	4	US-09-949-016-204606	Sequence 204606,	763	73.6	4.2	529885	4	US-09-949-016-14344	Sequence 14344, A
691	74.4	4.3	601	4	US-09-949-016-204607	Sequence 204607,	764	73.6	4.2	529885	4	US-09-949-016-14345	Sequence 14345, A
692	74.4	4.3	1740	4	US-09-709-103-45	Sequence 45, Appl	765	73.6	4.2	529885	4	US-09-949-016-14346	Sequence 14346, A
693	74.4	4.3	1740	4	US-09-709-103-45	Sequence 45, Appl	766	73.6	4.2	529885	4	US-09-949-016-14347	Sequence 14347, A
694	74.4	4.3	1801	4	US-09-709-103-3	Sequence 3, Appl	767	73.4	4.2	371	4	US-09-621-976-19223	Sequence 19223, A
695	74.4	4.3	1801	4	US-09-439-410A-3	Sequence 3, Appl	768	73.4	4.2	601	4	US-09-949-016-80449	Sequence 80449, A
696	74.4	4.3	5481	4	US-09-949-016-12049	Sequence 12049, A	769	73.4	4.2	1214	4	US-09-780-717-28	Sequence 28, Appl
697	74.4	4.3	5484	4	US-09-949-016-15589	Sequence 15589, A	770	73.4	4.2	13146	4	US-08-724-354D-3	Sequence 3, Appl
698	74.4	4.3	87734	4	US-09-949-016-17521	Sequence 17521, A	771	73.4	4.2	13146	3	US-09-270-984A-3	Sequence 3, Appl
699	74.4	4.3	124110	4	US-09-949-016-13353	Sequence 13353, A	772	73.4	4.2	11592	4	US-09-818-512-3	Sequence 3, Appl
700	74.2	4.3	208	1	US-08-686-878A-37	Sequence 37, Appl	773	73.4	4.2	254366	4	US-09-822-871-3	Sequence 3, Appl
701	74.2	4.3	208	3	US-09-175-928-37	Sequence 37, Appl	774	73.2	4.2	271	2	US-08-731-272A-29	Sequence 29, Appl
702	74.2	4.3	349	4	US-09-270-767-6612	Sequence 6612, Ap	775	73.2	4.2	347	4	US-09-621-976-16136	Sequence 16136, A
703	74.2	4.3	349	4	US-09-270-767-21894	Sequence 21894, A	776	73.2	4.2	351	4	US-09-621-976-16140	Sequence 16140, A
704	74.2	4.3	1046	1	US-08-361-467B-4	Sequence 4, Appl	777	73.2	4.2	601	4	US-09-949-016-149677	Sequence 149677, A
705	74.2	4.3	1046	1	US-08-484-332C-4	Sequence 4, Appl	778	73.2	4.2	1100	3	US-07-861-458C-4	Sequence 4, Appl
706	74.2	4.3	32721	4	US-09-949-016-14100	Sequence 14100, A	779	73.2	4.2	145928	4	US-09-949-016-15444	Sequence 15444, A
707	74	4.3	473	1	US-08-764-100-16	Sequence 16, Appl	780	73.2	4.2	189359	4	US-09-949-016-13125	Sequence 13125, A
708	74	4.3	601	4	US-09-949-016-179690	Sequence 179690,	781	73.2	4.2	237510	4	US-09-949-016-14273	Sequence 14273, A
709	74	4.3	601	4	US-09-949-016-182153	Sequence 182153,	782	73.2	4.2	312474	4	US-09-949-016-17434	Sequence 17434, A
710	74	4.3	601	4	US-09-949-016-182154	Sequence 182154,	783	73.2	4.2	73	4	US-09-621-976-14963	Sequence 14963, A
711	74	4.3	1544	4	US-09-187-999-14	Sequence 14, Appl	784	73	4.2	162	4	US-09-621-976-7813	Sequence 7813, Ap
712	74	4.3	2158	1	US-07-602-608-1	Sequence 1, Appl	785	73	4.2	1872	3	US-09-291-922-27	Sequence 27, Appl
713	74	4.3	2158	1	US-08-261-578-1	Sequence 1, Appl	786	73	4.2	2065	3	US-09-370-473-5	Sequence 5, Appl
714	74	4.3	3212	1	US-08-697-954-1	Sequence 1, Appl	787	73	4.2	2083	4	US-09-716-129-41	Sequence 41, Appl
715	74	4.3	4970	1	US-08-764-100-14	Sequence 14, Appl	788	72.8	4.2	232	4	US-09-621-976-17701	Sequence 17701, A
716	74	4.3	4970	1	US-08-764-100-20	Sequence 20, Appl	789	72.8	4.2	299	4	US-09-621-976-10211	Sequence 10211, A
717	74	4.3	15722	4	US-09-949-016-16709	Sequence 16709, A	790	72.8	4.2	746	3	US-09-013-810-1	Sequence 1, Appl
718	74	4.3	276687	4	US-09-949-016-13840	Sequence 13840, A	791	72.8	4.2	1558	1	US-08-455-550-7	Sequence 7, Appl
719	73.8	4.3	329	4	US-09-949-016-13840	Sequence 13840, A	792	72.8	4.2	58407	4	US-08-916-421B-2	Sequence 2, Appl
720	73.8	4.3	601	4	US-09-621-976-18052	Sequence 18052, A	793	72.8	4.2	58407	4	US-09-692-570-2	Sequence 2, Appl
721	73.8	4.3	1651	4	US-09-949-016-80451	Sequence 80451, A	794	72.8	4.2	199471	4	US-09-949-016-14083	Sequence 14083, A
722	73.8	4.3	6558	4	US-09-800-729-41	Sequence 41, Appl	795	72.6	4.2	73	4	US-09-621-976-14729	Sequence 14729, A
723	73.8	4.3	54033	4	US-09-491-356C-7	Sequence 7, Appl	796	72.6	4.2	1518	4	US-09-614-912-191	Sequence 191, App
724	73.8	4.3	54033	4	US-09-949-016-14325	Sequence 14325, A	797	72.6	4.2	65744	4	US-09-949-016-12591	Sequence 12591, A
725	73.8	4.3	421491	4	US-09-949-016-12805	Sequence 12805, A	798	72.6	4.2	65745	4	US-09-949-016-15871	Sequence 15871, A
726	73.8	4.3	421494	4	US-09-949-016-14060	Sequence 14060, A	799	72.6	4.2	73519	4	US-09-949-016-16344	Sequence 16344, A
727	73.6	4.2	227	2	US-08-520-678A-28	Sequence 28, Appl	800	72.6	4.2	105919	4	US-09-949-016-11769	Sequence 11769, A
728	73.6	4.2	227	3	US-08-897-126-28	Sequence 28, Appl	801	72.4	4.2	184	4	US-09-270-767-30942	Sequence 30942, A
729	73.6	4.2	348	4	US-09-621-976-16137	Sequence 16137, A	802	72.4	4.2	367	4	US-09-270-767-14713	Sequence 14713, A
730	73.6	4.2	601	4	US-09-949-016-161983	Sequence 161983,	803	72.4	4.2	413	3	US-09-227-357-71	Sequence 71, Appl
731	73.6	4.2	601	4	US-09-949-016-179687	Sequence 179687,	804	72.4	4.2	530	4	US-09-461-325-28	Sequence 28, Appl
732	73.6	4.2	958	2	US-08-757-046A-5	Sequence 5, Appl	805	72.4	4.2	530	4	US-10-012-542-28	Sequence 28, Appl
733	73.6	4.2	958	3	US-09-447-208-5	Sequence 5, Appl	806	72.4	4.2	530	4	US-10-115-123-28	Sequence 28, Appl
734	73.6	4.2	958	3	US-09-135-988-5	Sequence 5, Appl	807	72.4	4.2	601	4	US-09-949-016-80104	Sequence 80104, A
735	73.6	4.2	958	3	US-09-277-716-5	Sequence 5, Appl	808	72.4	4.2	601	4	US-09-949-016-179688	Sequence 179688,
736	73.6	4.2	958	3	US-08-597-274A-5	Sequence 5, Appl	809	72.4	4.2	730	4	US-09-270-767-14600	Sequence 14600, A
737	73.6	4.2	958	3	US-08-908-909-5	Sequence 5, Appl	810	72.4	4.2	756	4	US-09-614-912-93	Sequence 93, Appl
738	73.6	4.2	958	3	US-09-609-161B-5	Sequence 5, Appl	811	72.4	4.2	1798	2	US-08-557-128-12	Sequence 12, Appl
739	73.6	4.2	958	3	US-08-990-103-5	Sequence 5, Appl	812	72.4	4.2	2481	2	US-09-739-455-1	Sequence 1, Appl
740	73.6	4.2	958	4	US-09-746-485A-5	Sequence 5, Appl	813	72.4	4.2	2481	2	US-08-630-118A-1	Sequence 1, Appl
741	73.6	4.2	958	4	US-10-126-139-5	Sequence 5, Appl	814	72.4	4.2	2481	2	US-08-838-399-1	Sequence 1, Appl
742	73.6	4.2	958	4	US-10-126-798-5	Sequence 5, Appl	815	72.4	4.2	2481	3	US-09-235-839-1	Sequence 1, Appl
743	73.6	4.2	958	4	US-10-126-777-5	Sequence 5, Appl	816	72.4	4.2	2481	3	US-09-327-035-1	Sequence 1, Appl
744	73.6	4.2	2230	3	US-08-378-313-24	Sequence 24, Appl	817	72.4	4.2	2604	2	US-08-630-118A-3	Sequence 3, Appl
745	73.6	4.2	2389	4	US-09-799-875-7	Sequence 7, Appl	818	72.4	4.2	2604	2	US-08-838-399-3	Sequence 3, Appl
746	73.6	4.2	6530	2	US-08-146-930-1	Sequence 1, Appl	819	72.4	4.2	2604	3	US-09-235-839-3	Sequence 3, Appl
747	73.6	4.2	6530	2	US-08-458-240-1	Sequence 1, Appl	820	72.4	4.2	2604	3	US-09-327-035-3	Sequence 3, Appl
748	73.6	4.2	6530	5	PCF-US93-03993-1	Sequence 1, Appl	821	72.4	4.2	4880	3	US-09-031-563-1	Sequence 1, Appl
749	73.6	4.2	8648	4	US-10-029-907-5	Sequence 5, Appl	822	72.4	4.2	4880	3	US-09-392-277-1	Sequence 1, Appl
750	73.6	4.2	132438	4	US-09-949-016-14349	Sequence 14349, A	823	72.4	4.2	4880	4	US-09-258-000-1	Sequence 1, Appl
751	73.6	4.2	132438	4	US-09-949-016-14350	Sequence 14350, A	824	72.4	4.2	5125	3	US-09-031-563-4	Sequence 4, Appl
752	73.6	4.2	149543	4	US-09-949-016-15947	Sequence 15947, A	825	72.4	4.2	5125	3	US-09-392-277-4	Sequence 4, Appl
753	73.6	4.2	151089	4	US-09-949-016-14348	Sequence 14348, A	826	72.4	4.2	5125	4	US-09-258-000-4	Sequence 4, Appl
754	73.6	4.2	238815	4	US-09-949-016-14348	Sequence 14348, A	827	72.4	4.2	312470	4	US-09-949-016-14043	Sequence 14043, A
755	73.6	4.2	524032	4	US-09-949-016-16928	Sequence 16928, A	828	72.4	4.2	336024	4	US-09-949-016-12373	Sequence 12373, A
756	73.6	4.2	524032	4	US-09-949-016-16929	Sequence 16929, A	829	72.4	4.2	39416	4	US-09-949-016-16923	Sequence 16923, A
757	73.6	4.2	524032	4	US-09-949-016-16930	Sequence 16930, A	830	72.2	4.2	266	4	US-09-621-976-16813	Sequence 16813, A



831	72.2	4.2	601	4	US-09-949-016-193087	Sequence 193087,	904	71.6	4.1	601	4	US-09-949-016-47328	Sequence 47328, A
832	72.2	4.2	601	4	US-09-949-016-193088	Sequence 193088,	905	71.6	4.1	601	4	US-09-949-016-186943	Sequence 186943,
833	72.2	4.2	601	4	US-09-949-016-193180	Sequence 193180,	906	71.6	4.1	1810	4	US-09-800-729-77	Sequence 73, Appl
834	72.2	4.2	601	4	US-09-949-016-193181	Sequence 193181,	907	71.6	4.1	1811	4	US-09-800-729-77	Sequence 77, Appl
835	72.2	4.2	601	4	US-09-949-016-193273	Sequence 193273,	C 908	71.6	4.1	16073	4	US-09-949-016-12312	Sequence 12312, A
836	72.2	4.2	601	4	US-09-949-016-193274	Sequence 193274,	C 909	71.6	4.1	16073	4	US-09-949-016-12305	Sequence 12305, A
837	72.2	4.2	601	4	US-09-949-016-193366	Sequence 193366,	910	71.6	4.1	16073	4	US-09-949-016-12305	Sequence 12305, A
838	72.2	4.2	601	4	US-09-949-016-193367	Sequence 193367,	911	71.6	4.1	16073	4	US-09-949-016-12305	Sequence 12305, A
839	72.2	4.2	931	4	US-09-482-273-31	Sequence 31, Appl	C 912	71.6	4.1	152070	4	US-09-949-016-15402	Sequence 15402, A
840	72.2	4.2	1123	3	US-09-152-060-15	Sequence 15, Appl	C 913	71.6	4.1	211049	4	US-09-949-016-15770	Sequence 15770, A
C 841	72.2	4.2	12047	2	US-09-022-461-1	Sequence 1, Appl	914	71.4	4.1	100	4	US-09-621-976-13774	Sequence 12774, A
C 842	72.2	4.2	12047	3	US-09-033-556-3	Sequence 3, Appl	915	71.4	4.1	324	4	US-09-621-976-1323	Sequence 1323, Ap
C 843	72.2	4.2	12047	4	US-09-474-699-11	Sequence 11, Appl	916	71.4	4.1	324	4	US-09-621-976-1323	Sequence 1323, Ap
C 844	72.2	4.2	12047	4	US-09-151-376-3	Sequence 3, Appl	917	71.4	4.1	358	4	US-09-621-976-1323	Sequence 1323, Ap
C 845	72.2	4.2	12047	4	US-09-814-351-11	Sequence 11, Appl	C 918	71.4	4.1	985	4	US-09-322-409-25	Sequence 25, Appl
846	72.2	4.2	86213	4	US-09-949-016-17240	Sequence 17240, A	919	71.4	4.1	985	4	US-09-322-409-25	Sequence 25, Appl
847	72.2	4.2	86213	4	US-09-949-016-17241	Sequence 17241, A	C 920	71.4	4.1	985	4	US-09-451-527-25	Sequence 25, Appl
848	72.2	4.2	86213	4	US-09-949-016-17242	Sequence 17242, A	921	71.4	4.1	1206	3	US-09-451-527-25	Sequence 25, Appl
849	72.2	4.2	86213	4	US-09-949-016-17243	Sequence 17243, A	922	71.4	4.1	1813	5	US-09-451-527-25	Sequence 25, Appl
850	72.2	4.2	156942	4	US-09-949-016-12227	Sequence 12227, A	923	71.4	4.1	4456	3	PCT-US94-12883-3	Sequence 3, Appl
851	72.2	4.2	156942	4	US-09-949-016-15946	Sequence 15946, A	C 924	71.4	4.1	133559	4	US-09-949-016-15845	Sequence 15845, A
C 852	72.2	4.2	250352	4	US-09-949-016-14724	Sequence 14724, A	925	71.4	4.1	168174	4	US-10-071-411A-63	Sequence 63, Appl
853	72	4.2	72	4	US-09-621-976-10145	Sequence 10145, A	926	71.4	4.1	168273	4	US-10-071-411A-63	Sequence 63, Appl
854	72	4.2	72	4	US-09-621-976-14815	Sequence 14815, A	927	71.2	4.1	72	4	US-09-621-976-1837	Sequence 37, Ap
855	72	4.2	72	4	US-09-621-976-14815	Sequence 14815, A	928	71.2	4.1	422	4	US-09-854-133-9337	Sequence 337, Ap
856	72	4.2	101	3	US-09-404-879A-293	Sequence 293, App	929	71.2	4.1	1934	3	US-08-776-844-1	Sequence 1, Appl
C 857	72	4.2	101	4	US-09-338-933-293	Sequence 293, App	930	71.2	4.1	1934	3	US-09-909-325-1	Sequence 1, Appl
C 858	72	4.2	101	4	US-09-215-681-293	Sequence 293, App	931	71.2	4.1	1934	3	US-09-909-325-1	Sequence 1, Appl
C 859	72	4.2	101	4	US-09-216-003A-293	Sequence 293, App	C 932	71.2	4.1	2147	4	US-09-949-016-5245	Sequence 2, Appl
C 860	72	4.2	101	4	US-09-667-857-293	Sequence 293, App	933	71.2	4.1	2679	4	US-09-684-579-2	Sequence 2, Appl
861	72	4.2	253	4	US-09-621-976-12799	Sequence 12799, A	934	71.2	4.1	2908	4	US-09-904-615-35	Sequence 35, Appl
C 862	72	4.2	601	4	US-09-949-016-21578	Sequence 21578, A	935	71.2	4.1	3848	3	US-09-112-096-28	Sequence 28, Appl
C 863	72	4.2	601	4	US-09-949-016-21579	Sequence 21579, A	936	71.2	4.1	5668	3	US-09-112-096-14	Sequence 14, Appl
C 864	72	4.2	601	4	US-09-949-016-130330	Sequence 130330, A	937	71.2	4.1	5668	4	US-09-636-215-77	Sequence 77, App
C 865	72	4.2	601	4	US-09-949-016-130331	Sequence 130331, A	938	71.2	4.1	5668	4	US-09-685-168A-77	Sequence 77, App
C 866	72	4.2	601	4	US-09-949-016-179692	Sequence 179692, A	939	71.2	4.1	5668	4	US-09-679-426-777	Sequence 77, App
867	72	4.2	787	4	US-09-621-976-1878	Sequence 1878, Ap	940	71.2	4.1	5668	4	US-09-679-426-777	Sequence 77, App
C 868	72	4.2	890	4	US-09-621-976-2725	Sequence 2725, Ap	941	71.2	4.1	5668	4	US-09-651-236-777	Sequence 77, App
C 869	72	4.2	5852	1	US-07-867-106-2	Sequence 2, Appl	C 942	71.2	4.1	19818	4	US-09-949-016-12198	Sequence 12198, A
C 870	72	4.2	92227	4	US-09-949-016-11529	Sequence 11529, A	C 943	71.2	4.1	19819	4	US-09-949-016-16987	Sequence 16987, A
C 871	72	4.2	92232	4	US-09-949-016-15421	Sequence 15421, A	C 944	71.2	4.1	154023	4	US-09-949-016-17057	Sequence 17057, A
872	71.8	4.1	1926	3	US-09-249-585A-2	Sequence 2, Appl	C 945	71.2	4.1	250958	4	US-09-949-016-16061	Sequence 16061, A
873	71.8	4.1	1926	4	US-09-410-399-3	Sequence 3, Appl	946	71	4.1	71	4	US-09-621-976-14905	Sequence 14905, A
874	71.8	4.1	2580	3	US-09-050-863-2	Sequence 2, Appl	947	71	4.1	80	3	US-07-920-281C-25	Sequence 25, Appl
875	71.8	4.1	2580	3	US-09-359-081-2	Sequence 2, Appl	948	71	4.1	80	3	US-08-466-277-25	Sequence 25, Appl
C 876	71.8	4.1	4600	4	US-09-702-705-1797	Sequence 1797, Ap	949	71	4.1	80	4	US-09-688-842-25	Sequence 25, Appl
C 877	71.8	4.1	4600	4	US-09-736-457-1797	Sequence 1797, Ap	950	71	4.1	142	4	US-09-621-976-10801	Sequence 10801, A
C 878	71.8	4.1	4600	4	US-09-671-325-1797	Sequence 1797, Ap	951	71	4.1	1065	4	US-09-976-594-833	Sequence 833, App
C 879	71.8	4.1	5452	2	US-09-130-114-1	Sequence 1, Appl	952	71	4.1	2291	4	US-09-220-132-114	Sequence 114, App
880	71.8	4.1	6065	4	US-09-800-729-35	Sequence 35, Appl	953	71	4.1	2291	4	US-09-814-915A-95	Sequence 95, Appl
881	71.8	4.1	7286	3	US-09-331-581-3	Sequence 3, Appl	954	71	4.1	8100	4	US-09-554-337-4	Sequence 4, Appl
882	71.8	4.1	7338	3	US-09-331-581-14	Sequence 14, Appl	955	71	4.1	11517	1	US-07-920-281C-1	Sequence 1, Appl
C 883	71.8	4.1	8705	4	US-09-647-344A-14	Sequence 14, Appl	956	71	4.1	11517	3	US-08-466-277-1	Sequence 1, Appl
884	71.8	4.1	9600	3	US-08-910-647-1	Sequence 1, Appl	957	71	4.1	11517	4	US-09-688-842-1	Sequence 1, Appl
885	71.8	4.1	10596	3	US-09-620-925-1	Sequence 1, Appl	958	71	4.1	15538	4	US-09-554-337-4	Sequence 1, Appl
886	71.8	4.1	10596	1	US-07-884-811-15	Sequence 15, Appl	C 959	71	4.1	107458	4	US-09-949-016-15687	Sequence 15687, A
887	71.8	4.1	10596	1	US-07-885-971-15	Sequence 15, Appl	960	71	4.1	161124	4	US-09-949-016-11760	Sequence 11760, A
888	71.8	4.1	10596	1	US-08-087-783A-15	Sequence 15, Appl	961	70.8	4.1	298	4	US-09-621-976-1371	Sequence 3871, Ap
889	71.8	4.1	10596	1	US-08-194-088B-15	Sequence 15, Appl	962	70.8	4.1	336	4	US-09-248-796A-13866	Sequence 13866, A
890	71.8	4.1	10596	1	US-08-194-087-15	Sequence 15, Appl	963	70.8	4.1	361	3	US-09-018-584A-9	Sequence 9, Appl
891	71.8	4.1	10596	5	PCT-US93-04648-15	Sequence 15, Appl	964	70.8	4.1	361	4	US-09-784-423-9	Sequence 9, Appl
C 892	71.8	4.1	16080	4	US-09-724-566A-48	Sequence 48, Appl	965	70.8	4.1	601	4	US-09-949-016-19138	Sequence 19138, A
C 893	71.8	4.1	16080	4	US-09-471-669A-48	Sequence 48, Appl	966	70.8	4.1	601	4	US-09-949-016-19138	Sequence 19138, A
894	71.6	4.1	72	4	US-09-621-976-15064	Sequence 15064, A	967	70.8	4.1	601	4	US-09-949-016-19139	Sequence 19139, A
895	71.6	4.1	443	4	US-09-936-885A-1	Sequence 1, Appl	968	70.8	4.1	601	4	US-09-949-016-19140	Sequence 19140, A
896	71.6	4.1	601	4	US-09-949-016-29142	Sequence 29142, A	969	70.8	4.1	601	4	US-09-949-016-122875	Sequence 122875, A
897	71.6	4.1	601	4	US-09-949-016-29143	Sequence 29143, A	970	70.8	4.1	601	4	US-09-949-016-122876	Sequence 122876, A
898	71.6	4.1	601	4	US-09-949-016-29144	Sequence 29144, A	971	70.8	4.1	601	4	US-09-949-016-122877	Sequence 122877, A
899	71.6	4.1	601	4	US-09-949-016-29145	Sequence 29145, A	972	70.8	4.1	601	4	US-09-949-016-122878	Sequence 122878, A
900	71.6	4.1	601	4	US-09-949-016-41097	Sequence 41097, A	C 973	70.8	4.1	601	4	US-09-949-016-179689	Sequence 179689, A
901	71.6	4.1	601	4	US-09-949-016-41098	Sequence 41098, A	C 974	70.8	4.1	601	4	US-09-949-016-179691	Sequence 179691, A
902	71.6	4.1	601	4	US-09-949-016-41099	Sequence 41099, A	C 975	70.8	4.1	601	4	US-09-949-016-187282	Sequence 187282, A
903	71.6	4.1	601	4	US-09-949-016-41100	Sequence 41100, A	976	70.8	4.1	601	4	US-09-949-016-203158	Sequence 203158, A

977	70.8	4.1	601	4	US-09-949-016-203159	Sequence 203159,	c1050	70	4.0	601	4	US-09-949-016-19754	Sequence 19754, A
978	70.8	4.1	601	4	US-09-949-016-203160	Sequence 203160,	1051	70	4.0	601	4	US-09-949-016-45911	Sequence 45911, A
979	70.8	4.1	601	4	US-09-949-016-203161	Sequence 203161,	c1052	70	4.0	601	4	US-09-949-016-81973	Sequence 81973, A
980	70.8	4.1	601	4	US-09-949-016-203200	Sequence 203200,	1053	70	4.0	734	4	US-09-949-016-413	Sequence 413, App
981	70.8	4.1	601	4	US-09-949-016-203201	Sequence 203201,	1054	70	4.0	1383	4	US-09-735-846-1	Sequence 1, Appli
982	70.8	4.1	601	4	US-09-949-016-203202	Sequence 203202,	c1055	70	4.0	17797	4	US-09-949-016-14125	Sequence 14125, A
983	70.8	4.1	601	4	US-09-949-016-203203	Sequence 203203,	c1056	70	4.0	227979	4	US-09-949-016-11842	Sequence 11842, A
984	70.8	4.1	1898	1	US-08-342-411A-1	Sequence 1, Appli	1057	69.8	4.0	601	4	US-09-949-016-60625	Sequence 60625, A
985	70.8	4.1	2882	4	US-09-949-016-724	Sequence 724, App	1058	69.8	4.0	601	4	US-09-949-016-161232	Sequence 161232,
986	70.8	4.1	3200	1	US-08-444-405-1	Sequence 1, Appli	c1059	69.8	4.0	601	4	US-09-949-016-193438	Sequence 193438,
987	70.8	4.1	3200	1	US-08-384-850-1	Sequence 1, Appli	1060	69.8	4.0	687	4	US-09-774-639-106	Sequence 106, App
988	70.8	4.1	6920	4	US-09-949-016-152111	Sequence 152111, A	1061	69.8	4.0	20721	4	US-09-949-016-16257	Sequence 16257, A
c 989	70.8	4.1	12603	4	US-09-949-016-17096	Sequence 17096, A	1062	69.8	4.0	23221	4	US-09-949-016-14257	Sequence 14257, A
c 990	70.8	4.1	29227	4	US-09-949-016-11814	Sequence 11814, A	1063	69.8	4.0	20321	4	US-09-949-016-14258	Sequence 14258, A
c 991	70.8	4.1	29227	4	US-09-949-016-117474	Sequence 117474, A	1064	69.8	4.0	52298	4	US-09-491-356C-1	Sequence 1, Appli
c 992	70.8	4.1	29227	4	US-09-949-016-17475	Sequence 17475, A	c1065	69.8	4.0	175265	4	US-09-949-016-16089	Sequence 16089, A
c 993	70.8	4.1	37802	4	US-09-949-016-12639	Sequence 12639, A	1066	69.6	4.0	279	2	US-08-623-906A-3	Sequence 3, Appli
c 994	70.8	4.1	42348	4	US-09-949-016-17157	Sequence 17157, A	1067	69.6	4.0	350	4	US-09-621-976-15342	Sequence 15342, A
c 995	70.8	4.1	80411	4	US-09-949-016-15777	Sequence 15777, A	c1068	69.6	4.0	378	4	US-09-248-796A-11672	Sequence 11672, A
c 996	70.8	4.1	106256	4	US-09-949-016-16858	Sequence 16858, A	c1069	69.6	4.0	601	4	US-09-949-016-82606	Sequence 82606, A
c 997	70.8	4.1	236474	4	US-09-949-016-13418	Sequence 13418, A	1070	69.6	4.0	1062	4	US-09-796-766-3	Sequence 3, Appli
c 998	70.6	4.1	601	4	US-09-949-016-63658	Sequence 63658, A	1071	69.6	4.0	1412	4	US-09-614-912-197	Sequence 197, App
999	70.6	4.1	1138	4	US-09-800-729-44	Sequence 44, Appli	1072	69.6	4.0	2296	3	US-08-496-841C-137	Sequence 137, App
1000	70.6	4.1	1138	4	US-09-800-729-44	Sequence 44, Appli	1073	69.6	4.0	2445	6	5215909-9	Patent No. 5215909
1001	70.6	4.1	1637	4	US-09-065-040-2	Sequence 178, App	1074	69.6	4.0	2445	6	5215909-9	Patent No. 5215909
c1002	70.6	4.1	2633	3	US-09-205-258-178	Sequence 51, Appli	c1075	69.6	4.0	118067	4	US-09-497-855A-32	Sequence 32, Appli
c1003	70.6	4.1	58597	4	US-09-949-016-11598	Sequence 13598, A	1076	69.4	4.0	146	4	US-09-621-976-16115	Sequence 16115, A
1004	70.6	4.1	670889	4	US-09-949-016-12505	Sequence 12505, A	c1077	69.4	4.0	394	2	US-08-623-906A-7	Sequence 7, Appli
1005	70.6	4.1	670890	4	US-09-949-016-14207	Sequence 14207, A	c1078	69.4	4.0	601	4	US-09-949-016-88565	Sequence 88565, A
c1006	70.4	4.1	601	4	US-09-949-016-21580	Sequence 21580, A	c1079	69.4	4.0	601	4	US-09-949-016-88565	Sequence 88565, A
c1007	70.4	4.1	601	4	US-09-949-016-127893	Sequence 127893,	1080	69.4	4.0	601	4	US-09-949-016-122967	Sequence 122967,
c1008	70.4	4.1	601	4	US-09-949-016-127894	Sequence 127894,	1081	69.4	4.0	601	4	US-09-949-016-123061	Sequence 123061,
c1009	70.4	4.1	601	4	US-09-949-016-128230	Sequence 128230,	1082	69.4	4.0	601	4	US-09-949-016-123155	Sequence 123155,
c1010	70.4	4.1	601	4	US-09-949-016-128231	Sequence 128231,	1083	69.4	4.0	601	4	US-09-949-016-123249	Sequence 123249,
c1011	70.4	4.1	601	4	US-09-949-016-130332	Sequence 130332,	1084	69.4	4.0	601	4	US-09-949-016-123343	Sequence 123343,
1012	70.4	4.1	601	4	US-09-949-016-130332	Sequence 130332,	1085	69.4	4.0	601	4	US-09-949-016-123385	Sequence 123385,
1013	70.4	4.1	601	4	US-09-949-016-135435	Sequence 135435,	1086	69.4	4.0	601	4	US-09-949-016-123427	Sequence 123427,
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1016	70.4	4.1	1359	3	US-09-205-258-74	Sequence 74, Appli	1089	69.4	4.0	601	4	US-09-949-016-123553	Sequence 123553,
1017	70.4	4.1	1359	3	US-09-387-574-11	Sequence 11, Appli	1090	69.4	4.0	601	4	US-09-949-016-123595	Sequence 123595,
1018	70.4	4.1	1439	3	US-09-668-096-11	Sequence 11, Appli	1091	69.4	4.0	601	4	US-09-949-016-123637	Sequence 123637,
1019	70.4	4.1	1439	3	US-09-656-556-167	Sequence 167, App	1092	69.4	4.0	601	4	US-09-949-016-123679	Sequence 123679,
1020	70.4	4.1	1439	3	US-09-072-596-162	Sequence 162, App	1093	69.4	4.0	601	4	US-09-949-016-123721	Sequence 123721,
1021	70.4	4.1	1439	3	US-09-072-967-167	Sequence 167, App	1094	69.4	4.0	601	4	US-09-949-016-123763	Sequence 123763,
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1023	70.4	4.1	1518	3	US-09-055-699-20	Sequence 20, Appli	1096	69.4	4.0	612	4	US-09-270-767-12063	Sequence 12063, A
1024	70.4	4.1	1518	3	US-09-273-565-20	Sequence 20, Appli	1097	69.4	4.0	2460	4	US-09-270-767-12063	Sequence 12063, A
1025	70.4	4.1	1518	3	US-09-565-538-20	Sequence 20, Appli	1098	69.4	4.0	4184	4	US-09-949-016-4495	Sequence 4495, Ap
1026	70.4	4.1	1518	3	US-09-661-468-20	Sequence 20, Appli	1099	69.4	4.0	12191	4	US-09-949-016-16237	Sequence 16237, A
1027	70.4	4.1	1518	4	US-09-976-165-20	Sequence 20, Appli	c1100	69.4	4.0	12703	4	US-09-949-016-16685	Sequence 16685, A
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1029	70.4	4.1	2636	2	US-08-820-170A-21	Sequence 21, Appli	c1102	69.4	4.0	152486	4	US-09-949-016-12869	Sequence 12869, A
1030	70.4	4.1	2636	3	US-09-055-699-21	Sequence 21, Appli	c1103	69.4	4.0	152486	4	US-09-949-016-12869	Sequence 12869, A
1031	70.4	4.1	2636	3	US-09-273-565-21	Sequence 21, Appli	c1104	69.4	4.0	275110	4	US-09-949-016-12706	Sequence 12706, A
1032	70.4	4.1	2636	3	US-09-565-538-21	Sequence 21, Appli	1105	69.4	4.0	283538	4	US-09-949-016-16070	Sequence 16070, A
1033	70.4	4.1	2636	4	US-09-661-468-21	Sequence 21, Appli	1106	69.2	4.0	291	1	US-09-949-016-13506	Sequence 13506, A
1034	70.4	4.1	2636	4	US-09-976-165-21	Sequence 21, Appli	1107	69.2	4.0	291	1	US-07-922-723A-7	Sequence 7, Appli
1035	70.4	4.1	6200	3	US-09-439-923-1	Sequence 1, Appli	1108	69.2	4.0	291	1	US-07-799-828C-7	Sequence 7, Appli
1036	70.4	4.1	6200	4	US-09-711-205A-1	Sequence 1, Appli	1109	69.2	4.0	291	1	US-08-074-275-7	Sequence 7, Appli
1037	70.2	4.0	334	2	US-08-623-906A-9	Sequence 9, Appli	1110	69.2	4.0	291	2	US-07-952-277A-7	Sequence 7, Appli
c1038	70.2	4.0	2149	4	US-09-949-016-456	Sequence 456, App	1111	69.2	4.0	538	3	US-09-056-556-180	Sequence 180, App
c1039	70.2	4.0	25659	4	US-09-949-016-15052	Sequence 15052, A	1112	69.2	4.0	538	4	US-09-072-596-175	Sequence 175, App
1040	70.2	4.0	34539	4	US-09-949-016-12226	Sequence 12226, A	1113	69.2	4.0	538	4	US-09-072-596-175	Sequence 175, App
1041	70.2	4.0	34540	4	US-09-949-016-13156	Sequence 13156, A	c1114	69.2	4.0	601	4	US-09-949-016-127891	Sequence 127891,
1042	70.2	4.0	45546	3	US-09-146-053-6	Sequence 6, Appli	c1115	69.2	4.0	601	4	US-09-949-016-127892	Sequence 127892,
c1043	70.2	4.0	100836	4	US-09-949-016-12871	Sequence 12871, A	c1116	69.2	4.0	601	4	US-09-949-016-128228	Sequence 128228,
c1044	70.2	4.0	100837	4	US-09-949-016-17063	Sequence 17063, A	c1117	69.2	4.0	601	4	US-09-949-016-128229	Sequence 128229,
1045	70.2	4.0	142783	4	US-09-949-016-15127	Sequence 15127, A	c1118	69.2	4.0	601	4	US-09-949-016-193621	Sequence 193621,
1046	70	4.0	102	4	US-09-949-016-15127	Sequence 15127, A	1119	69.2	4.0	2381	1	US-08-021-608D-9	Sequence 9, Appli
1047	70	4.0	249	4	US-09-621-976-191436	Sequence 191436, A	1120	69.2	4.0	2381	1	US-08-726-160-9	Sequence 9, Appli
1048	70	4.0	366	4	US-09-621-976-19144	Sequence 19144, A	1121	69.2	4.0	2381	5	PCT-US94-011782-9	Sequence 9, Appli
c1049	70	4.0	599	3	US-09-328-111-147	Sequence 147, App	1122	69.2	4.0	2384	1	US-08-021-608D-1	Sequence 1, Appli

1123	69.2	4.0	2384	1	US-08-726-160-1	Sequence 1, Appl1	cl196	68.8	4.0	789	4	US-09-759-143-32	Sequence 32, Appl1
1124	69.2	4.0	2384	5	US-08-726-160-1	Sequence 1, Appl1	cl197	68.8	4.0	789	4	US-09-651-236-32	Sequence 32, Appl1
1125	69.2	4.0	67911	4	US-09-949-016-16979	Sequence 16979, A	cl198	68.8	4.0	796	1	US-08-104-073-2	Sequence 2, Appl1
1126	69.2	4.0	191433	4	US-09-949-016-16144	Sequence 16144, A	cl199	68.8	4.0	986	4	US-09-328-475C-141	Sequence 141, App
1127	69.2	4.0	304533	4	US-09-949-016-15371	Sequence 15371, A	cl200	68.8	4.0	8283	4	US-09-949-016-12261	Sequence 12261, A
1128	69.2	4.0	304533	4	US-09-949-016-15372	Sequence 15372, A	cl201	68.8	4.0	86639	4	US-09-949-016-17397	Sequence 17397, A
1129	69	4.0	69	4	US-09-621-976-14105	Sequence 14105, A	cl202	68.8	4.0	113701	4	US-09-949-016-13214	Sequence 13214, A
1130	69	4.0	69	4	US-09-621-976-14869	Sequence 14869, A	cl203	68.8	4.0	152331	3	US-09-128-155-16	Sequence 16, Appl
1131	69	4.0	69	4	US-09-573-080A-447	Sequence 447, App	cl204	68.8	4.0	176373	3	US-09-128-155-17	Sequence 17, Appl
1132	69	4.0	141	3	US-08-737-078A-1	Sequence 1, Appl1	cl205	68.6	4.0	69	4	US-09-621-976-14838	Sequence 14838, A
1133	69	4.0	183	5	US-09-621-976-13606	Sequence 1, Appl1	cl206	68.6	4.0	75	4	US-09-621-976-15073	Sequence 15073, A
1134	69	4.0	487	3	US-09-621-976-13606	Sequence 13606, A	cl207	68.6	4.0	601	4	US-09-621-976-13937	Sequence 13937, A
1135	69	4.0	487	3	US-09-621-976-13606	Sequence 13606, A	cl208	68.6	4.0	601	4	US-09-949-016-193622	Sequence 193622, A
1136	69	4.0	536	2	US-08-341-568-1	Sequence 1, Appl1	cl209	68.6	4.0	601	4	US-09-949-016-193623	Sequence 193623, A
1137	69	4.0	536	2	US-08-341-568-1	Sequence 1, Appl1	cl210	68.6	4.0	601	4	US-09-949-016-193624	Sequence 193624, A
1138	69	4.0	601	4	US-09-949-016-123063	Sequence 123063, A	cl211	68.6	4.0	2438	4	US-09-393-634-4	Sequence 4, Appl1
1139	69	4.0	601	4	US-09-949-016-123063	Sequence 123063, A	cl212	68.6	4.0	152070	4	US-09-949-016-15402	Sequence 15402, A
1140	69	4.0	601	4	US-09-949-016-123157	Sequence 123157, A	cl213	68.6	4.0	268449	4	US-09-949-016-17244	Sequence 17244, A
1141	69	4.0	601	4	US-09-949-016-123251	Sequence 123251, A	cl214	68.4	3.9	70	4	US-09-621-976-13579	Sequence 13579, A
1142	69	4.0	601	4	US-09-949-016-123345	Sequence 123345, A	cl215	68.4	3.9	70	4	US-09-621-976-14750	Sequence 14750, A
1143	69	4.0	601	4	US-09-949-016-123387	Sequence 123387, A	cl216	68.4	3.9	75	4	US-09-621-976-12516	Sequence 12516, A
1144	69	4.0	601	4	US-09-949-016-123429	Sequence 123429, A	cl217	68.4	3.9	283	4	US-09-621-976-16989	Sequence 16989, A
1145	69	4.0	601	4	US-09-949-016-123471	Sequence 123471, A	cl218	68.4	3.9	341	4	US-09-621-976-16135	Sequence 16135, A
1146	69	4.0	601	4	US-09-949-016-123513	Sequence 123513, A	cl219	68.4	3.9	415	3	US-09-018-584A-18	Sequence 18, Appl
1147	69	4.0	601	4	US-09-949-016-123555	Sequence 123555, A	cl220	68.4	3.9	415	4	US-09-784-423-1	Sequence 18, Appl
1148	69	4.0	601	4	US-09-949-016-123597	Sequence 123597, A	cl221	68.4	3.9	601	4	US-09-949-016-45912	Sequence 45912, A
1149	69	4.0	601	4	US-09-949-016-123639	Sequence 123639, A	cl222	68.4	3.9	601	4	US-09-949-016-45913	Sequence 45913, A
1150	69	4.0	601	4	US-09-949-016-123681	Sequence 123681, A	cl223	68.4	3.9	1660	4	US-09-722-971-9	Sequence 9, Appl1
1151	69	4.0	601	4	US-09-949-016-123723	Sequence 123723, A	cl224	68.4	3.9	1878	3	US-09-732-025-1	Sequence 1, Appl1
1152	69	4.0	601	4	US-09-949-016-123765	Sequence 123765, A	cl225	68.4	3.9	10877	4	US-09-674-311-1	Sequence 1, Appl1
1153	69	4.0	629	3	US-09-385-982-389	Sequence 389, App	cl226	68.4	3.9	30337	4	US-09-949-016-13053	Sequence 13053, A
1154	69	4.0	1702	4	US-09-799-451-574	Sequence 574, App	cl227	68.4	3.9	38566	4	US-09-949-016-15271	Sequence 15271, A
1155	69	4.0	21862	4	US-09-949-016-17319	Sequence 17319, A	cl228	68.4	3.9	38566	4	US-09-949-016-15272	Sequence 15272, A
1156	69	4.0	27555	4	US-09-949-016-17466	Sequence 17466, A	cl229	68.4	3.9	45844	4	US-09-949-016-12967	Sequence 12967, A
1157	69	4.0	236364	4	US-09-949-016-15753	Sequence 15753, A	cl230	68.4	3.9	98202	4	US-09-949-016-16433	Sequence 16433, A
1158	69	4.0	393753	4	US-09-949-016-14573	Sequence 14573, A	cl231	68.4	3.9	113876	4	US-09-949-016-14828	Sequence 14828, A
1159	69	4.0	393753	4	US-09-949-016-14574	Sequence 14574, A	cl232	68.4	3.9	113876	4	US-09-949-016-14828	Sequence 14828, A
1160	69	4.0	818128	4	US-09-949-016-14546	Sequence 14546, A	cl233	68.4	3.9	115508	4	US-09-949-016-11800	Sequence 11800, A
1161	69	4.0	818128	4	US-09-949-016-14547	Sequence 14547, A	cl234	68.4	3.9	115508	4	US-09-949-016-14826	Sequence 14826, A
1162	69	4.0	818128	4	US-09-949-016-14548	Sequence 14548, A	cl235	68.4	3.9	121068	4	US-09-949-016-14827	Sequence 14827, A
1163	69	4.0	818128	4	US-09-949-016-14549	Sequence 14549, A	cl236	68.4	3.9	121068	4	US-09-949-016-14138	Sequence 14138, A
1164	69	4.0	818128	4	US-09-949-016-14550	Sequence 14550, A	cl237	68.4	3.9	288031	4	US-09-949-016-14864	Sequence 14864, A
1165	69	4.0	818128	4	US-09-949-016-14551	Sequence 14551, A	cl238	68.2	3.9	235	4	US-09-621-976-16550	Sequence 16550, A
1166	69	4.0	818128	4	US-09-949-016-14552	Sequence 14552, A	cl239	68.2	3.9	412	3	US-09-018-584A-22	Sequence 22, Appl
1167	69	4.0	818128	4	US-09-949-016-14553	Sequence 14553, A	cl240	68.2	3.9	412	4	US-09-784-423-2	Sequence 22, Appl
1168	69	4.0	818128	4	US-09-949-016-14554	Sequence 14554, A	cl241	68.2	3.9	601	4	US-09-949-016-124397	Sequence 124397, A
1169	69	4.0	818128	4	US-09-949-016-14555	Sequence 14555, A	cl242	68.2	3.9	601	4	US-09-949-016-124398	Sequence 124398, A
1170	69	4.0	818128	4	US-09-949-016-14556	Sequence 14556, A	cl243	68.2	3.9	647	4	US-09-495-050A-54	Sequence 54, Appl
1171	69	4.0	818128	4	US-09-949-016-14557	Sequence 14557, A	cl244	68.2	3.9	1298	3	US-08-971-089-1	Sequence 1, Appl1
1172	69	4.0	818128	4	US-09-949-016-14558	Sequence 14558, A	cl245	68.2	3.9	1525	3	US-09-157-603-4	Sequence 4, Appl1
1173	69	4.0	818128	4	US-09-949-016-14559	Sequence 14559, A	cl246	68.2	3.9	1525	3	US-09-587-436-4	Sequence 4, Appl1
1174	69	4.0	818128	4	US-09-949-016-14560	Sequence 14560, A	cl247	68.2	3.9	1525	3	US-08-927-165A-4	Sequence 4, Appl1
1175	69	4.0	818128	4	US-09-949-016-14561	Sequence 14561, A	cl248	68.2	3.9	1578	3	US-09-416-050A-1	Sequence 1, Appl1
1176	69	4.0	818128	4	US-09-949-016-14562	Sequence 14562, A	cl249	68.2	3.9	1578	3	US-09-664-800-1	Sequence 1, Appl1
1177	69	4.0	818128	4	US-09-949-016-14563	Sequence 14563, A	cl250	68.2	3.9	1578	3	US-09-665-309-1	Sequence 1, Appl1
1178	69	4.0	818128	4	US-09-949-016-14564	Sequence 14564, A	cl251	68.2	3.9	1578	3	US-09-661-569-1	Sequence 1, Appl1
1179	69	4.0	818128	4	US-09-949-016-14565	Sequence 14565, A	cl252	68.2	3.9	1958	3	US-08-665-034A-3	Sequence 3, Appl1
1180	69	4.0	818128	4	US-09-949-016-14566	Sequence 14566, A	cl253	68.2	3.9	21193	4	US-09-949-016-17215	Sequence 17215, A
1181	68.8	4.0	389	4	US-09-513-999C-420	Sequence 420, App	cl254	68.2	3.9	31391	4	US-09-949-016-17200	Sequence 17200, A
1182	68.8	4.0	601	4	US-09-949-016-20852	Sequence 20852, A	cl255	68.2	3.9	42989	4	US-09-949-016-12291	Sequence 12291, A
1183	68.8	4.0	601	4	US-09-949-016-110199	Sequence 110199, A	cl256	68.2	3.9	42989	4	US-09-949-016-15428	Sequence 15428, A
1184	68.8	4.0	601	4	US-09-949-016-15266	Sequence 15266, A	cl257	68.2	3.9	113042	4	US-09-949-016-12343	Sequence 12343, A
1185	68.8	4.0	789	3	US-09-020-956-32	Sequence 32, Appl	cl258	68.2	3.9	113042	4	US-09-949-016-15246	Sequence 15246, A
1186	68.8	4.0	789	3	US-09-030-607-32	Sequence 32, Appl	cl259	68	3.9	69	1	US-08-702-344-7	Sequence 7, Appl
1187	68.8	4.0	789	3	US-09-439-313-32	Sequence 32, Appl	cl260	68	3.9	69	1	US-08-702-344-22	Sequence 22, Appl
1188	68.8	4.0	789	3	US-09-352-616A-32	Sequence 32, Appl	cl261	68	3.9	76	4	US-09-621-976-12446	Sequence 12446, A
1189	68.8	4.0	789	3	US-09-232-149A-32	Sequence 32, Appl	cl262	68	3.9	153	4	US-09-621-976-17451	Sequence 17451, A
1190	68.8	4.0	789	3	US-09-159-813-32	Sequence 32, Appl	cl263	68	3.9	214	4	US-09-621-976-9843	Sequence 9843, Ap
1191	68.8	4.0	789	4	US-09-636-215-32	Sequence 32, Appl	cl264	68	3.9	354	4	US-09-621-976-16145	Sequence 16145, A
1192	68.8	4.0	789	4	US-09-685-166A-32	Sequence 32, Appl	cl265	68	3.9	601	4	US-09-949-016-82607	Sequence 82607, A
1193	68.8	4.0	789	4	US-09-115-453-32	Sequence 32, Appl	cl266	68	3.9	601	4	US-09-949-016-162332	Sequence 162332, A
1194	68.8	4.0	789	4	US-09-688-489-32	Sequence 32, Appl	cl267	68	3.9	601	4	US-09-949-016-162333	Sequence 162333, A
1195	68.8	4.0	789	4	US-09-679-426-32	Sequence 32, Appl	cl268	68	3.9	601	4	US-09-949-016-162334	Sequence 162334, A

1269	68	3.9	601	4	US-09-949-016-162335	Sequence 162335,	c1342	67.8	3.9	64377	4	US-09-949-016-15212	Sequence 15212, A
1270	68	3.9	1486	4	US-09-461-325-73	Sequence 73, Appl	c1343	67.8	3.9	64377	4	US-09-949-016-15213	Sequence 15213, A
1271	68	3.9	1486	4	US-10-012-542-73	Sequence 73, Appl	c1344	67.8	3.9	64377	4	US-09-949-016-15214	Sequence 15214, A
1272	68	3.9	1486	4	US-10-115-123-73	Sequence 73, Appl	c1345	67.8	3.9	64377	4	US-09-949-016-15215	Sequence 15215, A
1273	68	3.9	1709	4	US-09-426-783-6	Sequence 29, Appl	c1346	67.8	3.9	64377	4	US-09-949-016-15216	Sequence 15216, A
1274	68	3.9	1766	4	US-09-904-615-29	Sequence 6, Appl	c1347	67.8	3.9	113701	4	US-09-949-016-13214	Sequence 13214, A
1275	68	3.9	1876	4	US-09-324-258-1	Sequence 1, Appl	c1348	67.8	3.9	389504	4	US-09-949-016-11774	Sequence 11774, A
1276	68	3.9	2028	4	US-09-426-783-9	Sequence 9, Appl	1349	67.6	3.9	333	4	US-09-248-766A-11241	Sequence 11241, A
1277	68	3.9	2187	3	US-09-127-2198-2	Sequence 2, Appl	1350	67.6	3.9	980	3	US-09-171-209-8	Sequence 8, Appl
1278	68	3.9	2329	4	US-09-800-729-11	Sequence 11, Appl	1351	67.6	3.9	1050	4	US-09-482-273-58	Sequence 58, Appl
1279	68	3.9	3636	3	US-09-074-579-2	Sequence 2, Appl	1352	67.6	3.9	2964	4	US-09-578-063-25	Sequence 25, Appl
1280	68	3.9	3636	3	US-09-388-774-2	Sequence 2, Appl	1353	67.6	3.9	3116	4	US-09-976-594-283	Sequence 283, App
c1281	68	3.9	14761	4	US-09-949-016-14181	Sequence 14181, A	1354	67.6	3.9	3137	4	US-09-620-312D-714	Sequence 714, App
c1282	68	3.9	14823	4	US-09-949-016-12124	Sequence 12124, A	c1355	67.6	3.9	19601	4	US-09-949-016-15629	Sequence 15629, A
1283	68	3.9	16549	4	US-09-949-016-16456	Sequence 16456, A	c1356	67.6	3.9	23907	4	US-09-949-016-15329	Sequence 15329, A
1284	68	3.9	30000	4	US-10-007-010-10	Sequence 10, Appl	1357	67.6	3.9	31111	4	US-09-949-016-15628	Sequence 15628, A
c1285	68	3.9	34534	4	US-09-949-016-15141	Sequence 15141, A	1358	67.6	3.9	39433	4	US-09-949-016-12014	Sequence 12014, A
1286	68	3.9	53562	4	US-09-949-016-16286	Sequence 16286, A	c1359	67.6	3.9	41743	4	US-09-949-016-13796	Sequence 13796, A
1287	68	3.9	101349	4	US-09-949-016-17433	Sequence 17433, A	c1360	67.6	3.9	96327	4	US-09-949-016-16541	Sequence 16541, A
1288	68	3.9	174029	4	US-09-949-016-12610	Sequence 12610, A	1361	67.6	3.9	225127	4	US-09-949-016-16480	Sequence 16480, A
1289	68	3.9	174030	4	US-09-949-016-13880	Sequence 13880, A	c1362	67.6	3.9	260247	4	US-09-949-016-13358	Sequence 13358, A
c1290	68	3.9	193169	4	US-09-949-016-15091	Sequence 15091, A	1363	67.4	3.9	69	4	US-09-621-976-13006	Sequence 12006, A
1291	67.8	3.9	115	4	US-09-621-976-14003	Sequence 14003, A	1364	67.4	3.9	91	4	US-09-621-976-14925	Sequence 14925, A
1292	67.8	3.9	146	4	US-09-621-976-16695	Sequence 16695, A	1365	67.4	3.9	146	4	US-09-621-976-16686	Sequence 16686, A
1293	67.8	3.9	601	4	US-09-949-016-122965	Sequence 122965, A	1366	67.4	3.9	250	4	US-09-621-976-17371	Sequence 17371, A
1294	67.8	3.9	601	4	US-09-949-016-122966	Sequence 122966, A	1367	67.4	3.9	601	4	US-09-949-016-69770	Sequence 69770, A
1295	67.8	3.9	601	4	US-09-949-016-123059	Sequence 123059, A	1368	67.4	3.9	601	4	US-09-949-016-69771	Sequence 69771, A
1296	67.8	3.9	601	4	US-09-949-016-123060	Sequence 123060, A	1369	67.4	3.9	601	4	US-09-949-016-122968	Sequence 122968, A
1297	67.8	3.9	601	4	US-09-949-016-123153	Sequence 123153, A	1370	67.4	3.9	601	4	US-09-949-016-123062	Sequence 123062, A
1298	67.8	3.9	601	4	US-09-949-016-123154	Sequence 123154, A	1371	67.4	3.9	601	4	US-09-949-016-123156	Sequence 123156, A
1299	67.8	3.9	601	4	US-09-949-016-123247	Sequence 123247, A	1372	67.4	3.9	601	4	US-09-949-016-123250	Sequence 123250, A
1300	67.8	3.9	601	4	US-09-949-016-123248	Sequence 123248, A	1373	67.4	3.9	601	4	US-09-949-016-123344	Sequence 123344, A
1301	67.8	3.9	601	4	US-09-949-016-123341	Sequence 123341, A	1374	67.4	3.9	601	4	US-09-949-016-123386	Sequence 123386, A
1302	67.8	3.9	601	4	US-09-949-016-123342	Sequence 123342, A	1375	67.4	3.9	601	4	US-09-949-016-123428	Sequence 123428, A
1303	67.8	3.9	601	4	US-09-949-016-123383	Sequence 123383, A	1376	67.4	3.9	601	4	US-09-949-016-123470	Sequence 123470, A
1304	67.8	3.9	601	4	US-09-949-016-123384	Sequence 123384, A	1377	67.4	3.9	601	4	US-09-949-016-123512	Sequence 123512, A
1305	67.8	3.9	601	4	US-09-949-016-123425	Sequence 123425, A	1378	67.4	3.9	601	4	US-09-949-016-123554	Sequence 123554, A
1306	67.8	3.9	601	4	US-09-949-016-123426	Sequence 123426, A	1379	67.4	3.9	601	4	US-09-949-016-123596	Sequence 123596, A
1307	67.8	3.9	601	4	US-09-949-016-123467	Sequence 123467, A	1380	67.4	3.9	601	4	US-09-949-016-123638	Sequence 123638, A
1308	67.8	3.9	601	4	US-09-949-016-123468	Sequence 123468, A	1381	67.4	3.9	601	4	US-09-949-016-123680	Sequence 123680, A
1309	67.8	3.9	601	4	US-09-949-016-123509	Sequence 123509, A	1382	67.4	3.9	601	4	US-09-949-016-123722	Sequence 123722, A
1310	67.8	3.9	601	4	US-09-949-016-123510	Sequence 123510, A	1383	67.4	3.9	601	4	US-09-949-016-123764	Sequence 123764, A
1311	67.8	3.9	601	4	US-09-949-016-123551	Sequence 123551, A	1384	67.4	3.9	601	4	US-09-805-545A-19	Sequence 19, Appl
1312	67.8	3.9	601	4	US-09-949-016-123552	Sequence 123552, A	1385	67.4	3.9	760	4	US-09-205-258-232	Sequence 232, App
1313	67.8	3.9	601	4	US-09-949-016-123593	Sequence 123593, A	1386	67.4	3.9	1166	5	PCT-US96-12129B-1	Sequence 1, Appl
1314	67.8	3.9	601	4	US-09-949-016-123594	Sequence 123594, A	1387	67.4	3.9	1485	3	US-09-372-422A-39	Sequence 39, Appl
1315	67.8	3.9	601	4	US-09-949-016-123635	Sequence 123635, A	c1388	67.4	3.9	1972	4	US-09-403-861A-1	Sequence 1, Appl
1316	67.8	3.9	601	4	US-09-949-016-123636	Sequence 123636, A	1389	67.4	3.9	2091	3	US-09-813-818-1	Sequence 1, Appl
1317	67.8	3.9	601	4	US-09-949-016-123677	Sequence 123677, A	1390	67.4	3.9	2091	3	US-10-199-333-1	Sequence 1, Appl
1318	67.8	3.9	601	4	US-09-949-016-123678	Sequence 123678, A	1391	67.4	3.9	2203	4	US-09-801-861-1	Sequence 1, Appl
1319	67.8	3.9	601	4	US-09-949-016-123719	Sequence 123719, A	1392	67.4	3.9	2203	4	US-10-224-562-1	Sequence 1, Appl
1320	67.8	3.9	601	4	US-09-949-016-123720	Sequence 123720, A	1393	67.4	3.9	2218	4	US-09-205-258-103	Sequence 103, App
1321	67.8	3.9	601	4	US-09-949-016-123761	Sequence 123761, A	1394	67.4	3.9	2442	4	US-09-575-081B-3	Sequence 3, Appl
1322	67.8	3.9	601	4	US-09-949-016-123762	Sequence 123762, A	1395	67.4	3.9	2718	4	US-09-667-135-1	Sequence 1, Appl
1323	67.8	3.9	991	3	US-08-924-747-25	Sequence 25, Appl	c1396	67.4	3.9	11890	4	US-09-949-016-13794	Sequence 13794, A
1324	67.8	3.9	991	3	US-09-247-373B-25	Sequence 25, Appl	c1397	67.4	3.9	39433	4	US-09-949-016-12014	Sequence 12014, A
1325	67.8	3.9	991	3	US-09-296-715-25	Sequence 25, Appl	c1398	67.4	3.9	258775	4	US-09-949-016-16435	Sequence 16435, A
1326	67.8	3.9	1558	3	US-09-123-030-7	Sequence 7, Appl	1399	67.2	3.9	81	4	US-09-513-998C-17324	Sequence 17324, A
1327	67.8	3.9	1965	4	US-09-482-273-27	Sequence 27, Appl	1400	67.2	3.9	233	4	US-09-621-976-16559	Sequence 16559, A
1328	67.8	3.9	1976	4	US-09-920-759-10	Sequence 10, Appl	c1401	67.2	3.9	234	4	US-09-621-976-16557	Sequence 16557, A
1329	67.8	3.9	2483	4	US-09-205-258-68	Sequence 68, Appl	c1402	67.2	3.9	509	3	US-09-603-607-202	Sequence 202, App
c1330	67.8	3.9	32379	4	US-09-949-016-15217	Sequence 15217, A	c1403	67.2	3.9	509	3	US-09-439-313-202	Sequence 202, App
c1331	67.8	3.9	32379	4	US-09-949-016-15218	Sequence 15218, A	c1404	67.2	3.9	509	3	US-09-352-616A-202	Sequence 202, App
c1332	67.8	3.9	32379	4	US-09-949-016-15219	Sequence 15219, A	c1405	67.2	3.9	509	3	US-09-233-149A-202	Sequence 202, App
c1333	67.8	3.9	32379	4	US-09-949-016-15220	Sequence 15220, A	c1406	67.2	3.9	509	4	US-09-159-812-202	Sequence 202, App
c1334	67.8	3.9	32379	4	US-09-949-016-15221	Sequence 15221, A	c1407	67.2	3.9	509	4	US-09-636-215-202	Sequence 202, App
c1335	67.8	3.9	32379	4	US-09-949-016-15222	Sequence 15222, A	c1408	67.2	3.9	509	4	US-09-685-166A-202	Sequence 202, App
c1336	67.8	3.9	32379	4	US-09-949-016-15223	Sequence 15223, A	c1409	67.2	3.9	509	4	US-09-115-453-202	Sequence 202, App
c1337	67.8	3.9	32379	4	US-09-949-016-15224	Sequence 15224, A	c1410	67.2	3.9	509	4	US-09-688-489-202	Sequence 202, App
c1338	67.8	3.9	32379	4	US-09-949-016-15225	Sequence 15225, A	c1411	67.2	3.9	509	4	US-09-679-426-202	Sequence 202, App
c1339	67.8	3.9	32379	4	US-09-949-016-15226	Sequence 15226, A	c1412	67.2	3.9	509	4	US-09-759-143-202	Sequence 202, App
c1340	67.8	3.9	35064	4	US-09-949-016-12778	Sequence 12778, A	c1413	67.2	3.9	509	4	US-09-651-236-202	Sequence 202, App
c1341	67.8	3.9	35065	4	US-09-949-016-13196	Sequence 13196, A	1414	67.2	3.9	601	4	US-09-949-016-20851	Sequence 20851, A



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RESULT 2
US-09-621-976-13367
; Sequence 13367, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13367
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 229
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-13367

Query Match          12.0%; Score 208; DB 4; Length 342;
Best Local Similarity 99.5%; Pred. No. 1.9e-31;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1431 GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 1490
DB 134  GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 193

QY 1491 CTCTGCGATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCAGACT 1550
DB 194  CTCTGCGATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCAGACT 253

QY 1551 CCCTCCTTTAAACACCACTCTCATCACTAATCTCAGCCCTTGCCTTGAATAAAGCT 1610
DB 254  CCCTCCTTTAAACACCACTCTCATCACTAATCTCAGCCCTTGCCTTGAATAAAGCT 313

QY 1611 TAGCTGCCCCACAAAAA 1639
DB 314  TAGCTGCCCCACAAAAA 342

RESULT 3
US-09-621-976-13384
; Sequence 13384, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13384
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13384

Query Match          11.8%; Score 204; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1431 GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 1490
DB 134  GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 193

RESULT 4
US-09-621-976-13398
; Sequence 13398, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13398
; LENGTH: 326
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13398

Query Match          10.9%; Score 189.8; DB 4; Length 326;
Best Local Similarity 97.4%; Pred. No. 6.4e-28;
Matches 188; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1431 GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 1490
DB 134  GAATTTTAATCCAGCTGGGTTTCATCACTGGGATGCCATAAAACAGGACGAGAGG 193

QY 1491 CTCTGCGATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCAGACT 1550
DB 194  CTCTGCGATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCAGACT 253

QY 1551 CCCTCCTTTAAACACCACTCTCATCACTAATCTCAGCCCTTGCCTTGAATAAAGCT 1610
DB 254  CCCTCCTTTAAACACCACTCTCATCACTAATCTCAGCCCTTGCCTTGAATAAAGCT 313

QY 1611 TAGCTGCCCCAC 1623
DB 314  TAGCTGCCCCACA 326

RESULT 5
US-09-621-976-13428
; Sequence 13428, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13428
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-621-976-13428

Query Match 9.4%; Score 163.8; DB 4; Length 365;  
Best Local Similarity 87.0%; Pred. No. 7.5e-23;  
Matches 180; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1431 GAATTTTAAATCAAGCTGGGTTTCATCACTGGGATGCCATAAACAAGGACCCAGAGAAG 1490  
|||  
Db 159 GAACTCTGAGAGCTCTCTCGGGATGTTTAACTTTTGACACTTTCTGGAAGGACCCAGAGAAG 218  
|||

QY 1491 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 1550  
|||  
Db 219 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 278  
|||

QY 1551 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 1610  
|||  
Db 279 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 338  
|||

QY 1611 TAGCTGCCCCACAAAAA 1637  
|||  
Db 339 TAGCTGCCCCACAAAAA 365  
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## RESULT 6

US-09-621-976-13359  
; Sequence 13359, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13359  
; LENGTH: 293  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-13359

Query Match 9.2%; Score 160; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.8e-22;  
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1431 GAATTTTAAATCAAGCTGGGTTTCATCACTGGGATGCCATAAACAAGGACCCAGAGAAG 1490  
|||  
Db 134 GAATTTTAAATCAAGCTGGGTTTCATCACTGGGATGCCATAAACAAGGACCCAGAGAAG 193  
|||

QY 1491 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 1550  
|||  
Db 194 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 253  
|||

QY 1551 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCC 1590  
|||  
Db 254 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCC 293  
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## RESULT 7

US-09-621-976-13392  
; Sequence 13392, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm  
; SEQ ID NO 13392  
; LENGTH: 361  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-13392

Query Match 9.2%; Score 158.8; DB 4; Length 361;  
Best Local Similarity 86.6%; Pred. No. 7e-22;  
Matches 175; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1431 GAATTTTAAATCAAGCTGGGTTTCATCACTGGGATGCCATAAACAAGGACCCAGAGAAG 1490  
|||  
Db 160 GAACTCTGAGAGCTCTCTCGGGATGTTTAACTTTTGACACTTTCTGGAAGGACCCAGAGAAG 219  
|||

QY 1491 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 1550  
|||  
Db 220 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 279  
|||

QY 1551 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 1610  
|||  
Db 280 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 339  
|||

QY 1611 TAGCTGCCCCACAAAAA 1632  
|||  
Db 340 TAGCTGCCCCACAAAAA 361  
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## RESULT 8

US-09-621-976-13407  
; Sequence 13407, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13407  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 254..256  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-13407

Query Match 8.8%; Score 151.8; DB 4; Length 357;  
Best Local Similarity 84.8%; Pred. No. 1.6e-20;  
Matches 168; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1431 GAATTTTAAATCAAGCTGGGTTTCATCACTGGGATGCCATAAACAAGGACCCAGAGAAG 1490  
|||  
Db 160 GAACTCTGAGAGCTCTCTCGGGATGTTTAACTTTTGACACTTTCTGGAAGGACCCAGAGAAG 219  
|||

QY 1491 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCACACT 1550  
|||  
Db 220 CTCTCGCATCCCGTGACCTCCAGACAAGGAGCCANNNGATTGGATGGGAGCCCCACACT 279  
|||

QY 1551 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 1610  
|||  
Db 280 CCCTCCTTAAACACACACCTCTCATCACTAATCTCAGCCCTTGGCCCTTGAATAAACCT 339  
|||

QY 1611 TAGCTGCCCCACAAAAA 1628  
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Db 340 TAGCTGCCCCACAAAAA 357  
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; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-16

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Matches 137; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1561 AACACACCCCTCTCATCTCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCC 1620
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QY 1621 ACAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1680
Db 115 CNAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 56

QY 1681 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1734
Db 55 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 13
US-09-713-550-16/c
; Sequence 16, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-16

Query Match
Best Local Similarity 7.3%; Score 126.2; DB 4; Length 396;
Matches 137; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1561 AACACACCCCTCTCATCTCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCC 1620
Db 175 ANNNCCCCCTTTNTTTTTTTTTTTTTTTTNNCCNNNNNTNTNAAAAAATTTNNCCCCC 116

QY 1621 ACAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1680
Db 115 CNAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 56

QY 1681 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1734
Db 55 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 14
US-09-825-294-16/c
; Sequence 16, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
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; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-16

Query Match
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Matches 137; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 1621 ACAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1680
Db 115 CNAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 56

QY 1681 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1734
Db 55 AAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 15
US-09-970-966-16/c
; Sequence 16, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesch, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 114, 121, 122, 123, 127, 134, 136, 138, 140, 141, 142, 143,
; LOCATION: 144, 148, 163, 166, 172, 173, 174, 176, 177, 183, 184, 185,
; LOCATION: 187, 195, 198, 199, 202, 203, 206, 213, 214, 215, 216,
; LOCATION: 217, 218, 219, 223, 225, 226, 227, 229, 230, 236, 238
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 239, 252, 256, 257, 261, 262, 268, 269, 273, 278, 280, 288,
; LOCATION: 289, 290, 292, 293, 303, 312, 325, 327, 333, 335, 336, 341,
; LOCATION: 342, 347, 354, 359, 365, 371, 383, 384, 386, 388, 391
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-16

Query Match
Best Local Similarity 7.3%; Score 126.2; DB 4; Length 396;
Matches 137; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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Qy	1621	ACAAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1680
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Qy	1681	AAAAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1734
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#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
146	1734	100.0	1734	14	US-10-066-269-105
514	1734	100.0	1734	14	Sequence 105, App
520	1734	100.0	1734	15	Sequence 149, App
563	1734	100.0	1734	15	Sequence 155, App
564	1734	100.0	1734	15	Sequence 149, App
565	1734	100.0	1734	15	Sequence 149, App
571	1734	100.0	1734	15	Sequence 149, App
584	1734	100.0	1734	15	Sequence 149, App
590	1734	100.0	1734	15	Sequence 149, App
616	1734	100.0	1734	16	Sequence 201, App
686	1734	100.0	1734	16	Sequence 51, Appl
762	1734	100.0	1734	16	Sequence 51, Appl

767	1734	100.0	1734	16	US-10-223-081-149	Sequence 149, App
805	1734	100.0	1734	16	US-10-223-082-149	Sequence 149, App
837	1734	100.0	1734	17	US-10-305-654-149	Sequence 149, App
846	1734	100.0	1734	17	US-10-081-056-149	Sequence 149, App
858	1734	100.0	1734	19	US-10-972-317-51	Sequence 51, Appl
859	1244.4	71.8	1441	14	US-10-050-704-14	Sequence 14, Appl
860	1244.4	71.8	1441	18	US-10-798-512-14	Sequence 14, Appl
861	209	12.1	410	10	US-09-803-719-37	Sequence 37, Appl
862	170.4	9.8	349	10	US-09-764-891-190	Sequence 190, App
863	156.4	9.0	587	10	US-09-918-995-15078	Sequence 15078, App
864	132	7.6	3673778	16	US-10-312-841-1	Sequence 1, Appl
865	128.2	7.4	313	18	US-10-021-323-13390	Sequence 13390, A
866	127.8	7.4	472	18	US-10-425-115-88743	Sequence 88743, A
867	126.8	7.3	597	18	US-10-021-323-138	Sequence 138, App
868	126.2	7.3	396	9	US-09-825-294-16	Sequence 16, Appl
869	126.2	7.3	396	9	US-09-970-966-16	Sequence 16, Appl
870	126.2	7.3	396	15	US-10-212-677-16	Sequence 16, Appl
871	126.2	7.3	396	17	US-10-361-811-16	Sequence 16, Appl
872	126.2	7.3	396	17	US-10-369-186-16	Sequence 16, Appl
873	125.4	7.2	434	18	US-10-437-963-44960	Sequence 44960, A
874	125.2	7.2	574	18	US-10-021-323-7391	Sequence 7391, App
875	125	7.2	602	18	US-10-370-715B-283	Sequence 283, App
876	124.6	7.2	1309	18	US-10-425-115-55991	Sequence 55991, A
877	123.8	7.1	447	18	US-10-425-115-148961	Sequence 148961, A
878	123.6	7.1	2487	10	US-09-746-783-165	Sequence 165, App
879	123.6	7.1	5586	17	US-10-257-166-86	Sequence 86, Appl
880	123.6	7.1	15832	14	US-10-239-676-106	Sequence 106, App
881	123.6	7.1	15832	15	US-10-311-455-1316	Sequence 1316, App
882	123.6	7.1	15832	15	US-10-240-453-118	Sequence 118, App
883	123.2	7.1	8946	15	US-10-311-455-884	Sequence 884, App
884	123.2	7.1	3673778	16	US-10-312-841-2	Sequence 2, Appl
885	123	7.1	392	10	US-09-814-353-2829	Sequence 2829, App
886	123	7.1	392	10	US-09-814-353-9159	Sequence 9159, App
887	123	7.1	524	18	US-10-425-115-11283	Sequence 11283, A
888	122.6	7.1	499	18	US-10-425-115-133060	Sequence 133060, A
889	122.6	7.1	558	18	US-10-425-115-112505	Sequence 112505, A
890	122.2	7.0	554	18	US-10-021-323-4489	Sequence 4489, App
891	122.2	7.0	2924	15	US-10-205-219-103	Sequence 103, App
892	122.2	7.0	3260	18	US-10-437-963-80144	Sequence 80144, A
893	121.8	7.0	404	10	US-09-803-719-335	Sequence 335, App
894	121.8	7.0	529	18	US-10-425-115-171364	Sequence 171364, A
895	121.8	7.0	686	9	US-09-873-536-364	Sequence 364, App
896	121.8	7.0	1201	17	US-10-115-831-152	Sequence 152, App
897	121.8	7.0	1579	17	US-10-108-260A-1142	Sequence 1142, App
898	121.8	7.0	1608	18	US-10-723-860-7385	Sequence 7385, App
899	121.8	7.0	11416	15	US-10-311-455-91	Sequence 91, Appl
900	121.8	7.0	11416	17	US-10-221-613-19	Sequence 19, Appl
901	121.8	7.0	21354	17	US-10-221-714A-512	Sequence 512, App
902	121.6	7.0	389	18	US-10-437-963-96437	Sequence 96437, A
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908	121	7.0	277	17	US-10-085-783A-16143	Sequence 16143, A
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910	121	7.0	490	18	US-10-021-323-16197	Sequence 16197, A
911	121	7.0	555	18	US-10-425-115-90821	Sequence 90821, A
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913	120.8	7.0	810	10	US-09-814-353-12127	Sequence 12127, App
914	120.8	7.0	2235	19	US-10-887-553A-987	Sequence 987, App
915	120.6	7.0	480	18	US-10-021-323-6568	Sequence 6568, App
916	120.6	7.0	501	10	US-09-814-353-18888	Sequence 18888, A
917	120.6	7.0	547	18	US-10-437-963-20806	Sequence 20806, A
918	120.6	7.0	761	18	US-10-425-115-17031	Sequence 17031, A
919	120.6	7.0	1404	18	US-10-425-115-54171	Sequence 54171, A
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921	120.6	7.0	5306	15	US-10-311-455-484	Sequence 484, App
922	120.6	7.0	6486	18	US-10-433-793-80	Sequence 80, Appl
923	120.6	7.0	8899	15	US-10-311-455-810	Sequence 810, App
924	120.6	7.0	8899	17	US-10-257-166-156	Sequence 156, App
925	120.4	6.9	490	18	US-10-357-930-57078	Sequence 57078, A
926	120.4	6.9	503	18	US-10-425-115-104818	Sequence 104818, A

927	120.4	6.9	1792	18	US-10-425-115-73188	Sequence 73188, A	1000	119	6.9	3583	18	US-10-723-860-6471	Sequence 6471, Ap
928	120.4	6.9	3950	18	US-10-723-860-5594	Sequence 5594, Ap	c1001	118.8	6.9	508	18	US-10-021-323-5403	Sequence 5403, Ap
929	120.2	6.9	510	18	US-10-437-963-1928	Sequence 1928, Ap	c1002	118.8	6.9	522	18	US-10-021-323-1498	Sequence 1498, Ap
930	120.2	6.9	559	18	US-10-021-323-17353	Sequence 17353, A	1003	118.8	6.9	546	18	US-10-021-323-6273	Sequence 6273, Ap
931	120.2	6.9	1074	9	US-09-764-864-184	Sequence 184, App	1004	118.8	6.9	565	18	US-10-425-115-110392	Sequence 110392, A
932	120.2	6.9	1294	18	US-10-425-115-72107	Sequence 72107, A	1005	118.8	6.9	605	18	US-10-425-115-76155	Sequence 76155, A
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934	120.2	6.9	4080	17	US-10-424-599-115754	Sequence 115754, A	c1007	118.8	6.9	684	18	US-10-425-115-110165	Sequence 110165, A
935	120	6.9	396	18	US-10-425-115-93010	Sequence 93010, A	c1008	118.8	6.9	805	10	US-09-814-353-2363	Sequence 2363, Ap
936	120	6.9	524	17	US-10-424-598-11691	Sequence 11691, A	c1009	118.8	6.9	805	10	US-09-814-353-8701	Sequence 8701, Ap
937	120	6.9	545	18	US-10-021-323-6099	Sequence 6099, Ap	1010	118.8	6.9	836	18	US-10-767-795-61	Sequence 61, Appl
938	120	6.9	580	18	US-10-357-930-58036	Sequence 58036, A	1011	118.8	6.9	1638	17	US-10-424-599-96402	Sequence 96402, A
939	120	6.9	1769	14	US-10-234-432-45	Sequence 45, Appl	1012	118.8	6.9	1816	18	US-10-723-860-7371	Sequence 7371, Ap
940	120	6.9	7061	17	US-10-311-455-969	Sequence 969, App	c1013	118.8	6.9	5198	15	US-10-311-455-252	Sequence 252, App
941	120	6.9	7061	17	US-10-221-613-147	Sequence 147, App	c1014	118.8	6.9	6171	15	US-10-311-455-761	Sequence 761, App
942	120	6.9	15518	15	US-10-311-455-2145	Sequence 2145, Ap	c1015	118.6	6.8	237	9	US-09-834-975-725	Sequence 725, App
943	120	6.9	15518	15	US-10-240-485-177	Sequence 177, App	1016	118.6	6.8	305	17	US-10-231-956A-85	Sequence 85, Appl
944	119.8	6.9	425	10	US-09-814-353-15543	Sequence 15543, A	1017	118.6	6.8	394	18	US-10-357-930-13555	Sequence 13555, A
945	119.8	6.9	464	15	US-10-106-698-307	Sequence 307, App	1018	118.6	6.8	408	18	US-10-357-930-34697	Sequence 34697, A
946	119.8	6.9	560	18	US-10-021-323-12602	Sequence 12602, A	1019	118.6	6.8	408	18	US-10-357-930-43554	Sequence 43554, A
947	119.8	6.9	621	17	US-10-424-599-92208	Sequence 92208, A	1020	118.6	6.8	500	18	US-10-425-115-170711	Sequence 170711, A
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950	119.8	6.9	3275	9	US-09-738-973-151	Sequence 151, App	c1023	118.6	6.8	584	18	US-10-021-323-6395	Sequence 6395, Ap
951	119.8	6.9	3275	9	US-09-854-133-151	Sequence 151, App	1024	118.6	6.8	698	9	US-09-764-846-131	Sequence 131, App
952	119.8	6.9	3775	15	US-10-144-649A-151	Sequence 151, App	1025	118.6	6.8	698	14	US-10-091-483-131	Sequence 131, App
953	119.8	6.9	7765	15	US-09-814-353-19180	Sequence 19180, A	1026	118.6	6.8	1494	13	US-10-062-254-259	Sequence 259, App
954	119.8	6.9	7765	14	US-10-198-846-9735	Sequence 9735, Ap	1027	118.6	6.8	1781	18	US-10-723-860-7200	Sequence 7200, Ap
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957	119.6	6.9	319	17	US-10-242-533A-15028	Sequence 15028, A	c1030	118.6	6.8	4255	15	US-10-311-455-2006	Sequence 2006, Ap
958	119.6	6.9	319	17	US-10-085-783A-15028	Sequence 15028, A	c1031	118.6	6.8	5195	15	US-10-311-455-894	Sequence 894, App
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960	119.6	6.9	521	18	US-10-425-115-28564	Sequence 28564, A	c1033	118.6	6.8	6944	18	US-10-311-507-114	Sequence 114, App
961	119.6	6.9	569	17	US-10-424-599-26107	Sequence 26107, A	c1034	118.6	6.8	6944	18	US-10-480-846-112	Sequence 112, App
962	119.6	6.9	662	18	US-10-425-115-104281	Sequence 104281, A	1035	118.4	6.8	431	18	US-10-021-323-15250	Sequence 15250, A
963	119.6	6.9	668	18	US-10-425-115-12149	Sequence 12149, A	1036	118.4	6.8	472	18	US-10-357-930-49926	Sequence 49926, A
964	119.6	6.9	876	18	US-10-424-599-45096	Sequence 45096, A	c1037	118.4	6.8	681	9	US-09-729-674-23	Sequence 23, Appl
965	119.6	6.9	980	17	US-10-723-860-4894	Sequence 4894, Ap	1038	118.4	6.8	1132	9	US-09-822-830A-26	Sequence 26, Appl
966	119.6	6.9	1093	18	US-10-425-115-55902	Sequence 55902, A	1039	118.4	6.8	1132	18	US-10-913-553-23	Sequence 23, Appl
967	119.6	6.9	1331	17	US-10-159-563-200	Sequence 200, App	1040	118.4	6.8	1225	9	US-09-908-711-53	Sequence 53, Appl
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969	119.6	6.9	3466	9	US-09-726-643-35	Sequence 35, Appl	1069	118.4	6.8	2755	18	US-10-425-115-32936	Sequence 32936, A
970	119.6	6.9	3466	13	US-10-042-141-35	Sequence 35, Appl	1069	118.4	6.8	2846	10	US-09-997-428-230	Sequence 230, App
971	119.6	6.9	3466	18	US-10-919-272-35	Sequence 35, Appl							
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973	119.4	6.9	515	18	US-10-357-930-54538	Sequence 54538, A							
974	119.4	6.9	579	18	US-10-425-115-44286	Sequence 44286, A							
975	119.4	6.9	637	18	US-10-425-115-48251	Sequence 48251, A							
976	119.4	6.9	660	17	US-10-424-599-24054	Sequence 24054, A							
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979	119.4	6.9	685	18	US-10-425-115-131293	Sequence 131293, A							
980	119.4	6.9	1189	18	US-10-437-963-40780	Sequence 40780, A							
981	119.4	6.9	1504	18	US-10-425-115-63627	Sequence 63627, A							
982	119.4	6.9	2501	18	US-10-473-126-364	Sequence 364, App							
983	119.4	6.9	3002	18	US-10-311-401-5	Sequence 5, Appli							
984	119.4	6.9	4824	18	US-10-723-860-5191	Sequence 5191, Ap							
985	119.4	6.9	35362	18	US-10-473-126-244	Sequence 244, App							
986	119.2	6.9	196	14	US-10-066-543-2605	Sequence 2605, Ap							
987	119.2	6.9	341	18	US-10-425-115-77243	Sequence 77243, A							
988	119.2	6.9	568	17	US-10-424-599-117111	Sequence 117111, A							
989	119.2	6.9	592	18	US-10-425-115-105613	Sequence 105613, A							
990	119.2	6.9	598	18	US-10-021-323-11423	Sequence 11423, A							
991	119.2	6.9	600	18	US-10-425-115-76887	Sequence 76887, A							
992	119.2	6.9	1138	18	US-10-425-115-108606	Sequence 108606, A							
993	119.2	6.9	1708	17	US-10-310-154-71	Sequence 71, Appl							
994	119.2	6.9	7306	15	US-10-311-455-1610	Sequence 1610, Ap							
995	119.2	6.9	15749	18	US-10-723-860-6482	Sequence 6482, Ap							
996	119	6.9	317	18	US-10-357-930-58782	Sequence 58782, A							
997	119	6.9	376	18	US-10-425-115-53779	Sequence 53779, A							
998	119	6.9	533	18	US-10-425-115-69699	Sequence 69699, A							
999	119	6.9	555	18	US-10-021-323-4846	Sequence 4846, Ap							

Search completed: May 15, 2005, 06:02:17

Job time : 1066 secs

DE Human PRO protein, Seq ID No 156.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
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RESULT 7  
ID AG95876 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 8  
ID AB84891 standard; protein; 440 AA.  
DE Human PRO1411 protein sequence SEQ ID NO:150.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 9  
ID AB95497 standard; protein; 440 AA.  
DE Human angiogenesis related protein PRO1411 SEQ ID NO: 150.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
PA (BAKE) BAKER K P.  
PA (PERR) FERRARA N.  
PA (GERB) GERBER H.  
PA (GERR) GERRITSEN M E.  
PA (GODD) GODDARD A.  
PA (GODO) GODOWSKI P J.  
PA (GURN) GURNEY A L.  
PA (HILL) HILLAN K J.  
PA (MARS) MARSTERS S A.  
PA (PANJ) PAN J.  
PA (PAON) PAONI N F.  
PA (STEP) STEPHAN J F.  
PA (WATA) WATANABE C K.  
PA (WILL) WILLIAMS P M.  
PA (WOOD) WOOD W I.  
Query Match 100.0%; Score 2363; DB 5; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 10  
ID AU58500 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 11  
ID ABU8048 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 12  
ID ABU84363 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 13  
ID ABR66237 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
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Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 14  
ID ABR65627 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003036159-A1.  
PD 20-FEB-2003.  
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Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 15  
ID ABU9567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 16  
ID ABU82806 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
FN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 17  
ID ABU89927 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003036147-A1.  
PD 20-FEB-2003.  
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Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 18  
ID ABR68176 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 19  
ID ABU96229 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 20  
ID ABU92660 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 21  
ID ABU80816 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
FN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 22  
ID ABO08737 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 23  
ID ABO02789 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 24  
ID ABR74943 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 25  
ID ABR94705 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 26  
ID ABO25176 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 27  
ID ABO33782 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 28  
ID ABU85678 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
FN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 29  
ID ABU98838 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US200303153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 30  
ID ABU98053 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 31  
ID ABU91759 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 32  
ID ABU89452 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
FN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 33  
ID ABU86293 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 34

ID ABU67506 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 35  
ID ABU80534 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 36  
ID ABU90901 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 37  
ID ABO33960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO411.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 38  
ID ABR99452 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 39  
ID ABR98842 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 40  
ID ABO16365 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 41  
ID ABR92265 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 42  
ID ABO18906 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 43  
ID ABR78327 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 44  
ID ABU71977 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 45  
ID ABU85063 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 46  
ID ABO0202 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 47  
ID ABO11534 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 48  
ID ABO02179 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 49  
ID ABU8753 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 50  
ID ABU67294 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 51  
ID ABU83448 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 52  
ID ABO06249 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 53  
ID ABR59285 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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RESULT 54
ID ABO09347 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 55
ID ABO19211 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 56
ID ABO11229 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 57
ID ABR66847 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 58
ID ABO16060 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 59
ID ABO13766 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US200304916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 60
ID ABU71531 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 61
ID ABU65669 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, SEQ ID 202.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 62
ID ABO07517 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 63
ID ABO03704 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 64
ID ABR67152 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 65
ID ABO15755 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 66
ID ABU56036 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 67
ID ABU72312 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 68
ID ABU65364 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 69
ID ABU95309 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 70
ID ABU71212 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 71
ID ABO07822 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 72
ID ABR70063 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 73
ID ABR69396 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;
RESULT 74
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ID ABO01537 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 75  
ID ABU81339 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 76  
ID ABR60136 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 77  
ID ABU90985 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 78  
ID ABR67871 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 79  
ID ABR65259 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 80  
ID ABR68481 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 81  
ID ABR71893 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 82  
ID ABU85373 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 83  
ID ABU89063 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 84  
ID ABU72062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

ID ABU83143 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 85  
ID ABU94999 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 86  
ID ABU90547 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 87  
ID ABU84058 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 88  
ID ABU93709 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 89  
ID ABR64954 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 90  
ID ABR68786 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 91  
ID ABO06602 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 92  
ID ABR99147 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 93  
ID ABU57031 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 94  
ID ABU72062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.

PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 95  
ID ABUS5983 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 96  
ID ABUS2270 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 97  
ID ABUS7281 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 98  
ID ABUS7163 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 99  
ID ABUS3753 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 100  
ID ABUS8127 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 101  
ID ABUS2501 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 102  
ID ABUS1838 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 103  
ID ABUS6002 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 104  
ID ABUS1171 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411.

PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 105  
ID ABR59831 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 106  
ID ABUS4019 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 107  
ID ABUS9872 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 108  
ID ABUS2125 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 109  
ID ABR6542 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 110  
ID ABR90960 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 111  
ID ABO53286 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 112  
ID ABUS4387 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 113  
ID ABUS7269 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 114  
ID ABUS6598 standard; protein; 440 AA.

DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 115  
ID ABU91144 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 116  
ID ABU94692 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 117  
ID ABO04619 standard; protein; 440 AA.  
DE Human secreted polypeptide #101.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 118  
ID ABR70368 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 119  
ID ABU98533 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 120  
ID ABR65932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 121  
ID ABR64649 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027362-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 122  
ID ABU79574 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 123  
ID ABU92965 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 124  
ID ABU95924 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036145-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 125  
ID ABU91144 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 126  
ID ABU90237 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 127  
ID ABO09652 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 128  
ID ABO10924 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 129  
ID ABR70978 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 130  
ID ABU98288 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 131  
ID ABU87586 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 132  
ID ABU91454 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 133  
ID ABU89293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 134  
ID ABU84668 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032116-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 135  
ID ABR69758 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 136  
ID ABU80135 standard; protein; 440 AA.  
DE Human PRO protein #101.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 137  
ID ABU82500 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 138  
ID ABU93404 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 139  
ID ABO09957 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 140  
ID ABO09042 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 141  
ID ABU96464 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 142  
ID ABU10610 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein #101.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 143  
ID ABU72134 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 144  
ID ABU95619 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003032115-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 145  
ID ABU79805 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 146  
ID ABU96828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 147  
ID ABR70673 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 148  
ID ABO05024 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 149  
ID ABO08432 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 150  
ID ABO05639 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 151  
ID ABR74028 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 152  
ID ABR95620 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 153  
ID ABR80917 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 154  
ID ABR81222 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 155  
ID ABM00918 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 156  
ID ABR88520 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 157  
ID ABR77341 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 158  
ID ABO28825 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 159  
ID ABO31570 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 160  
ID ABM07987 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 161  
ID ABO40467 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 162  
ID ABO35992 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 163  
ID ABO44031 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.

PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 164  
ID ADA77954 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 165  
ID ABM24826 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 166  
ID ABO03094 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 167  
ID ABR90350 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 168  
ID ABM17264 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 169  
ID ABR95010 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 170  
ID ABR95315 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 171  
ID ABJ72305 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 172  
ID ADB17109 standard; protein; 440 AA.  
DE Human transmembrane PRO polypeptide (SeqID 52).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

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RESULT 173
ID ABO21553 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 174
ID ABR97817 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 175
ID ABR87605 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 176
ID ABR77646 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 177
ID ABR27876 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 178
ID ABR06157 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 179
ID ABR03663 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 180
ID ABR35114 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 181
ID ABR26351 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 182
ID ABO48133 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 183
ID ABR92875 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 184
ID ABO24636 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 185
ID ABR11647 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 186
ID ABR02748 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 187
ID ABR16044 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 188
ID ABO27605 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 189
ID ABR29096 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 190
ID ABR07072 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 2363; DB 6; Length 440;
  Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 191
ID ABR21166 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
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PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 192  
ID ABM09512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 193  
ID AB041382 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 194  
ID AB036197 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 195  
ID AB043726 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 196  
ID ABM76426 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 197  
ID ABM76122 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 198  
ID ABM25741 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 199  
ID ABM26046 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 200  
ID AB003399 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 201  
ID AB002484 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 202  
ID AB044264 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 203  
ID ABR90655 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 204  
ID ABR73723 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 205  
ID ABO16975 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 206  
ID ABR94400 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 207  
ID ABR75907 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 208  
ID ABR71283 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 209  
ID ABR93180 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 210  
ID ABR93485 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054478-A1.  
PD 20-MAR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 211
ID ABR87910 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 212
ID ABO33596 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 213
ID ABO27910 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 214
ID ABO33254 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 215
ID ABO33254 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 216
ID ABO4942 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 217
ID ABO08902 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 218
ID ABO36502 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 219
ID ABO35587 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 220
ID ABO3552 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 221
ID ABO10427 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 222
ID ABO11952 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 223
ID ABO52098 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 224
ID ABO52403 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 225
ID ADA19914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003068394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 226
ID ABO23721 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #101.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 227
ID ADB17297 standard; protein; 440 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 228
ID ABR97207 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
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RESULT 229  
ID ABO40772 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 230  
ID ABM11037 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 231  
ID ABM28181 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 232  
ID ABO32180 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 233  
ID ABM15307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 234  
ID ABM06462 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 235  
ID ABM04273 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 236  
ID ABM22386 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 237  
ID ABM07682 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 238  
ID ABO40772 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 239  
ID ABM35419 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 240  
ID ABM33182 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 241  
ID ABO52708 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 242  
ID ABO50268 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 243  
ID ABU9262 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 244  
ID ABO04314 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 245  
ID ABO05944 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 246  
ID ABM18484 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 247  
ID ABR97512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 248  
 ID ABR80612 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003049740-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 249  
 ID ABR01223 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003049770-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 250  
 ID ABR88825 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003073169-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 251  
 ID ABR13477 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003064457-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 252  
 ID ABR20861 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003068711-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 253  
 ID ABR041992 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049745-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 254  
 ID ABR042602 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003049751-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 255  
 ID ABR10122 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003067478-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 256  
 ID ABR038637 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003068773-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 257  
 ID ABR32877 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003073185-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 258  
 ID ABR22691 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003087373-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 259  
 ID ABR74902 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003096353-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 260  
 ID ADA79746 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein (PRO) #101.  
 PN US2003073173-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 261  
 ID ABR96292 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003054458-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 262  
 ID ABR02443 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003059886-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 263  
 ID ABR86385 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003049758-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 264  
 ID ABR86690 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003049772-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 265  
 ID ABR16654 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003064448-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 266  
 ID ABR29706 standard; protein; 440 AA.  
 DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
 PN US2003064456-A1.  
 PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 267  
ID ABO29130 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 268  
ID ABM23911 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 269  
ID ABM23301 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 270  
ID ADA47278 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
FN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 271  
ID ABM22081 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 272  
ID ABO37722 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 273  
ID ABM28486 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 274  
ID ABM28791 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 275  
ID ABM66435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;

RESULT 276  
ID ABM75817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 277  
ID ABM34097 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 278  
ID ABM34402 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 279  
ID ABO20333 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 280  
ID ABO21248 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 281  
ID ABO22163 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 282  
ID ADA20086 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 283  
ID ABR65597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 284  
ID ABR85775 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 285  
ID ABR99757 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 286  
ID ABM00613 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 287  
ID ABM00308 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 288  
ID ABO29740 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 289  
ID ABM23606 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 290  
ID ABM29401 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 291  
ID ABO38332 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 292  
ID ABO45632 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 293  
ID ABM20556 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 294  
ID ADA81473 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 295  
ID ABO16670 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 296  
ID ABO18296 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 297  
ID ABO22723 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 298  
ID ABO23028 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 299  
ID ABR92570 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 300  
ID ABR81527 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 301  
ID ABM77951 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 302  
ID ABR89740 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 303  
ID ABM26656 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 304  
ID ABM13782 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064458-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 305  
ID ABO28520 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 306  
ID ABO30350 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 307  
ID ABO30377 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 308  
ID ABO3968 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 309  
ID ABO37112 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 310  
ID ABO41687 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 311  
ID ABO35282 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 312  
ID ABO25131 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 313  
ID ABO47523 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 314  
ID ABO47828 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 315  
ID ABO48438 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 316  
ID ABO51488 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 317  
ID ABO51793 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 318  
ID ABO50573 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 319  
ID ABR79697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 320  
ID ABM16959 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 321  
ID ABO17991 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 322  
ID ABO20943 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 323  
ID ABR96902 standard; protein; 440 AA.

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DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 324  
ID ABM12257 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 325  
ID ABM16349 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 326  
ID ABM24216 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 327  
ID ABM14697 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 328  
ID ABM04578 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 329  
ID ABM06767 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 330  
ID ABM09207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 331  
ID ABO39247 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 332  
ID ABM75512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104545-A1.  
PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 333  
ID ABM25436 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 334  
ID ABM19946 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 335  
ID ABO46852 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 336  
ID ABO47157 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 337  
ID ADA83271 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 338  
ID ABR71588 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 339  
ID ABR72198 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 340  
ID ABR98537 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 341  
ID ABO06907 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 342  
ID ABR84860 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 343  
ID ABR73418 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 344  
ID ABR76512 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 345  
ID ABR73113 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 346  
ID ABR72433 standard; protein; 440 AA.  
DE Human PRO1411 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 347  
ID ABR18179 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 348  
ID ABO20638 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 349  
ID ABO25381 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 350  
ID ABO25696 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 351  
ID ABR94095 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 352  
ID ABR80002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 353  
ID ABR11342 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 354  
ID ABO32949 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 355  
ID ABO30855 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 356  
ID ABO30960 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 357  
ID ABR27266 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 358  
ID ABR30011 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 359  
ID ABR05547 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 360  
ID ABR15612 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 361  
ID ABR08597 standard; protein; 440 AA.

DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 362  
ID ABO42297 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 363  
ID ABO38027 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 364  
ID ABO45937 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 365  
ID ABO66740 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 366  
ID ADB20314 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 367  
ID ABM19641 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 368  
ID ABO49353 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 369  
ID ABO49658 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 370  
ID ADA78566 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003073181-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 371  
ID ABO34328 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 372  
ID ABR88215 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 373  
ID ADA00383 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO 411.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 374  
ID ABM26361 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 375  
ID ABM03358 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 376  
ID ABO39857 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 6; Length 440;  
RESULT 377  
ID ABO49963 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 7; Length 440;  
RESULT 378  
ID ABO50878 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2363; DB 7; Length 440;  
RESULT 379  
ID ABO05334 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036126-A1.  
PD 20-FEB-2003.



Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 380  
ID ABR74638 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 381  
ID ABO44449 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 382  
ID ABR77117 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 383  
ID ABM17874 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 384  
ID ABR95925 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 385  
ID ABO21858 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 386  
ID ABO20028 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 387  
ID ABO24331 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 388  
ID ABR86080 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 389  
ID ABM10732 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064455-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 390  
ID ABM76731 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 391  
ID ABR89435 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 392  
ID ABM12562 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 393  
ID ABM05852 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 394  
ID ABO34977 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 395  
ID ABM03053 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 396  
ID ABM19031 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 397  
ID ABM19336 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 398  
ID ABO46547 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 399  
ID ABO43048 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 400  
ID ABR69091 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 401  
ID ABR89130 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 402  
ID ABR72503 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 403  
ID ABR74333 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 404  
ID ABO18601 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 405  
ID ABR80307 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 406  
ID ABO01528 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 407  
ID ABO2138 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 408  
ID ABR87300 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.

PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 409  
ID ABM12867 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 410  
ID ABM30621 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003084443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 411  
ID ABM24521 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 412  
ID ABO29435 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 413  
ID ABO31265 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003088710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 414  
ID ABM4392 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 415  
ID ABM09817 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 416  
ID ABO38942 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003088774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 417  
ID ABM34707 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104538-A1.

PD 05-JUN-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 418  
ID ABO51183 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 419  
ID ABO4009 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 420  
ID ABO10479 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 421  
ID ABR7722 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 422  
ID ABR78932 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 423  
ID ABO24026 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003054452-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 424  
ID ABR93790 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 425  
ID ARM01833 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 426  
ID ABR78256 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 427  
ID ABO33473 standard; protein; 440 AA.

DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 428  
ID ABR90045 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 429  
ID ABM27571 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003084442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 430  
ID ABM13172 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 431  
ID ABO31875 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 432  
ID ABM14087 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003086883-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 433  
ID ABM08292 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 434  
ID ABO40162 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 435  
ID ABM74597 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 436  
ID ABM33792 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003096358-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 437  
ID ABM20251 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 438  
ID ABO48743 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 439  
ID ABR72808 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 440  
ID ABO15450 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 441  
ID ABR85165 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 442  
ID ABO15145 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 443  
ID ABO17280 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 444  
ID ABO19863 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 445  
ID ABM17569 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 446  
ID ABJ72135 standard; protein; 440 AA.  
DE Human membrane bound receptor/protein PRO1411 amino acid sequence.

PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 447  
ID ABR85470 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 448  
ID ABM77036 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 449  
ID ABO28215 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 450  
ID ABM22996 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 451  
ID ABM30316 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003088723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 452  
ID ABM21776 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 453  
ID ABM21471 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 454  
ID ABM15002 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
PN US2003088766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 455  
ID ABO41077 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003068694-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 456  
ID ABO36807 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 457  
ID ABO37417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 458  
ID ABM75207 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 459  
ID ABM33487 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 460  
ID ABO46242 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
FN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 461  
ID ADA82637 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 462  
ID ADB85625 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 463  
ID ADB83646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 464  
ID ADB80752 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003088068-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 465  
ID ADB73293 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 466  
ID ABM31841 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 467  
ID ADB78375 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 468  
ID ABM31231 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003086762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 469  
ID ADB85023 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
FN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 470  
ID ADB78129 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 471  
ID ADB85945 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 472  
ID ABM32146 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 473  
ID ABM32451 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.  
FN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 474  
ID ADB80752 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003088068-A1.  
PD 08-MAY-2003.

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Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 474
ID ADB87195 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 475
ID ADB84777 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 476
ID ADB68304 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 477
ID ADB68111 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 478
ID ADB31536 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 479
ID ADB30926 standard; protein; 440 AA.
DE Human secreted polypeptide PRO1411, SEQ ID NO:202.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 480
ID ADB83892 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 481
ID ADB73047 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 482
ID ADB90928 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 483
ID ADC07008 standard; protein; 440 AA.
DE Human PRO1411 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 484
ID ADC17921 standard; protein; 440 AA.
DE Human PRO polypeptide #15.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 485
ID ADC17187 standard; protein; 440 AA.
DE Mammalian PRO polypeptide (seqid 52).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 486
ID ADC14885 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 487
ID ADC36885 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 488
ID ADC52380 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 489
ID ADC21875 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096469-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 490
ID ADC49906 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 491
ID ADC49105 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 492
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ID ADC49622 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 493  
ID ADC47483 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 494  
ID ADC47228 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 495  
ID ADC78103 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 496  
ID ADD06338 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 497  
ID ADD05675 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 498  
ID ADD10439 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 499  
ID ADC77857 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 500  
ID ADD11399 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 501  
ID ADD50820 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 502  
ID ADD51066 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 503  
ID ADD70567 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 504  
ID ADD39644 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 505  
ID ADD70090 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 506  
ID ADD37192 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 507  
ID ADD36056 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 508  
ID ADD38211 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 509  
ID ADD39167 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 510  
ID ADD50547 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.

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PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 511
ID ADD50301 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 512
ID ADD38690 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 513
ID ADD40121 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 514
ID ADD51312 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003105289-A1.
PD 03-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 515
ID ADE50342 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 516
ID ADE19954 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 517
ID ADE49865 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 518
ID ADE21423 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 519
ID ADF29848 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204053-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 520
ID ADF55741 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 521
ID ADG01057 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 522
ID ADG08610 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 523
ID ADG02670 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 524
ID ADG01377 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 525
ID ADF95552 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 526
ID ADF95231 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 527
ID ADG12367 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 528
ID ADH24084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 529  
ID ADH34110 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 530  
ID ADH29943 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 531  
ID ADH23914 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 532  
ID ADH09027 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 533  
ID ADH85318 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 534  
ID ADH24594 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 535  
ID ADH37450 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 536  
ID ADH02039 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 537  
ID ADH37620 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 538  
ID ADH85658 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 539  
ID ADH24254 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 540  
ID ADH38548 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 541  
ID ADG63787 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 542  
ID ADH83669 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 543  
ID ADH29477 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 544  
ID ADH27593 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 545  
ID ADH37790 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO1411.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 546  
ID ADH37967 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 547  
ID ADH37620 standard; protein; 440 AA.  
DE Human secreted and transmembrane protein PRO411.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;

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RESULT 547
ID ADH57387 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180920-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 548
ID ADH53529 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 549
ID ADH53699 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 550
ID ADH52035 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 551
ID ADH49890 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 552
ID ADI25400 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 553
ID ADH90193 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 554
ID ADI25570 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 555
ID ADH97744 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 556
ID ADH98084 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 557
ID ADI03592 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 558
ID ADI11949 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 559
ID ADH90023 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 560
ID ADH98424 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 561
ID ADI11099 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 562
ID ADI11609 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 563
ID ADH98254 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 564
ID ADH98594 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 565
ID ADH98084 standard; protein; 440 AA.
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DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 566
ID ADI05072 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 567
ID ADI03422 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 568
ID ADI04817 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 569
ID ADH78271 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 570
ID ADI19615 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 571
ID ADH90363 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 572
ID ADI03082 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 573
ID ADH77931 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 574
ID ADH97914 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 575
ID ADI01299 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 576
ID ADI01994 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 577
ID ADI03252 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 578
ID ADI11439 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 579
ID ADI02341 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 580
ID ADI11779 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 581
ID ADI05416 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 582
ID ADH79488 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 583
ID ADI19445 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181675-A1.
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PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 584  
ID ADI05246 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 585  
ID ADH79658 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 586  
ID ADI01484 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 587  
ID ADI01654 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 588  
ID ADI01824 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 589  
ID ADH79828 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 590  
ID ADI04646 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 591  
ID ADI02782 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 592  
ID ADH78101 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 593  
ID ADI25740 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 594  
ID ADI25910 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 595  
ID ADK65422 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 596  
ID ADH98764 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 597  
ID ADH80005 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 598  
ID ADM30342 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 599  
ID ADL93736 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 7; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 600  
ID ADC48859 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 601  
ID ADC52190 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 611  
ID ADD73613 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
FN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 612  
ID ADD78453 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 613  
ID AD841400 standard; protein; 440 AA.  
DE Human secreted/transmembrane PRO polypeptide #75.  
FN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 614  
ID AD874339 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
FN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 615  
ID AD821276 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 616  
ID AD877391 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 617  
ID AD820538 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
FN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 618  
ID AD875603 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
FN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 619  
ID AD874119 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
FN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 620

ID ADD74365 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 621  
ID ADD76095 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 622  
ID ADD85587 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 623  
ID ADE05136 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 624  
ID ADD75349 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 625  
ID ADD76893 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 626  
ID ADD86661 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 627  
ID ADE41201 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 628  
ID ADD78129 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 629  
ID ADE74951 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #101.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 630  
ID ADD77637 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 631  
ID ADD77883 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 632  
ID ADD85341 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 633  
ID ADD73873 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 634  
ID ADD74611 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 635  
ID ADD77139 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 636  
ID ADD85833 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 637  
ID ADE05382 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 638  
ID ADD74857 standard; protein; 440 AA.  
DE Human PRO polypeptide #78.  
PN US2003100724-A1.

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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 648
ID ADG04435 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 649
ID ADG12065 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 650
ID ADG00595 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 651
ID ADF94622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 652
ID ADG06718 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 653
ID ADH06622 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 654
ID ADH06452 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 655
ID ADG6873 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 656
ID ADH27763 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 639
ID ADE96425 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 640
ID ADF25736 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 641
ID ADF24635 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 642
ID ADF29371 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 643
ID ADE96902 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 644
ID ADG05669 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 645
ID ADG27223 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 646
ID ADF96164 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;
RESULT 647
ID ADG11286 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2363; DB 8; Length 440;

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Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 657  
ID ADH25104 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 658  
ID ADH33736 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 659  
ID ADG82851 standard; protein; 440 AA.  
DE Human PRO polypeptide #101.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 660  
ID ADH02940 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 661  
ID ADH02379 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 662  
ID ADH07986 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 663  
ID ADG69383 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 664  
ID ADH39204 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 665  
ID ADH03894 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 666  
ID ADH03417 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 667  
ID ADH26132 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 668  
ID ADG83944 standard; protein; 440 AA.  
DE Human PRO polypeptide #26.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 669  
ID ADH39062 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 670  
ID ADG85488 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 671  
ID ADG63636 standard; protein; 440 AA.  
DE Human secreted/transmembrane polypeptide PRO1411.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 672  
ID ADH06282 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 673  
ID ADH30112 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 674  
ID ADH24424 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 675  
ID ADH03894 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO1411.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;



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ID ADH33101 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 676
ID ADG69553 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 677
ID ADH07816 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 678
ID ADG59828 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 679
ID ADH39374 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 680
ID ADH33566 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 681
ID ADH33906 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 682
ID ADH01116 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 683
ID ADG69723 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 684
ID ADH02209 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 685
ID ADG69213 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 686
ID ADG85998 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 687
ID ADH24934 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 688
ID ADH39551 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 689
ID ADH02549 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 690
ID ADG69043 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 691
ID ADH07646 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 692
ID ADG86168 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 693
ID ADH24764 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
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PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 694
ID ADH25812 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 695
ID ADH3378 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 696
ID ADH57217 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 697
ID ADH43583 standard; protein; 440 AA.
DE Human PRO polypeptide #75.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 698
ID ADH52323 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 699
ID ADG34152 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 700
ID ADH04371 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 701
ID ADH49571 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 702
ID ADH90533 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181700-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 703
ID ADH11269 standard; protein; 440 AA.
DE Human PRO polypeptide #26.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 704
ID ADH98934 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 705
ID ADI33622 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 706
ID ADI02164 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 707
ID ADH69716 standard; protein; 440 AA.
DE Human PRO polypeptide #78.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 708
ID ADH61372 standard; protein; 440 AA.
DE Human secreted/transmembrane protein PRO1411.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 709
ID ADH90703 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 710
ID ADI29877 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO1411.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2363; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
RESULT 711
ID ADJ54840 standard; protein; 440 AA.
DE Human PRO polypeptide #101.
PN US2004023321-A1.
PD 05-FEB-2004.
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PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 712  
 ID ADJ98578 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187197-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 713  
 ID ADJ98748 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187228-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 714  
 ID ADH78907 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003181703-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 715  
 ID ADJ99141 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003186408-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 716  
 ID ADJ99311 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187196-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 717  
 ID ADJ98929 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187242-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 718  
 ID ADH79077 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003181702-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 719  
 ID ADK00937 standard; protein; 440 AA.  
 DE Human PRO polypeptide #26.  
 PN US2003186407-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 720  
 ID ADK14458 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187229-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 721  
 ID ADM27274 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2004044179-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 722  
 ID ADK82928 standard; protein; 440 AA.  
 DE Human PRO polypeptide #75.  
 PN US2004043927-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 723  
 ID ADJ64611 standard; protein; 440 AA.  
 DE Human PRO polypeptide #101.  
 PN US2004038337-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 724  
 ID ADK66632 standard; protein; 440 AA.  
 DE Human PRO polypeptide #78.  
 PN US2004044180-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 725  
 ID ADM31507 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2004048334-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 726  
 ID ADM36554 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2004053358-A1.  
 PD 18-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 727  
 ID ADM40359 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2004048335-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 728  
 ID ADM80907 standard; protein; 440 AA.  
 DE Human PRO polypeptide #26.  
 PN US2004058411-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 729  
 ID ADL94571 standard; protein; 440 AA.  
 DE Human secreted/transmembrane protein PRO1411.  
 PN US2004073015-A1.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2363; DB 8; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
 RESULT 730  
 ID ADK14458 standard; protein; 440 AA.  
 DE Novel human secreted and transmembrane protein PRO1411.  
 PN US2003187229-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 730  
ID ADN37967 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2363; DB 8; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.4e-137;  
RESULT 731  
ID ADL32808 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO1411.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 2357; DB 7; Length 440;  
Best Local Similarity 99.8%; Pred. No. 5.5e-137;  
RESULT 732  
ID AAB38324 standard; protein; 387 AA.  
DE Human secreted protein encoded by gene 4 clone HKAJK47.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 85.9%; Score 2030; DB 3; Length 387;  
Best Local Similarity 87.5%; Pred. No. 6e-117;  
RESULT 733  
ID RAY50941 standard; protein; 479 AA.  
DE Human adult skin cDNA clone vd4\_1 derived protein.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 85.1%; Score 2010.5; DB 3; Length 479;  
Best Local Similarity 87.6%; Pred. No. 1.2e-115;  
RESULT 734  
ID ABO27306 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO411.  
PN US200309012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 7.5e-113;  
RESULT 735  
ID ABO34192 standard; protein; 372 AA.  
DE Human secreted/transmembrane polypeptide PRO 1411.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 83.1%; Score 1963; DB 6; Length 372;  
Best Local Similarity 84.5%; Pred. No. 7.5e-113;  
RESULT 736  
ID RAY50940 standard; protein; 369 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #2.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 81.5%; Score 1925.5; DB 3; Length 369;  
Best Local Similarity 83.4%; Pred. No. 1.5e-110;  
RESULT 737  
ID AAY50939 standard; protein; 358 AA.  
DE Human adult skin cDNA clone vd3\_1 derived protein #1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 71.6%; Score 1692; DB 3; Length 358;  
Best Local Similarity 95.8%; Pred. No. 3.2e-96;  
RESULT 738  
ID ADP07783 standard; protein; 186 AA.  
DE Human secreted protein, seq id 266.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 37.1%; Score 875.5; DB 8; Length 186;  
Best Local Similarity 92.3%; Pred. No. 2.5e-46;

RESULT 739  
ID AAY60056 standard; protein; 230 AA.  
DE Human endometrium tumour EST encoded protein 116.  
PN DE19817948-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 28.3%; Score 669; DB 2; Length 230;  
Best Local Similarity 98.4%; Pred. No. 1.5e-33;  
RESULT 740  
ID ABO23519 standard; protein; 1079 AA.  
DE Mycobacterium tuberculosis outlier protein #3.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 19.1%; Score 450.5; DB 7; Length 1079;  
Best Local Similarity 30.5%; Pred. No. 1.7e-19;  
RESULT 741  
ID ABU36481 standard; protein; 1306 AA.  
DE Protein encoded by Prokaryotic essential gene #22008.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 18.6%; Score 439.5; DB 6; Length 1306;  
Best Local Similarity 30.9%; Pred. No. 9.6e-19;  
RESULT 742  
ID AAO16495 standard; protein; 400 AA.  
DE Kukulcania hibernalis spider silk protein #2.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 18.4%; Score 434; DB 6; Length 400;  
Best Local Similarity 33.4%; Pred. No. 6.8e-19;  
RESULT 743  
ID ABU36971 standard; protein; 1381 AA.  
DE Protein encoded by Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.6%; Score 415.5; DB 6; Length 1381;  
Best Local Similarity 29.9%; Pred. No. 3e-17;  
RESULT 744  
ID ABM15873 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:111.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 745  
ID ABU36943 standard; protein; 484 AA.  
DE Protein encoded by Prokaryotic essential gene #22470.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.5%; Score 412.5; DB 6; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 746  
ID ABO23518 standard; protein; 484 AA.  
DE Mycobacterium tuberculosis outlier protein #2.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 17.5%; Score 412.5; DB 7; Length 484;  
Best Local Similarity 33.6%; Pred. No. 1.7e-17;  
RESULT 747  
ID AAM16105 standard; protein; 357 AA.  
DE Peptide #2539 encoded by probe for measuring cervical gene expression.

PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 748  
ID ABB35090 standard; peptide; 357 AA.  
DE Peptide #2596 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 749  
ID AAM28596 standard; protein; 357 AA.  
DE Peptide #2633 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 750  
ID ABB29912 standard; peptide; 357 AA.  
DE Peptide #2563 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 751  
ID ABB20509 standard; protein; 357 AA.  
DE Protein #2508 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 752  
ID AAM68282 standard; protein; 357 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28598.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 753  
ID AAM55912 standard; protein; 357 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28017.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 754  
ID ABG49940 standard; peptide; 357 AA.  
DE Human liver peptide, SEQ ID NO 28598.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 755  
ID AAM03832 standard; protein; 357 AA.  
DE Peptide #2514 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 4; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 756  
ID ABG37823 standard; peptide; 357 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 27488.  
PN WO200186003-A2.

PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 17.2%; Score 406.5; DB 5; Length 357;  
Best Local Similarity 31.6%; Pred. No. 3e-17;  
RESULT 757  
ID ABB36734 standard; protein; 532 AA.  
DE Protein encoded by Prokaryotic essential gene #22261.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 17.1%; Score 404.5; DB 6; Length 532;  
Best Local Similarity 32.2%; Pred. No. 5.8e-17;  
RESULT 758  
ID AAP80940 standard; protein; 1177 AA.  
DE SLPIII protein comprising the gagage of silk fibroin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR-) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 1; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 759  
ID AAR05307 standard; protein; 1177 AA.  
DE SLP III (Silk-fibroin like protein).  
PN WO9005177-A.  
PD 17-MAY-1990.  
PA (SYTR-) SYNTRO CORP.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 760  
ID AAR95105 standard; protein; 1177 AA.  
DE Silk like protein (SLP)III.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 761  
ID AAW26342 standard; protein; 1177 AA.  
DE Silk-like protein SlpIII.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 2; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 762  
ID AAY78277 standard; peptide; 1177 AA.  
DE SLPIII amino acid sequence SEQ ID NO:64.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 3; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 763  
ID AAB63995 standard; protein; 1177 AA.  
DE SLPIII protein sequence SEQ ID 31.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 764  
ID AAB72725 standard; protein; 1177 AA.  
DE Repetitive protein polymer protein sequence #25.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 17.0%; Score 402.5; DB 4; Length 1177;  
Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
RESULT 765  
ID ABB69267 standard; protein; 1177 AA.  
DE Silk-like protein SLPIII.  
PN US6355776-B1.  
PD 12-MAR-2002.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 5; Length 1177;  
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
 RESULT 766  
 ID ADE44959 standard; protein; 1177 AA.  
 DE Silk fibroin protein repeating peptide related protein seq id 64.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 7; Length 1177;  
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
 RESULT 767  
 ID AAR41007 standard; protein; 1178 AA.  
 DE Silk-like protein Slp-III multimer.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
 RESULT 768  
 ID AAW53518 standard; protein; 1178 AA.  
 DE Amino acid sequence of the synthetic SlpIII protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 17.0%; Score 402.5; DB 2; Length 1178;  
 Best Local Similarity 30.4%; Pred. No. 1.6e-16;  
 RESULT 769  
 ID AAP82962 standard; protein; 1059 AA.  
 DE SEPLA protein comprising gagags of silk fibroin.  
 PN WO8803533-A.  
 PD 19-MAY-1988.  
 PA (SYTR) SYNTRO CORP.  
 Query Match 17.0%; Score 401; DB 1; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 1.8e-16;  
 RESULT 770  
 ID AAW53524 standard; protein; 1023 AA.  
 DE Amino acid sequence of the SLP4 protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1023;  
 Best Local Similarity 30.4%; Pred. No. 2.3e-16;  
 RESULT 771  
 ID AAR41013 standard; protein; 1059 AA.  
 DE SLP4 multimeric protein.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 2.4e-16;  
 RESULT 772  
 ID AAW26348 standard; protein; 1059 AA.  
 DE SLP4 synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 2; Length 1059;  
 Best Local Similarity 30.4%; Pred. No. 2.4e-16;  
 RESULT 773  
 ID AAY78283 standard; protein; 1101 AA.  
 DE SELP4 amino acid sequence SEQ ID NO:83.  
 PN US6018030-A.  
 PD 23-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 3; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
 RESULT 774  
 ID ABG69273 standard; protein; 1101 AA.  
 DE Silk/Elastin-like protein SELP4.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 5; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
 RESULT 775  
 ID ADE44978 standard; protein; 1101 AA.  
 DE Recombinant structural protein SLP4 protein seq id 83.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 16.9%; Score 399; DB 7; Length 1101;  
 Best Local Similarity 30.4%; Pred. No. 2.5e-16;  
 RESULT 776  
 ID ABU36550 standard; protein; 923 AA.  
 DE Protein encoded by Prokaryotic essential gene #22077.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.8%; Score 392.5; DB 6; Length 923;  
 Best Local Similarity 27.7%; Pred. No. 5.3e-16;  
 RESULT 777  
 ID ABP53453 standard; protein; 1062 AA.  
 DE Pre-gelled protein polymer SLP3 related amino acid sequence #2.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPE/) CAPPELLO J.  
 Query Match 16.4%; Score 386.5; DB 5; Length 1062;  
 Best Local Similarity 31.5%; Pred. No. 1.4e-15;  
 RESULT 778  
 ID ABU36827 standard; protein; 778 AA.  
 DE Protein encoded by Prokaryotic essential gene #22354.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.3%; Score 386; DB 6; Length 778;  
 Best Local Similarity 31.2%; Pred. No. 1.1e-15;  
 RESULT 779  
 ID RAY28843 standard; protein; 641 AA.  
 DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1).  
 PN WO9947647-A1.  
 PD 23-SEP-1999.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Query Match 16.2%; Score 383; DB 2; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 780  
 ID AAY95856 standard; protein; 641 AA.  
 DE Epstein Barr virus nuclear antigen 1 protein (EBNA1).  
 PN WO200047778-A1.  
 PD 17-AUG-2000.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Query Match 16.2%; Score 383; DB 3; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 781  
 ID AAB62332 standard; protein; 641 AA.  
 DE EBV tethering protein EBNA1.  
 PN WO200125484-A2.  
 PD 12-APR-2001.  
 PA (UNMI) UNIV MICHIGAN  
 Query Match 16.2%; Score 383; DB 4; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 782  
 ID ABP72663 standard; protein; 641 AA.  
 DE Epstein-Barr virus nuclear antigen 1.  
 PN WO2003018754-A2.  
 PD 06-MAR-2003.  
 PA (NEUR-) NEURONZ LTD.  
 Query Match 16.2%; Score 383; DB 6; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 783  
 ID AAE34812 standard; protein; 641 AA.  
 DE Epstein-barr virus nuclear antigen 1 (EBNA1).  
 PN WO200290558-A1.  
 PD 14-NOV-2002.

PA (FITB-) FIT BIOTECH OVJ PLC.  
 Query Match 16.2%; Score 383; DB 6; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 784  
 ID ADK6581 standard; protein; 641 AA.  
 DE Human herpesvirus 4 nuclear antigen-1 protein.  
 PN DE10207135-A1.  
 PD 11-SEP-2003.  
 PA (EURO-) EUROIMMUN GMBH.  
 Query Match 16.2%; Score 383; DB 7; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 785  
 ID ADJ57052 standard; protein; 641 AA.  
 DE Epstein-Barr virus nuclear antigen 1.  
 PN WO2004007536-A2.  
 PD 22-JAN-2004.  
 PA (AFRI-) AFFINIUM PHARM INC.  
 Query Match 16.2%; Score 383; DB 8; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 786  
 ID ADP12515 standard; protein; 641 AA.  
 DE Protein encoded by mRNA of the invention #125.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Query Match 16.2%; Score 383; DB 9; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 787  
 ID ADQ94586 standard; protein; 641 AA.  
 DE Epstein-Barr virus EBNA1 protein.  
 PN US2004141995-A1.  
 PD 22-JUL-2004.  
 PA (WANG/) WANG R.  
 PA (VOOK/) VOOK K.  
 Query Match 16.2%; Score 383; DB 8; Length 641;  
 Best Local Similarity 31.0%; Pred. No. 1.4e-15;  
 RESULT 788  
 ID ABU36438 standard; protein; 837 AA.  
 DE Protein encoded by Prokaryotic essential gene #21965.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.1%; Score 380.5; DB 6; Length 837;  
 Best Local Similarity 30.5%; Pred. No. 2.7e-15;  
 RESULT 789  
 ID ABP53456 standard; protein; 996 AA.  
 DE Pre-gelated protein polymer SLP4 related amino acid sequence #2.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPP/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 16.0%; Score 379; DB 5; Length 996;  
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;  
 RESULT 790  
 ID AAE18319 standard; protein; 1002 AA.  
 DE Silk-like protein, SLP4.  
 PN WO200200016-A1.  
 PD 03-JAN-2002.  
 PA (LUMI-) LUMINIS PTY LTD.  
 PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
 Query Match 16.0%; Score 379; DB 5; Length 1002;  
 Best Local Similarity 31.8%; Pred. No. 3.9e-15;  
 RESULT 791  
 ID ABU36945 standard; protein; 588 AA.  
 DE Protein encoded by Prokaryotic essential gene #22472.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 16.0%; Score 378; DB 6; Length 588;  
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;  
 RESULT 792  
 ID ADM40790 standard; protein; 588 AA.  
 DE Mycobacterial disease detection method related Rv3367 protein.

PN WO2003073101-A2.  
 PD 04-SEP-2003.  
 PA (UYNV) UNIV NEW YORK STATE.  
 Query Match 16.0%; Score 378; DB 7; Length 588;  
 Best Local Similarity 30.1%; Pred. No. 2.7e-15;  
 RESULT 793  
 ID AAW27178 standard; protein; 646 AA.  
 DE Nephila clavipes spider silk protein.  
 PN WO9708315-A1.  
 PD 06-MAR-1997.  
 PA (BASE/) BASEL R M.  
 PA (ELIO/) ELION G R.  
 Query Match 16.0%; Score 378; DB 2; Length 646;  
 Best Local Similarity 29.0%; Pred. No. 3e-15;  
 RESULT 794  
 ID ADB61321 standard; protein; 646 AA.  
 DE Spider silk related MaSpi protein.  
 PN WO2003060099-A2.  
 PD 24-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 PA (ALWA/) ALWATTARI A.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 795  
 ID ADC35240 standard; protein; 646 AA.  
 DE MaSpi silk protein, SEQ ID 1.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 796  
 ID ADM46149 standard; protein; 646 AA.  
 DE Nephila clavipes spidroin 1 (MaSpi) protein.  
 PN WO2003057720-A2.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 16.0%; Score 378; DB 7; Length 646;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 RESULT 797  
 ID AAR95107 standard; protein; 1038 AA.  
 DE Fibronectin cell binding seq. contg. silk like protein (SLP)III.  
 PN US5514581-A.  
 PD 07-MAY-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 2; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 798  
 ID AAB63997 standard; protein; 1038 AA.  
 DE FCB-SLP protein from pSV1521 SEQ ID 36.  
 PN US6140072-A.  
 PD 31-OCT-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 799  
 ID AAB72727 standard; protein; 1038 AA.  
 DE Repetitive protein polymer protein sequence #27.  
 PN US6184348-B1.  
 PD 06-FEB-2001.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.9%; Score 376.5; DB 4; Length 1038;  
 Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
 RESULT 800  
 ID ADO08760 standard; protein; 452 AA.  
 DE Novel surgical dressing-related protein SeqID47.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN-) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 15.9%; Score 375.5; DB 8; Length 452;  
 Best Local Similarity 29.9%; Pred. No. 3e-15;  
 RESULT 801

ID ABU36682 standard; protein; 914 AA.  
DE Protein encoded by Prokaryotic essential gene #22209.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.9%; Score 375; DB 6; Length 914;  
Best Local Similarity 33.0%; Pred. No. 6.3e-15;  
RESULT 802  
ID AAM50037 standard; protein; 1255 AA.  
DE N. clavipes spidroin synthetic homologue S01S01 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1255;  
Best Local Similarity 30.5%; Pred. No. 9.8e-15;  
RESULT 803  
ID AAM50039 standard; protein; 1880 AA.  
DE N. clavipes spidroin synthetic homologue S01S01S01 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.8%; Score 374; DB 5; Length 1880;  
Best Local Similarity 30.5%; Pred. No. 1.4e-14;  
RESULT 804  
ID AAO16497 standard; protein; 520 AA.  
DE Argiope trifasciata spider silk protein #1.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.8%; Score 373.5; DB 6; Length 520;  
Best Local Similarity 30.0%; Pred. No. 4.5e-15;  
RESULT 805  
ID ABU36979 standard; protein; 584 AA.  
DE Protein encoded by Prokaryotic essential gene #22506.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 584;  
Best Local Similarity 32.3%; Pred. No. 5.1e-15;  
RESULT 806  
ID ABU36570 standard; protein; 667 AA.  
DE Protein encoded by Prokaryotic essential gene #22097.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.8%; Score 373.5; DB 6; Length 667;  
Best Local Similarity 28.5%; Pred. No. 5.7e-15;  
RESULT 807  
ID ADE28209 standard; protein; 203 AA.  
DE Human MDTT protein - SEQ ID 59.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.8%; Score 373; DB 7; Length 203;  
Best Local Similarity 58.9%; Pred. No. 2e-15;  
RESULT 808  
ID ABU36802 standard; protein; 694 AA.  
DE Protein encoded by Prokaryotic essential gene #22329.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 372; DB 6; Length 694;  
Best Local Similarity 30.3%; Pred. No. 7.4e-15;  
RESULT 809  
ID ABU36862 standard; protein; 615 AA.  
DE Protein encoded by Prokaryotic essential gene #22389.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 371; DB 6; Length 615;  
Best Local Similarity 31.0%; Pred. No. 7.6e-15;  
RESULT 810  
ID AAY40097 standard; protein; 651 AA.  
DE Spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.7%; Score 371; DB 2; Length 651;  
Best Local Similarity 30.1%; Pred. No. 8e-15;  
RESULT 811  
ID AAU11781 standard; protein; 651 AA.  
DE Spider natural silk protein Spidroin 1.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.7%; Score 371; DB 5; Length 651;  
Best Local Similarity 30.1%; Pred. No. 8e-15;  
RESULT 812  
ID AAR14308 standard; protein; 718 AA.  
DE N. clavipes dragline silk protein-1.  
PN EP452925-A.  
PD 23-OCT-1991.  
PA (UYWY-) UNIV OF WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 813  
ID AAW53346 standard; protein; 718 AA.  
DE Nephila clavipes spider silk protein.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 2; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 814  
ID AAY59070 standard; protein; 718 AA.  
DE N. clavipes spider silk protein 1.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.7%; Score 371; DB 3; Length 718;  
Best Local Similarity 30.1%; Pred. No. 8.8e-15;  
RESULT 815  
ID ABU36634 standard; protein; 491 AA.  
DE Protein encoded by Prokaryotic essential gene #22161.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.7%; Score 370.5; DB 6; Length 491;  
Best Local Similarity 28.3%; Pred. No. 6.6e-15;  
RESULT 816  
ID AAR81318 standard; protein; 980 AA.  
DE Adhesion protein.  
PN WO9519793-A1.  
PD 27-JUL-1995.  
PA (USNA) US SEC OF NAVY.  
PA (CELL-) CELLCO INC.  
Query Match 15.7%; Score 370.5; DB 2; Length 980;  
Best Local Similarity 29.6%; Pred. No. 1.3e-14;  
RESULT 817  
ID AAR05312 standard; protein; 1066 AA.  
DE Sequence encoding SLP-11 monomer (similar to silk fibroin).  
PN WO9005177-A.  
PD 17-MAY-1990.  
PA (SYTR) SYNTRO CORP.  
Query Match 15.7%; Score 370; DB 2; Length 1066;  
Best Local Similarity 27.9%; Pred. No. 1.5e-14;  
RESULT 818  
ID AAM50038 standard; protein; 989 AA.  
DE N. clavipes spidroin synthetic homologue S01SM12 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 15.6%; Score 369.5; DB 5; Length 989;  
Best Local Similarity 30.8%; Pred. No. 1.5e-14;  
RESULT 819  
ID AAR41010 standard; protein; 2025 AA.



DE SELP1 multimeric protein.  
 PN US5243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.6%; Score 369; DB 2; Length 2025;  
 Best Local Similarity 27.4%; Pred. No. 3.1e-14;  
 RESULT 820  
 ID AAF82959 standard; protein; 2107 AA.  
 DE SELP1 protein comprising gags of silk fibroin and gvgvp of elastin.  
 PN WO803533-A.  
 PD 19-MAY-1988.  
 PA (SYTR ) SYNTRO CORP.  
 Query Match 15.6%; Score 369; DB 1; Length 2107;  
 Best Local Similarity 27.4%; Pred. No. 3.3e-14;  
 RESULT 821  
 ID AAY78287 standard; protein; 1011 AA.  
 DE SELPF amino acid sequence SEQ ID NO:94.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 3; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 822  
 ID ABG5277 standard; protein; 1011 AA.  
 DE Silk/Elastin-like protein SELPF.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 5; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 823  
 ID ADE44989 standard; protein; 1170 AA.  
 DE Recombinant structural protein SELPF protein seq id 94.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 7; Length 1011;  
 Best Local Similarity 27.8%; Pred. No. 2.1e-14;  
 RESULT 824  
 ID AAW26351 standard; protein; 1170 AA.  
 DE SELPF synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 367; DB 2; Length 1170;  
 Best Local Similarity 27.8%; Pred. No. 2.5e-14;  
 RESULT 825  
 ID ABB67896 standard; protein; 610 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 30480.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 15.5%; Score 366; DB 4; Length 610;  
 Best Local Similarity 32.5%; Pred. No. 1.5e-14;  
 RESULT 826  
 ID AAE36887 standard; protein; 691 AA.  
 DE Dolomedes tenebrosus fibroin 2 protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWT-) UNIV WYOMING.  
 Query Match 15.5%; Score 366; DB 6; Length 691;  
 Best Local Similarity 27.0%; Pred. No. 1.7e-14;  
 RESULT 827  
 ID AAW53526 standard; protein; 695 AA.  
 DE Amino acid sequence of FCB-SLP1II protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 695;  
 Best Local Similarity 27.3%; Pred. No. 1.7e-14;  
 RESULT 828  
 ID AAW26349 standard; protein; 766 AA.  
 DE FCB-SLP1II (57 kDa) synthetic protein.

PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 829  
 ID AAY78285 standard; peptide; 766 AA.  
 DE FCB-SLP1II amino acid sequence SEQ ID NO:88.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 3; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 830  
 ID ABG6275 standard; protein; 766 AA.  
 DE Fibronectin FCB portion/silk-like protein, FCB-SLP1II #1.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 5; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 831  
 ID ADE44983 standard; protein; 766 AA.  
 DE Recombinant structural protein FCB-SLP1II protein seq id 88.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 7; Length 766;  
 Best Local Similarity 27.3%; Pred. No. 1.9e-14;  
 RESULT 832  
 ID AAY78286 standard; protein; 979 AA.  
 DE FCB-SLP1II amino acid sequence SEQ ID NO:89.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 3; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 833  
 ID ABG6276 standard; protein; 979 AA.  
 DE Fibronectin FCB portion/silk-like protein, FCB-SLP1II #2.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 5; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 834  
 ID ADE44984 standard; protein; 979 AA.  
 DE Recombinant structural protein FCB-SLP1II protein seq id 89.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 7; Length 979;  
 Best Local Similarity 27.3%; Pred. No. 2.4e-14;  
 RESULT 835  
 ID AAW26350 standard; protein; 1050 AA.  
 DE FCB-SLP1II (72 kDa) synthetic protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 1050;  
 Best Local Similarity 27.3%; Pred. No. 2.6e-14;  
 RESULT 836  
 ID AAW53527 standard; protein; 1170 AA.  
 DE Amino acid sequence of SELPF protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 15.5%; Score 366; DB 2; Length 1170;  
 Best Local Similarity 27.8%; Pred. No. 2.8e-14;  
 RESULT 837  
 ID AAM50042 standard; protein; 630 AA.  
 DE N. clavipes spideroin synthetic homologue SO1 protein.  
 PN DE10113781-A1.

PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.  
Query Match 15.4%; Score 365.5; DB 5; Length 630;  
Best Local Similarity 29.6%; Pred. No. 1.7e-14;  
RESULT 838  
ID AAM50047 standard; protein; 676 AA.  
DE N. clavipes spidroin synthetic homologue S01 protein #2.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENTIK & KULTURPFLANZE.  
Query Match 15.5%; Score 365.5; DB 5; Length 676;  
Best Local Similarity 29.6%; Pred. No. 1.8e-14;  
RESULT 839  
ID ABU36623 standard; protein; 576 AA.  
DE Protein encoded by Prokaryotic essential gene #22150.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.4%; Score 365; DB 6; Length 576;  
Best Local Similarity 30.2%; Pred. No. 1.7e-14;  
RESULT 840  
ID ABU36439 standard; protein; 591 AA.  
DE Protein encoded by Prokaryotic essential gene #21966.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.4%; Score 365; DB 6; Length 591;  
Best Local Similarity 29.4%; Pred. No. 1.7e-14;  
RESULT 841  
ID ABG69270 standard; protein; 2018 AA.  
DE Silk/Elastin-like protein SELP1.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364.5; DB 5; Length 2018;  
Best Local Similarity 27.4%; Pred. No. 5.9e-14;  
RESULT 842  
ID ADE44975 standard; protein; 2018 AA.  
DE Recombinant structural protein SELP1 protein seq id 80.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364.5; DB 7; Length 2018;  
Best Local Similarity 27.4%; Pred. No. 5.9e-14;  
RESULT 843  
ID AAY78280 standard; peptide; 2100 AA.  
DE SELP1 amino acid sequence SEQ ID NO:80.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364.5; DB 3; Length 2100;  
Best Local Similarity 27.4%; Pred. No. 6.1e-14;  
RESULT 844  
ID ABU36540 standard; protein; 606 AA.  
DE Protein encoded by Prokaryotic essential gene #22067.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.4%; Score 364; DB 6; Length 606;  
Best Local Similarity 29.8%; Pred. No. 2e-14;  
RESULT 845  
ID AAR95112 standard; protein; 649 AA.  
DE Silk like protein (SLP)-L2.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 2; Length 649;  
Best Local Similarity 27.7%; Pred. No. 2.1e-14;  
RESULT 846  
ID AAB64002 standard; protein; 649 AA.  
DE SLP-L1 protein SEQ ID 49.  
PN US6140072-A.  
PD 31-OCT-2000.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 4; Length 649;  
Best Local Similarity 27.7%; Pred. No. 2.1e-14;  
RESULT 847  
ID AAB72732 standard; protein; 649 AA.  
DE Repetitive protein polymer protein sequence #32.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 4; Length 649;  
Best Local Similarity 27.7%; Pred. No. 2.1e-14;  
RESULT 848  
ID AAR95111 standard; protein; 784 AA.  
DE Silk like protein (SLP)-L1.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 2; Length 784;  
Best Local Similarity 31.3%; Pred. No. 2.6e-14;  
RESULT 849  
ID AAB64001 standard; protein; 784 AA.  
DE SLP-L1 protein SEQ ID 48.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 4; Length 784;  
Best Local Similarity 31.3%; Pred. No. 2.6e-14;  
RESULT 850  
ID AAB72731 standard; protein; 784 AA.  
DE Repetitive protein polymer protein sequence #31.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 4; Length 784;  
Best Local Similarity 31.3%; Pred. No. 2.6e-14;  
RESULT 851  
ID AAR05309 standard; protein; 946 AA.  
DE SLP-L2 polymer (similar to silk fibroin).  
PN WO9005177-A.  
PD 17-MAY-1990.  
PA (SYTR ) SYNTRO CORP.  
Query Match 15.4%; Score 364; DB 2; Length 946;  
Best Local Similarity 27.7%; Pred. No. 3.1e-14;  
RESULT 852  
ID AAW01496 standard; protein; 1018 AA.  
DE Silk-like protein SLP-L3.0 polymer.  
PN WO9501998-A2.  
PD 19-JAN-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 2; Length 1018;  
Best Local Similarity 30.5%; Pred. No. 3.3e-14;  
RESULT 853  
ID AAW26345 standard; protein; 2107 AA.  
DE SELP1 synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 2; Length 2107;  
Best Local Similarity 27.4%; Pred. No. 6.6e-14;  
RESULT 854  
ID AAW53521 standard; protein; 2107 AA.  
DE Amino acid sequence of the SELP1 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.4%; Score 364; DB 2; Length 2107;  
Best Local Similarity 27.4%; Pred. No. 6.6e-14;  
RESULT 855  
ID ABU36685 standard; protein; 639 AA.  
DE Protein encoded by Prokaryotic essential gene #22212.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.

Query Match 15.4%; Score 363; DB 6; Length 639;  
Best Local Similarity 30.5%; Pred. No. 2.4e-14;  
RESULT 856  
ID AAR99057 standard; protein; 604 AA.  
DE Spider dragline variant, DP-1B.16 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.3%; Score 362; DB 2; Length 604;  
Best Local Similarity 29.7%; Pred. No. 2.7e-14;  
RESULT 857  
ID AAR95109 standard; protein; 1332 AA.  
DE Silk like protein (SLP)-C.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 2; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 858  
ID AAB63999 standard; protein; 1332 AA.  
DE SLP-C protein sequence SEQ ID 41.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 859  
ID AAB72729 standard; protein; 1332 AA.  
DE Repetitive protein polymer protein sequence #29.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 860  
ID AAP82960 standard; protein; 2055 AA.  
DE SELP2 protein comprising gagags of silk fibroin and gvgvp of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR) SYNTRO CORP.  
Query Match 15.3%; Score 360.5; DB 1; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.1e-13;  
RESULT 861  
ID ABU36590 standard; protein; 562 AA.  
DE Protein encoded by Prokaryotic essential gene #22117.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 360; DB 6; Length 562;  
Best Local Similarity 28.9%; Pred. No. 3.3e-14;  
RESULT 862  
ID ABB76672 standard; protein; 655 AA.  
DE Protein related to Bombyx mori silk fibroin.  
PN WO200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 15.2%; Score 360; DB 5; Length 655;  
Best Local Similarity 28.7%; Pred. No. 3.8e-14;  
RESULT 863  
ID ABU36665 standard; protein; 1011 AA.  
DE Protein encoded by Prokaryotic essential gene #22192.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 359.5; DB 6; Length 1011;  
Best Local Similarity 31.2%; Pred. No. 6.2e-14;  
RESULT 864  
ID AAE36926 standard; protein; 490 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #1.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWT-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 490;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
Query Match 15.4%; Score 363; DB 6; Length 639;  
Best Local Similarity 30.5%; Pred. No. 2.4e-14;  
RESULT 856  
ID AAR99057 standard; protein; 604 AA.  
DE Spider dragline variant, DP-1B.16 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.3%; Score 362; DB 2; Length 604;  
Best Local Similarity 29.7%; Pred. No. 2.7e-14;  
RESULT 857  
ID AAR95109 standard; protein; 1332 AA.  
DE Silk like protein (SLP)-C.  
PN US5514581-A.  
PD 07-MAY-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 2; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 858  
ID AAB63999 standard; protein; 1332 AA.  
DE SLP-C protein sequence SEQ ID 41.  
PN US6140072-A.  
PD 31-OCT-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 362; DB 4; Length 1332;  
Best Local Similarity 28.3%; Pred. No. 5.7e-14;  
RESULT 859  
ID AAB72729 standard; protein; 1332 AA.  
DE Repetitive protein polymer protein sequence #29.  
PN US6184348-B1.  
PD 06-FEB-2001.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.3%; Score 360.5; DB 1; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.1e-13;  
RESULT 861  
ID ABU36590 standard; protein; 562 AA.  
DE Protein encoded by Prokaryotic essential gene #22117.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 360; DB 6; Length 562;  
Best Local Similarity 28.9%; Pred. No. 3.3e-14;  
RESULT 862  
ID ABB76672 standard; protein; 655 AA.  
DE Protein related to Bombyx mori silk fibroin.  
PN WO200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 15.2%; Score 360; DB 5; Length 655;  
Best Local Similarity 28.7%; Pred. No. 3.8e-14;  
RESULT 863  
ID ABU36665 standard; protein; 1011 AA.  
DE Protein encoded by Prokaryotic essential gene #22192.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.2%; Score 359.5; DB 6; Length 1011;  
Best Local Similarity 31.2%; Pred. No. 6.2e-14;  
RESULT 864  
ID AAE36926 standard; protein; 490 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #1.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWT-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 490;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 3.6e-14;  
RESULT 866  
ID AAE36893 standard; protein; 525 AA.  
DE Phidippus audax fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWT-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 525;  
Best Local Similarity 28.9%; Pred. No. 3.6e-14;  
RESULT 867  
ID AAE36886 standard; protein; 854 AA.  
DE Dolomedes tenebrosus fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWT-) UNIV WYOMING.  
Query Match 15.2%; Score 359; DB 6; Length 854;  
Best Local Similarity 26.2%; Pred. No. 5.7e-14;  
RESULT 868  
ID AAY40099 standard; protein; 615 AA.  
DE Spider silk protein spidroine minor 1.  
PN PR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358.5; DB 2; Length 615;  
Best Local Similarity 28.7%; Pred. No. 4.4e-14;  
RESULT 869  
ID AAR41011 standard; protein; 2055 AA.  
DE SELP2 multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 870  
ID AAW26346 standard; protein; 2055 AA.  
DE SELP2 synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 871  
ID AAW53522 standard; protein; 2055 AA.  
DE Amino acid sequence of the SELP2 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 2; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 872  
ID AAY78281 standard; peptide; 2055 AA.  
DE SELP2 amino acid sequence SEQ ID NO:81.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 3; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;  
RESULT 873  
ID ADE44976 standard; protein; 2055 AA.  
DE Recombinant structural protein SELP2 protein seq id 81.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.2%; Score 358.5; DB 7; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 1.4e-13;

RESULT 874  
ID AAR99053 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1A.9 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 29.2%; Pred. No. 4.7e-14;  
RESULT 875  
ID AAR99055 standard; protein; 606 AA.  
DE Spider dragline variant, DP-1B.9 polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 876  
ID AAY40101 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 877  
ID AAY40102 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 30.3%; Pred. No. 4.7e-14;  
RESULT 878  
ID AAY40100 standard; protein; 606 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 1.  
PN FR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA) L'OREAL SA.  
Query Match 15.2%; Score 358; DB 2; Length 606;  
Best Local Similarity 29.2%; Pred. No. 4.7e-14;  
RESULT 879  
ID AAU11793 standard; protein; 809 AA.  
DE Dragline protein 1 analogue DP-1B 8mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 809;  
Best Local Similarity 30.3%; Pred. No. 6.2e-14;  
RESULT 880  
ID AAU11797 standard; protein; 818 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 8mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 818;  
Best Local Similarity 30.3%; Pred. No. 6.3e-14;  
RESULT 881  
ID AAU11794 standard; protein; 1617 AA.  
DE Dragline protein 1 analogue DP-1B 16mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1617;  
Best Local Similarity 30.3%; Pred. No. 1.2e-13;  
RESULT 882  
ID AAU11798 standard; protein; 1626 AA.  
DE Dragline protein 1 analogue DP-1B/his tag 16mer.  
PN WO200190389-A2.  
PD 29-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 15.2%; Score 358; DB 5; Length 1626;  
Best Local Similarity 30.3%; Pred. No. 1.2e-13;  
RESULT 883

ID AAO16494 standard; protein; 761 AA.  
DE Kukulcania hibernalis spider silk protein #1.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 15.1%; Score 357; DB 6; Length 761;  
Best Local Similarity 28.1%; Pred. No. 6.7e-14;  
RESULT 884  
ID ASG69271 standard; protein; 2055 AA.  
DE Silk/Elastin-like protein SLP2.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 15.0%; Score 354.5; DB 5; Length 2055;  
Best Local Similarity 25.6%; Pred. No. 2.5e-13;  
RESULT 885  
ID AAW01494 standard; protein; 945 AA.  
DE Silk-like protein SLP-F9 polymer.  
PN WO9501998-A2.  
PD 19-JAN-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES.  
Query Match 15.0%; Score 354; DB 2; Length 945;  
Best Local Similarity 25.8%; Pred. No. 1.3e-13;  
RESULT 886  
ID ABU34417 standard; protein; 505 AA.  
DE Protein encoded by Prokaryotic essential gene #19944.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 353; DB 6; Length 505;  
Best Local Similarity 32.4%; Pred. No. 8e-14;  
RESULT 887  
ID AAP82961 standard; protein; 2257 AA.  
DE SLP3 protein comprising gagags of silk fibroin and gvgvp of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR) SYNTRO CORP.  
Query Match 14.9%; Score 352.5; DB 1; Length 2257;  
Best Local Similarity 29.6%; Pred. No. 3.6e-13;  
RESULT 888  
ID ABU36613 standard; protein; 603 AA.  
DE Protein encoded by Prokaryotic essential gene #22140.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 352; DB 6; Length 603;  
Best Local Similarity 30.0%; Pred. No. 1.1e-13;  
RESULT 889  
ID AAR80254 standard; peptide; 1056 AA.  
DE Polymer SLP3.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 14.9%; Score 351.5; DB 2; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2e-13;  
RESULT 890  
ID ABP53475 standard; protein; 1056 AA.  
DE Protein polymer SLP3 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPPE/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 14.9%; Score 351.5; DB 5; Length 1056;  
Best Local Similarity 26.5%; Pred. No. 2e-13;  
RESULT 891  
ID ABU36437 standard; protein; 957 AA.  
DE Protein encoded by Prokaryotic essential gene #21964.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.9%; Score 351; DB 6; Length 957;  
Best Local Similarity 28.0%; Pred. No. 2e-13;  
RESULT 892

ID ABU36826 standard; protein; 461 AA.  
 DE Protein encoded by Prokaryotic essential gene #22353.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.8%; Score 350.5; DB 6; Length 461;  
 Best Local Similarity 31.3%; Pred. No. 1e-13;  
 RESULT 893  
 ID AAR41012 standard; protein; 2257 AA.  
 DE SELP3 multimeric protein.  
 PN US243038-A.  
 PD 07-SEP-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 894  
 ID AAW26347 standard; protein; 2257 AA.  
 DE SELP3 synthetic elastomeric protein.  
 PN US5641648-A.  
 PD 24-JUN-1997.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 895  
 ID AAW3523 standard; protein; 2257 AA.  
 DE Amino acid sequence of the SELP3 protein.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 2; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 896  
 ID AAY78282 standard; peptide; 2257 AA.  
 DE SELP3 amino acid sequence SEQ ID NO:82.  
 PN US6018030-A.  
 PD 25-JAN-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 3; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 897  
 ID ARG69272 standard; protein; 2257 AA.  
 DE Silk/Elastin-like protein SELP3.  
 PN US6355776-B1.  
 PD 12-MAR-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 5; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 898  
 ID ADE44977 standard; protein; 2257 AA.  
 DE Recombinant structural protein SELP3 protein seq id 82.  
 PN US2003083464-A1.  
 PD 01-MAY-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 14.8%; Score 350.5; DB 7; Length 2257;  
 Best Local Similarity 29.6%; Pred. No. 4.8e-13;  
 RESULT 899  
 ID ADQ19957 standard; protein; 316 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 14.8%; Score 350; DB 8; Length 316;  
 Best Local Similarity 35.3%; Pred. No. 7.8e-14;  
 RESULT 900  
 ID ABU36684 standard; protein; 618 AA.  
 DE Protein encoded by Prokaryotic essential gene #22211.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.8%; Score 349; DB 6; Length 618;  
 Best Local Similarity 29.9%; Pred. No. 1.7e-13;  
 RESULT 901  
 ID AAB82611 standard; protein; 528 AA.

DE Spider recombinant silk protein pETNCDS.  
 PN WO20015333-A1.  
 PD 26-JUL-2001.  
 PA (WELL/) MELLO C M.  
 PA (ARCI/) ARCIDIACONO S.  
 PA (BUTL/) BUTLER M M.  
 PA (USSA) US SEC OF ARMY.  
 Query Match 14.7%; Score 348.5; DB 4; Length 528;  
 Best Local Similarity 29.0%; Pred. No. 1.6e-13;  
 RESULT 902  
 ID AAR80168 standard; protein; 831 AA.  
 DE PMISS1 WISP spider silk protein insert product.  
 PN WO9525155-A1.  
 PD 21-SEP-1995.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 14.7%; Score 348.5; DB 2; Length 831;  
 Best Local Similarity 28.1%; Pred. No. 2.4e-13;  
 RESULT 903  
 ID AAB36869 standard; protein; 648 AA.  
 DE Argiope trifasciata major ampullate spidroin 1 (Maspl) protein.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 14.6%; Score 346; DB 6; Length 648;  
 Best Local Similarity 27.3%; Pred. No. 2.7e-13;  
 RESULT 904  
 ID ADO8772 standard; protein; 441 AA.  
 DE Novel surgical dressing-related protein SeqID59.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 14.6%; Score 345.5; DB 8; Length 441;  
 Best Local Similarity 27.2%; Pred. No. 2e-13;  
 RESULT 905  
 ID AAW31853 standard; protein; 898 AA.  
 DE Mycobacterium tuberculosis 77 Kda protein.  
 PN WO9741252-A2.  
 PD 06-NOV-1997.  
 PA (GBPB) GBF GES BIOTECH FORSCHUNG GMBH.  
 Query Match 14.6%; Score 344.5; DB 2; Length 898;  
 Best Local Similarity 26.8%; Pred. No. 4.6e-13;  
 RESULT 906  
 ID AAM17023 standard; protein; 283 AA.  
 DE Peptide #3457 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 907  
 ID ABB36017 standard; peptide; 283 AA.  
 DE Peptide #3523 encoded by human foetal liver single exon probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 908  
 ID AAW29514 standard; protein; 283 AA.  
 DE Peptide #3551 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.8%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 909  
 ID ABB30839 standard; peptide; 283 AA.  
 DE Peptide #3490 encoded by breast cell single exon nucleic acid probe.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;

Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 910  
 ID ABB21422 standard; protein; 283 AA.  
 DE Protein #3421 encoded by probe for measuring heart cell gene expression.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 911  
 ID AAM69190 standard; protein; 283 AA.  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29496.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 912  
 ID AAM56810 standard; protein; 283 AA.  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28915.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 913  
 ID AAG50867 standard; peptide; 283 AA.  
 DE Human liver peptide, SEQ ID No 29515.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 914  
 ID AAM04731 standard; protein; 283 AA.  
 DE Peptide #3413 encoded by probe for measuring breast gene expression.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 4; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 915  
 ID AAG38794 standard; peptide; 283 AA.  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 28459.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 14.6%; Score 344; DB 5; Length 283;  
 Best Local Similarity 34.4%; Pred. No. 1.6e-13;  
 RESULT 916  
 ID ABU36839 standard; protein; 525 AA.  
 DE Protein encoded by Prokaryotic essential gene #22366.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.6%; Score 344; DB 6; Length 525;  
 Best Local Similarity 30.4%; Pred. No. 3e-13;  
 RESULT 917  
 ID AAE36884 standard; protein; 651 AA.  
 DE Argiope trifasciata flagelliform silk protein (Flag).  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 14.6%; Score 344; DB 6; Length 651;  
 Best Local Similarity 28.4%; Pred. No. 3.6e-13;  
 RESULT 918  
 ID AAB82609 standard; protein; 681 AA.  
 DE Spider recombinant silk protein PQE((SP1)4/(SP2)1)4.  
 PN WO200153333-A1.  
 PD 26-JUL-2001.  
 PA (MELL/) MELLO C M.  
 PA (ARCI/) ARCIDIACONO S.  
 PA (BUTL/) BUTLER M M.

PA (USSA ) US SEC OF ARMY.  
 Query Match 14.5%; Score 343; DB 4; Length 681;  
 Best Local Similarity 28.3%; Pred. No. 4.4e-13;  
 RESULT 919  
 ID AAB82610 standard; protein; 691 AA.  
 DE Spider recombinant silk protein pET((SP1)4/(SP2)1)4.  
 PN WO200153333-A1.  
 PD 26-JUL-2001.  
 PA (MELL/) MELLO C M.  
 PA (ARCI/) ARCIDIACONO S.  
 PA (BUTL/) BUTLER M M.  
 PA (USSA ) US SEC OF ARMY.  
 Query Match 14.5%; Score 343; DB 4; Length 691;  
 Best Local Similarity 28.3%; Pred. No. 4.4e-13;  
 RESULT 920  
 ID ADB61323 standard; protein; 629 AA.  
 DE Spider silk related ADF-3 protein.  
 PN WO2003060099-A2.  
 PD 24-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 PA (ALWA/) ALWATTARI A.  
 Query Match 14.5%; Score 342.5; DB 7; Length 629;  
 Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
 RESULT 921  
 ID ADC35242 standard; protein; 629 AA.  
 DE ADF-3 silk protein, SEQ ID 3.  
 PN WO2003057727-A1.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 14.5%; Score 342.5; DB 7; Length 629;  
 Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
 RESULT 922  
 ID ADM46151 standard; protein; 629 AA.  
 DE Nephila clavipes ADF-3 protein.  
 PN WO2003057720-A2.  
 PD 17-JUL-2003.  
 PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
 Query Match 14.5%; Score 342.5; DB 7; Length 629;  
 Best Local Similarity 29.5%; Pred. No. 4.4e-13;  
 RESULT 923  
 ID AAM50045 standard; protein; 773 AA.  
 DE N. clavipes spidroin homologue SM12-70xELP for plant expression.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 14.5%; Score 342.5; DB 5; Length 773;  
 Best Local Similarity 29.4%; Pred. No. 5.3e-13;  
 RESULT 924  
 ID AAM50046 standard; protein; 777 AA.  
 DE N. clavipes spidroin homologue SM12-70xELP for E. coli expression.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 14.5%; Score 342.5; DB 5; Length 777;  
 Best Local Similarity 29.4%; Pred. No. 5.3e-13;  
 RESULT 925  
 ID ADO08787 standard; protein; 482 AA.  
 DE Novel surgical dressing-related protein SeqID74.  
 PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN ) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 14.5%; Score 342; DB 8; Length 482;  
 Best Local Similarity 27.1%; Pred. No. 3.6e-13;  
 RESULT 926  
 ID ABU36689 standard; protein; 515 AA.  
 DE Protein encoded by Prokaryotic essential gene #22216.  
 PN WO200271183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 14.5%; Score 342; DB 6; Length 515;  
 Best Local Similarity 29.3%; Pred. No. 3.9e-13;  
 RESULT 927

ID ABU36423 standard; protein; 487 AA.  
DE Protein encoded by Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.4%; Score 339.5; DB 6; Length 487;  
Best Local Similarity 29.9%; Pred. No. 5.2e-13;  
RESULT 928  
ID AAE36885 standard; protein; 1002 AA.  
DE Argiope trifasciata flag protein fragment.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.3%; Score 337; DB 6; Length 1002;  
Best Local Similarity 29.9%; Pred. No. 1.5e-12;  
RESULT 929  
ID AAE18320 standard; protein; 968 AA.  
DE Silk elastin combination protein, SELP3.  
PN WO200200016-A1.  
PD 03-JAN-2002.  
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
Query Match 14.2%; Score 336.5; DB 5; Length 968;  
Best Local Similarity 29.6%; Pred. No. 1.5e-12;  
RESULT 930  
ID ABP53479 standard; protein; 1169 AA.  
DE Protein polymer SELPF polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPF-) CAPPELLO J.  
PA (STED-) STEDRONSKY E R.  
Query Match 14.2%; Score 336; DB 5; Length 1169;  
Best Local Similarity 30.5%; Pred. No. 2e-12;  
RESULT 931  
ID ADO08775 standard; protein; 482 AA.  
DE Novel surgical dressing-related protein SeqID62.  
PN JF2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 14.2%; Score 335; DB 8; Length 482;  
Best Local Similarity 30.6%; Pred. No. 9.8e-13;  
RESULT 932  
ID ADP31119 standard; protein; 8973 AA.  
DE Human secreted protein SEQ ID #1886.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 14.2%; Score 335; DB 8; Length 8973;  
Best Local Similarity 29.9%; Pred. No. 1.6e-11;  
RESULT 933  
ID AAW79137 standard; protein; 261 AA.  
DE FLGA Gly-ala insert present in chimeric IkappaB construct.  
PN WO9822577-A1.  
PD 28-MAY-1998.  
PA (MASU/) MASUCCI M G.  
Query Match 14.2%; Score 334.5; DB 2; Length 261;  
Best Local Similarity 29.1%; Pred. No. 5.8e-13;  
RESULT 934  
ID AAE36927 standard; protein; 440 AA.  
DE Nephila clavipes minor ampullate spidroin 1 consensus protein #2.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.1%; Score 334; DB 6; Length 440;  
Best Local Similarity 27.9%; Pred. No. 1e-12;  
RESULT 935  
ID ABP72662 standard; protein; 498 AA.  
DE Rv181c gene product of Mycobacterium tuberculosis.  
PN WO2003018754-A2.  
PD 05-MAR-2003.  
PA (NEUR-) NEURONZ LTD.  
PA (NEUR-) NEURONZ BIOSCIENCES INC.  
Query Match 14.1%; Score 334; DB 6; Length 498;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 936  
ID ABU36686 standard; protein; 498 AA.  
DE Protein encoded by Prokaryotic essential gene #22213.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.1%; Score 334; DB 6; Length 498;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 937  
ID ABB68951 standard; protein; 342 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33645.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 14.1%; Score 332.5; DB 4; Length 342;  
Best Local Similarity 29.5%; Pred. No. 1e-12;  
RESULT 938  
ID AAM50043 standard; protein; 364 AA.  
DE N. clavipes spidroin synthetic homologue SM12 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 14.0%; Score 331.5; DB 5; Length 364;  
Best Local Similarity 29.3%; Pred. No. 1.2e-12;  
RESULT 939  
ID AAE36868 standard; protein; 447 AA.  
DE Argiope aurantia major ampullate spidroin 1 (MaSp1) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 14.0%; Score 330; DB 6; Length 447;  
Best Local Similarity 29.5%; Pred. No. 1.8e-12;  
RESULT 940  
ID ADK51951 standard; protein; 780 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 19.  
PN WO2003099465-A1.  
PD 04-DEC-2003.  
PA (DOWO) DOW CORNING CORP.  
PA (GEWV) GENECOR INT INC.  
Query Match 13.9%; Score 329; DB 8; Length 780;  
Best Local Similarity 26.9%; Pred. No. 3.6e-12;  
RESULT 941  
ID ADR70468 standard; protein; 780 AA.  
DE Silk-elastin polymer SELP47K.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KOMA/) KOMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.9%; Score 329; DB 8; Length 780;  
Best Local Similarity 26.9%; Pred. No. 3.6e-12;  
RESULT 942  
ID ADO08759 standard; protein; 302 AA.  
DE Novel surgical dressing-related protein SeqID46.  
PN JF2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.8%; Score 326.5; DB 8; Length 302;  
Best Local Similarity 29.8%; Pred. No. 2.1e-12;  
RESULT 943  
ID ABB81230 standard; protein; 334 AA.  
DE Mycobacterium bovis BCG strain Pasteur PE-PGRS protein sequence.  
PN WO954487-A2.  
PD 28-OCT-1999.  
PA (INSP-) INST PASTEUR.  
Query Match 13.8%; Score 326.5; DB 3; Length 334;  
Best Local Similarity 30.0%; Pred. No. 2.3e-12;  
RESULT 944  
ID ABU36981 standard; protein; 439 AA.  
DE Protein encoded by Prokaryotic essential gene #22508.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.8%; Score 325.5; DB 6; Length 439;  
Best Local Similarity 29.0%; Pred. No. 3.4e-12;  
RESULT 945  
ID ADO08784 standard; protein; 471 AA.  
DE Novel surgical dressing-related protein SeqID71.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.7%; Score 324.5; DB 8; Length 471;  
Best Local Similarity 28.1%; Pred. No. 4.2e-12;  
RESULT 946  
ID ADO08764 standard; protein; 482 AA.  
DE Novel surgical dressing-related protein SeqID51.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.7%; Score 324; DB 8; Length 482;  
Best Local Similarity 29.3%; Pred. No. 4.6e-12;  
RESULT 947  
ID ADR70478 standard; protein; 1038 AA.  
DE Silk-elastin polymer SCLP 67K.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KOMA/) KOMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.7%; Score 324; DB 8; Length 1038;  
Best Local Similarity 25.0%; Pred. No. 9.6e-12;  
RESULT 948  
ID AAR80255 standard; peptide; 972 AA.  
DE Polymer SCLP4.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 13.6%; Score 322.5; DB 2; Length 972;  
Best Local Similarity 24.8%; Pred. No. 1.1e-11;  
RESULT 949  
ID ABP53476 standard; protein; 972 AA.  
DE Protein polymer SCLP4 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 13.6%; Score 322.5; DB 5; Length 972;  
Best Local Similarity 24.8%; Pred. No. 1.1e-11;  
RESULT 950  
ID AAB70185 standard; peptide; 504 AA.  
DE Peptide dendrimer carrier #10.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 504;  
Best Local Similarity 29.1%; Pred. No. 6.9e-12;  
RESULT 951  
ID AAB70186 standard; peptide; 1016 AA.  
DE Peptide dendrimer carrier #11.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 1016;  
Best Local Similarity 29.1%; Pred. No. 1.3e-11;  
RESULT 952  
ID AAB70187 standard; peptide; 2040 AA.  
DE Peptide dendrimer carrier #12.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.6%; Score 321.5; DB 4; Length 2040;  
Best Local Similarity 29.1%; Pred. No. 2.6e-11;  
RESULT 953

ID ABU36473 standard; protein; 594 AA.  
DE Protein encoded by Prokaryotic essential gene #22000.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 320; DB 6; Length 594;  
Best Local Similarity 31.4%; Pred. No. 1e-11;  
RESULT 954  
ID ABB70834 standard; protein; 620 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39294.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 13.5%; Score 320; DB 4; Length 620;  
Best Local Similarity 26.7%; Pred. No. 1e-11;  
RESULT 955  
ID AAB36881 standard; protein; 1953 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 13.5%; Score 320; DB 6; Length 1953;  
Best Local Similarity 26.9%; Pred. No. 3.1e-11;  
RESULT 956  
ID ADP31118 standard; protein; 5820 AA.  
DE Human secreted protein SEQ ID #1885.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 13.5%; Score 318.5; DB 8; Length 5820;  
Best Local Similarity 29.2%; Pred. No. 1.1e-10;  
RESULT 957  
ID ABB81229 standard; protein; 318 AA.  
DE Mycobacterium tuberculosis strain H37Rv PE-PCR protein sequence.  
PN WO954487-A2.  
PD 28-OCT-1999.  
PA (INSP) INST PASTEUR.  
Query Match 13.5%; Score 318; DB 3; Length 318;  
Best Local Similarity 32.2%; Pred. No. 7.3e-12;  
RESULT 958  
ID ADR70473 standard; protein; 884 AA.  
DE Silk-elastin polymer SCLP 47-E13.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KOMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.5%; Score 318; DB 8; Length 884;  
Best Local Similarity 26.6%; Pred. No. 1.9e-11;  
RESULT 959  
ID AAR80253 standard; peptide; 988 AA.  
DE Polymer SCLP7.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 13.4%; Score 317.5; DB 2; Length 988;  
Best Local Similarity 28.6%; Pred. No. 2.3e-11;  
RESULT 960  
ID ABP53474 standard; protein; 988 AA.  
DE Protein polymer SCLP7 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPE/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 13.4%; Score 317.5; DB 5; Length 988;  
Best Local Similarity 28.6%; Pred. No. 2.3e-11;  
RESULT 961  
ID ADO59401 standard; protein; 2655 AA.  
DE Antheraea yamamai fibroin.  
PN KR2002094304-A.  
PD 18-DEC-2002.  
PA (KURA-) RURAL DEV ADMINISTRATION.  
Query Match 13.4%; Score 317; DB 7; Length 2655;  
Best Local Similarity 25.6%; Pred. No. 6.4e-11;



RESULT 962  
ID ADO8778 standard; protein; 506 AA.  
DE Novel surgical dressing-related protein SeqID65.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.4%; Score 316; DB 8; Length 506;  
Best Local Similarity 28.3%; Pred. No. 1.5e-11;  
RESULT 963  
ID ADR70479 standard; protein; 965 AA.  
DE Silk-elastin polymer SEMP 58.  
PN US2004180027-A1.  
PD 16-SEP-2004.  
PA (KUMA/) KUMAR M.  
PA (CUEV/) CUEVAS W A.  
Query Match 13.4%; Score 315.5; DB 8; Length 965;  
Best Local Similarity 26.4%; Pred. No. 3e-11;  
RESULT 964  
ID AAM94219 standard; protein; 116 AA.  
DE Human reproductive system related antigen SEQ ID NO: 2877.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.3%; Score 314; DB 4; Length 116;  
Best Local Similarity 98.2%; Pred. No. 4.9e-12;  
RESULT 965  
ID AAB70180 standard; peptide; 1488 AA.  
DE Peptide dendrimer carrier #5.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 13.2%; Score 312; DB 4; Length 1488;  
Best Local Similarity 28.9%; Pred. No. 7.4e-11;  
RESULT 966  
ID ADG88556 standard; protein; 200 AA.  
DE Poly Gly flexible linker.  
PN US2003176333-A1.  
PD 18-SEP-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 13.1%; Score 309.5; DB 7; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 967  
ID ADJ84541 standard; protein; 200 AA.  
DE T2R G-protein coupled receptor related linker seq id 94.  
PN US2004038312-A1.  
PD 26-FEB-2004.  
PA (ZUKER/) ZUKER C S.  
PA (ADLER/) ADLER J E.  
PA (HOON/) HOON M.  
PA (RYBA/) RYBA N.  
PA (MUELL/) MUELLER K.  
Query Match 13.1%; Score 309.5; DB 8; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 968  
ID ADM96215 standard; protein; 200 AA.  
DE Poly Gly flexible linker.  
PN US2004071708-A1.  
PD 15-APR-2004.  
PA (IMMU-) IMMUSOL INC.  
Query Match 13.1%; Score 309.5; DB 8; Length 200;  
Best Local Similarity 32.3%; Pred. No. 1.6e-11;  
RESULT 969  
ID ADO8771 standard; protein; 296 AA.  
DE Novel surgical dressing-related protein SeqID58.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 13.1%; Score 309.5; DB 8; Length 296;  
Best Local Similarity 27.3%; Pred. No. 2.3e-11;  
RESULT 970  
ID ABG71303 standard; protein; 201 AA.  
DE PINPOINT poly-Gly linker protein.  
PN US6444421-B1.  
PD 03-SEP-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 13.1%; Score 309; DB 5; Length 201;  
Best Local Similarity 31.9%; Pred. No. 1.7e-11;  
RESULT 971  
ID AAW05704 standard; peptide; 235 AA.  
DE Glycine-rich repeat sequence of EBV nuclear antigen.  
PN WO9632483-A1.  
PD 17-OCT-1996.  
PA (MASU/) MASUCCI M.  
Query Match 13.0%; Score 308; DB 2; Length 235;  
Best Local Similarity 29.6%; Pred. No. 2.2e-11;  
RESULT 972  
ID AAW79126 standard; protein; 235 AA.  
DE Epstein Barr Virus EBNA1 protein gly-ala repeat region.  
PN WO9822577-A1.  
PD 28-MAY-1998.  
PA (MASU/) MASUCCI M G.  
Query Match 13.0%; Score 308; DB 2; Length 235;  
Best Local Similarity 29.6%; Pred. No. 2.2e-11;  
RESULT 973  
ID AAB70188 standard; peptide; 465 AA.  
DE Peptide dendrimer carrier #13.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 12.9%; Score 305.5; DB 4; Length 465;  
Best Local Similarity 27.9%; Pred. No. 6.1e-11;  
RESULT 974  
ID ABB61734 standard; protein; 1039 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11994.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.9%; Score 305.5; DB 4; Length 1039;  
Best Local Similarity 27.5%; Pred. No. 1.3e-10;  
RESULT 975  
ID ADP31138 standard; protein; 1350 AA.  
DE Human secreted protein SEQ ID #1905.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.9%; Score 304.5; DB 8; Length 1350;  
Best Local Similarity 26.0%; Pred. No. 2e-10;  
RESULT 976  
ID ADP31137 standard; protein; 1719 AA.  
DE Human secreted protein SEQ ID #1904.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.9%; Score 304.5; DB 8; Length 1719;  
Best Local Similarity 26.0%; Pred. No. 2.5e-10;  
RESULT 977  
ID ADO8774 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SeqID61.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.8%; Score 303.5; DB 8; Length 322;  
Best Local Similarity 31.6%; Pred. No. 5.7e-11;  
RESULT 978  
ID ADS28501 standard; protein; 592 AA.  
DE Bacterial polypeptide #17534.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

Query Match 12.8%; Score 302; DB 8; Length 592;  
Best Local Similarity 27.7%; Pred. No. 1.3e-10;  
RESULT 979  
ID AAR99059 standard; protein; 714 AA.  
DE Spider dragline variant, DP-2A polymer.  
PN WO9429450-A2.  
PD 22-DEC-1994.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 1.5e-10;  
RESULT 980  
ID AAY40103 standard; protein; 714 AA.  
DE Polymer of an analogue of spider silk protein spidroine major 2.  
PN PR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 12.8%; Score 302; DB 2; Length 714;  
Best Local Similarity 28.4%; Pred. No. 1.5e-10;  
RESULT 981  
ID ADO08790 standard; protein; 506 AA.  
DE Novel surgical dressing-related protein SeqID77.  
PN JF2004049521-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.7%; Score 301; DB 8; Length 506;  
Best Local Similarity 26.6%; Pred. No. 1.3e-10;  
RESULT 982  
ID ADS88365 standard; protein; 622 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 220.  
PN WO2004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZOME AG.  
Query Match 12.7%; Score 300.5; DB 8; Length 622;  
Best Local Similarity 26.2%; Pred. No. 1.6e-10;  
RESULT 983  
ID ABP53481 standard; protein; 768 AA.  
DE Protein polymer SELP8K polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.7%; Score 300.5; DB 5; Length 768;  
Best Local Similarity 26.8%; Pred. No. 2e-10;  
RESULT 984  
ID AAR0341 standard; protein; 884 AA.  
DE Protein polymer adhesive substrate SELP8K.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 985  
ID AA09213 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 986  
ID AA053541 standard; protein; 884 AA.  
DE Expected amino acid sequence of pPT0345 encoding SELP8K polymer.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 987  
ID AA049728 standard; protein; 884 AA.  
DE SELP8K polymer.  
PN US5773577-A.  
PD 30-JUN-1998.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 2; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 988  
ID AAY51882 standard; protein; 884 AA.  
DE Plasmid pPT0345 protein fragment containing SELP8K polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 3; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 989  
ID ABG31412 standard; protein; 884 AA.  
DE SELP8K polymer encoded by plasmid pPT0345.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 5; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 990  
ID ABW01628 standard; protein; 884 AA.  
DE Plasmid pPT0345 SELP8K polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.7%; Score 300.5; DB 7; Length 884;  
Best Local Similarity 26.8%; Pred. No. 2.3e-10;  
RESULT 991  
ID AAW56163 standard; protein; 738 AA.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JP10080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIVAKU KK.  
Query Match 12.7%; Score 300; DB 2; Length 738;  
Best Local Similarity 24.4%; Pred. No. 2.1e-10;  
RESULT 992  
ID AAE36879 standard; protein; 373 AA.  
DE Latrodectus geometricus major ampullate spidroin 2 (MaSp2) protein #1.  
PN WO20031020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.7%; Score 299; DB 6; Length 373;  
Best Local Similarity 28.0%; Pred. No. 1.2e-10;  
RESULT 993  
ID AAR80256 standard; peptide; 1024 AA.  
DE Polymer SELP5.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.5%; Score 296.5; DB 2; Length 1024;  
Best Local Similarity 21.8%; Pred. No. 4.7e-10;  
RESULT 994  
ID ABP53477 standard; protein; 1024 AA.  
DE Protein polymer SELP5 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.5%; Score 296.5; DB 5; Length 1024;  
Best Local Similarity 21.8%; Pred. No. 4.7e-10;  
RESULT 995  
ID AAY40098 standard; protein; 531 AA.  
DE Spider silk protein spidroine major 2.  
PN PR2774588-A1.  
PD 13-AUG-1999.  
PA (OREA ) L'OREAL SA.  
Query Match 12.5%; Score 296; DB 2; Length 531;  
Best Local Similarity 27.7%; Pred. No. 2.7e-10;  
RESULT 996  
ID AAR14309 standard; protein; 595 AA.  
DE N-clavipes dragline silk protein-2.  
PN EP452925-A.  
PD 23-OCT-1991.

PA (UYWY-) UNIV OF WYOMING.  
Query Match 12.5%; Score 296; DB 2; Length 595;  
Best Local Similarity 27.7%; Pred. No. 3e-10;  
RESULT 997  
ID RAW53347 standard; protein; 595 AA.  
DE Nephila clavipes spider silk protein.  
PN US5728810-A.  
PD 17-MAR-1998.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.5%; Score 296; DB 2; Length 595;  
Best Local Similarity 27.7%; Pred. No. 3e-10;  
RESULT 998  
ID AAY59071 standard; protein; 595 AA.  
DE N. clavipes spider silk protein 2.  
PN US5989894-A.  
PD 23-NOV-1999.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.5%; Score 296; DB 3; Length 595;  
Best Local Similarity 27.7%; Pred. No. 3e-10;  
RESULT 999  
ID AAO16488 standard; protein; 624 AA.  
DE Nephila clavipes dragline silk fibronin protein.  
PN WO20029082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.5%; Score 296; DB 6; Length 624;  
Best Local Similarity 27.7%; Pred. No. 3.1e-10;  
RESULT 1000  
ID ADC3241 standard; protein; 627 AA.  
DE Maspil silk protein, SEQ ID 2.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 12.5%; Score 296; DB 7; Length 627;  
Best Local Similarity 27.7%; Pred. No. 3.1e-10;  
RESULT 1001  
ID AAR80252 standard; peptide; 832 AA.  
DE Polymer SELP8.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.5%; Score 294.5; DB 2; Length 832;  
Best Local Similarity 27.1%; Pred. No. 5.1e-10;  
RESULT 1002  
ID ABP53473 standard; protein; 832 AA.  
DE Protein polymer SELP8 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.5%; Score 294.5; DB 5; Length 832;  
Best Local Similarity 27.1%; Pred. No. 5.1e-10;  
RESULT 1003  
ID AAB23358 standard; protein; 674 AA.  
DE Human trophinin protein from residue 69 to 749.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Query Match 12.4%; Score 294; DB 3; Length 674;  
Best Local Similarity 28.7%; Pred. No. 4.4e-10;  
RESULT 1004  
ID ADC86917 standard; protein; 821 AA.  
DE Human GPCR protein SEQ ID NO.1370.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 12.4%; Score 294; DB 7; Length 821;  
Best Local Similarity 31.1%; Pred. No. 5.4e-10;  
RESULT 1005  
ID ABB67074 standard; protein; 586 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28014.  
PN WO200171042-A2.

PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.4%; Score 293.5; DB 4; Length 586;  
Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
RESULT 1006  
ID ABB62822 standard; protein; 586 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15258.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 12.4%; Score 293.5; DB 4; Length 586;  
Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
RESULT 1007  
ID ADS96696 standard; protein; 586 AA.  
DE Drosophila melanogaster protein, SEQ ID 317.  
PN WO2004039999-A2.  
PD 13-MAY-2004.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 12.4%; Score 293.5; DB 8; Length 586;  
Best Local Similarity 26.6%; Pred. No. 4.2e-10;  
RESULT 1008  
ID ADA07852 standard; protein; 611 AA.  
DE Pinctada margaritifera nacrein.  
PN US2003027258-A1.  
PD 06-FEB-2003.  
PA (CHAN/) CHANG F F.  
PA (LIHH/) LI H.  
PA (HSIEH/) HSIEH-LI H M.  
Query Match 12.4%; Score 293.5; DB 6; Length 611;  
Best Local Similarity 26.5%; Pred. No. 4.3e-10;  
RESULT 1009  
ID ABO23517 standard; protein; 256 AA.  
DE Mycobacterium tuberculosis outlier protein #1.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match 12.4%; Score 293; DB 7; Length 256;  
Best Local Similarity 31.1%; Pred. No. 2e-10;  
RESULT 1010  
ID ADO08786 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SeqID73.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.4%; Score 292.5; DB 8; Length 322;  
Best Local Similarity 28.8%; Pred. No. 2.7e-10;  
RESULT 1011  
ID AAE36889 standard; protein; 912 AA.  
DE Plecteurys tristis fibroin 1 protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.4%; Score 292; DB 6; Length 912;  
Best Local Similarity 23.4%; Pred. No. 7.9e-10;  
RESULT 1012  
ID AAR94895 standard; protein; 749 AA.  
DE Human trophinin.  
PN WO9610414-A1.  
PD 11-APR-1996.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match 12.3%; Score 290.5; DB 2; Length 749;  
Best Local Similarity 27.6%; Pred. No. 8.1e-10;  
RESULT 1013  
ID AAB23357 standard; protein; 749 AA.  
DE Human trophinin protein.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Query Match 12.3%; Score 290.5; DB 3; Length 749;

Best Local Similarity 27.6%; Pred. No. 8.1e-10;  
RESULT 1014  
ID ABO60408 standard; protein; 805 AA.  
DE Human genome derived single exon protein #6642.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 12.3%; Score 290.5; DB 8; Length 805;  
Best Local Similarity 27.6%; Pred. No. 8.6e-10;  
RESULT 1015  
ID AAB94744 standard; protein; 814 AA.  
DE Human protein sequence SEQ ID NO:15790.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.3%; Score 290.5; DB 4; Length 814;  
Best Local Similarity 27.6%; Pred. No. 8.7e-10;  
RESULT 1016  
ID AAM94034 standard; protein; 814 AA.  
DE Human stomach cancer expressed polypeptide SEQ ID NO 139.  
PN WO200109317-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.3%; Score 290.5; DB 4; Length 814;  
Best Local Similarity 27.6%; Pred. No. 8.7e-10;  
RESULT 1017  
ID AAU32728 standard; protein; 1406 AA.  
DE Novel human secreted protein #3219.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.3%; Score 290.5; DB 4; Length 1406;  
Best Local Similarity 27.6%; Pred. No. 1.5e-09;  
RESULT 1018  
ID AAY04999 standard; protein; 388 AA.  
DE Mycobacterium species protein sequence 50C.  
PN WO9090186-A2.  
PD 25-FEB-1999.  
PA (INSP-) INST PASTEUR.  
Query Match 12.2%; Score 289; DB 2; Length 388;  
Best Local Similarity 30.4%; Pred. No. 5.3e-10;  
RESULT 1019  
ID ADB61322 standard; protein; 627 AA.  
DE Spider silk related MasP11 protein.  
PN WO2003060099-A2.  
PD 24-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
PA (ALWA/) ALWATTARI A.  
Query Match 12.2%; Score 289; DB 7; Length 627;  
Best Local Similarity 28.2%; Pred. No. 8.4e-10;  
RESULT 1020  
ID ADM46150 standard; protein; 627 AA.  
DE Nephila clavipes spidroin 2 (MasP11) protein.  
PN WO2003057720-A2.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 12.2%; Score 289; DB 7; Length 627;  
Best Local Similarity 28.2%; Pred. No. 8.4e-10;  
RESULT 1021  
ID ABP53466 standard; protein; 768 AA.  
DE SLP8 related amino acid sequence #2.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 12.2%; Score 288.5; DB 5; Length 768;  
Best Local Similarity 26.6%; Pred. No. 1.1e-09;  
RESULT 1022  
ID AAR80335 standard; protein; 877 AA.  
DE Protein polymeric adhesion substrate 1-G.  
PN WO9523611-A1.

PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.2e-09;  
RESULT 1023  
ID AAW49724 standard; protein; 877 AA.  
DE Protein polymer adhesive substrate PPAS1-G.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 12.2%; Score 288.5; DB 2; Length 877;  
Best Local Similarity 26.6%; Pred. No. 1.2e-09;  
RESULT 1024  
ID ADO8763 standard; protein; 322 AA.  
DE Novel surgical dressing-related protein SeqID50.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.1%; Score 286; DB 8; Length 322;  
Best Local Similarity 29.8%; Pred. No. 6.8e-10;  
RESULT 1025  
ID AAE36882 standard; protein; 563 AA.  
DE Nephila madagascariensis major ampullate spidroin 2 (MasP2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 12.1%; Score 286; DB 6; Length 563;  
Best Local Similarity 26.3%; Pred. No. 1.2e-09;  
RESULT 1026  
ID ABB60403 standard; protein; 2112 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 12.1%; Score 286; DB 4; Length 2112;  
Best Local Similarity 24.3%; Pred. No. 4.1e-09;  
RESULT 1027  
ID AAM78356 standard; protein; 536 AA.  
DE Human protein SEQ ID NO 1018.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 285; DB 4; Length 536;  
Best Local Similarity 29.6%; Pred. No. 1.3e-09;  
RESULT 1028  
ID AAM50044 standard; protein; 271 AA.  
DE N. clavipes spidroin synthetic homologue SF1 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 12.0%; Score 283.5; DB 5; Length 271;  
Best Local Similarity 29.7%; Pred. No. 8.2e-10;  
RESULT 1029  
ID AAB06023 standard; protein; 401 AA.  
DE Polar gelatin P tetramer, P4.  
PN EP1014176-A2.  
PD 28-JUN-2000.  
PA (FUJF) FUJII PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 3; Length 401;  
Best Local Similarity 33.9%; Pred. No. 1.2e-09;  
RESULT 1030  
ID AAY72375 standard; protein; 599 AA.  
DE Amphiphilic recombinant collagen-like polymer, N1N2P4.  
PN EP1063565-A1.  
PD 27-DEC-2000.  
PA (FUJF) FUJII PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 4; Length 599;  
Best Local Similarity 33.9%; Pred. No. 1.8e-09;  
RESULT 1031  
ID AAY72374 standard; protein; 599 AA.  
DE Amphiphilic recombinant collagen-like polymer, N1N1P4.  
PN EP1063565-A1.

PD 27-DEC-2000.  
PA (FUJIF ) FUJI PHOTO FILM BV.  
Query Match 12.0%; Score 283.5; DB 4; Length 599;  
Best Local Similarity 33.9%; Pred. No. 1.8e-09;  
RESULT 1032  
ID AAB23367 standard; protein; 1160 AA.  
DE Mouse trophinin protein.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Query Match 12.0%; Score 283; DB 3; Length 1160;  
Best Local Similarity 29.6%; Pred. No. 3.5e-09;  
RESULT 1033  
ID ADO08783 standard; protein; 316 AA.  
DE Novel surgical dressing-related protein SeqID70.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN ) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 12.0%; Score 282.5; DB 8; Length 316;  
Best Local Similarity 27.6%; Pred. No. 1.1e-09;  
RESULT 1034  
ID ADH59864 standard; protein; 258 AA.  
DE Silk protein related protein #SEQ ID 33.  
PN WO2003100065-A1.  
PD 04-DEC-2003.  
PA (UYNI-) UNIV JAPAN TOKYO AGR.  
Query Match 11.9%; Score 280.5; DB 8; Length 258;  
Best Local Similarity 29.4%; Pred. No. 1.2e-09;  
RESULT 1035  
ID AAB36876 standard; protein; 444 AA.  
DE Argiopoie trifasciata major ampullate spidroin 2 (MasP2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 11.8%; Score 280; DB 6; Length 444;  
Best Local Similarity 27.1%; Pred. No. 2.2e-09;  
RESULT 1036  
ID ADN35278 standard; protein; 1028 AA.  
DE Helical domain of type III collagen #2.  
PN WO2004028404-A2.  
PD 08-APR-2004.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.8%; Score 280; DB 8; Length 1028;  
Best Local Similarity 27.4%; Pred. No. 4.8e-09;  
RESULT 1037  
ID ADN35277 standard; protein; 1313 AA.  
DE Helical domain of type III collagen.  
PN WO2004028404-A2.  
PD 08-APR-2004.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.8%; Score 280; DB 8; Length 1313;  
Best Local Similarity 27.4%; Pred. No. 6.1e-09;  
RESULT 1038  
ID ADE61480 standard; protein; 1380 AA.  
DE Rat Protein AAC05725, SEQ ID NO 7400.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.8%; Score 280; DB 7; Length 1380;  
Best Local Similarity 31.7%; Pred. No. 6.4e-09;  
RESULT 1039  
ID ABB50291 standard; protein; 1466 AA.  
DE Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 11.8%; Score 280; DB 4; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1040  
ID ABB90747 standard; protein; 1466 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.

PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.8%; Score 280; DB 5; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1041  
ID ABUS4454 standard; protein; 1466 AA.  
DE Human tumour endothelial marker TEM 15.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.8%; Score 280; DB 6; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1042  
ID ABR47418 standard; protein; 1466 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:68.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 11.8%; Score 280; DB 6; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1043  
ID ADP65248 standard; protein; 1466 AA.  
DE Human alpha 1 type III collagen preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 11.8%; Score 280; DB 7; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1044  
ID ADP65210 standard; protein; 1466 AA.  
DE Human alpha 1 type III collagen preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 11.8%; Score 280; DB 7; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1045  
ID ADQ26091 standard; protein; 1466 AA.  
DE Type III, alpha 1 collagen.  
PN WO2004056386-A2.  
PD 08-JUL-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1046  
ID ADQ29677 standard; protein; 1466 AA.  
DE Human colorectal cancer-associated protein #32.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1047  
ID ADR16802 standard; protein; 1466 AA.  
DE Human collagen III alpha2 (III) fragment protein.  
PN US2004151731-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1048  
ID ADR16427 standard; protein; 1466 AA.  
DE Human collagen I alpha2 (III) fragment protein.  
PN US2004151732-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
PA (PELU/) PELUSE S.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1049  
ID AEM80366 standard; protein; 1466 AA.

DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.  
PN WO2004030615-A2.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 11.8%; Score 278.5; DB 5; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1058  
ID ADI26117 standard; protein; 526 AA.  
DE Human protein that promotes STAT6 activation #41.  
PN WO2003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH) ASAH KASEI KK.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1059  
ID ABM81732 standard; protein; 526 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO82568, SEQ:4466.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1060  
ID ADS88302 standard; protein; 526 AA.  
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 157.  
PN WO2004035783-A2.  
PD 29-APR-2004.  
PA (CELL-) CELLZONE AG.  
Query Match 11.8%; Score 278.5; DB 8; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1061  
ID ABB61650 standard; protein; 2280 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11742.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 11.8%; Score 278.5; DB 4; Length 2280;  
Best Local Similarity 26.3%; Pred. No. 1.3e-08;  
RESULT 1062  
ID AAR71704 standard; protein; 1078 AA.  
DE Collagen alpha 1 (III) chain precursor.  
PN WO9508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.8%; Score 278; DB 2; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 6.7e-09;  
RESULT 1063  
ID ABU40120 standard; protein; 237 AA.  
DE Protein encoded by Prokaryotic essential gene #25647.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.7%; Score 277; DB 6; Length 237;  
Best Local Similarity 30.7%; Pred. No. 1.8e-09;  
RESULT 1064  
ID ABP53461 standard; protein; 768 AA.  
DE SELP5 related amino acid sequence #3.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPE/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.7%; Score 276.5; DB 5; Length 768;  
Best Local Similarity 23.1%; Pred. No. 6e-09;  
RESULT 1065  
ID ADE59683 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5579.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1066  
ID ADD45148 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 10581.

DE Tumour-associated antigenic target (TAT) polypeptide PRO2665, SEQ:922.  
PN WO2004030615-A2.  
PA (GETH) GENENTECH INC.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1050  
ID ADR67267 standard; protein; 1466 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (HAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 11.8%; Score 280; DB 8; Length 1466;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1051  
ID ABG15191 standard; protein; 1469 AA.  
DE Novel human diagnostic protein #15182.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 280; DB 4; Length 1469;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1052  
ID ADE09399 standard; protein; 1470 AA.  
DE Novel protein-related contig polypeptide sequence #465.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 280; DB 7; Length 1470;  
Best Local Similarity 27.4%; Pred. No. 6.8e-09;  
RESULT 1053  
ID ABR42661 standard; protein; 1726 AA.  
DE Decorin-modified pro-alpha chain.  
PN WO2003035692-A2.  
PD 01-MAY-2003.  
PA (UYMA-) UNIV VICTORIA MANCHESTER.  
Query Match 11.8%; Score 280; DB 6; Length 1726;  
Best Local Similarity 27.4%; Pred. No. 7.9e-09;  
RESULT 1054  
ID ADO08777 standard; protein; 338 AA.  
DE Novel surgical dressing-related protein SeqID64.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 11.8%; Score 279; DB 8; Length 338;  
Best Local Similarity 29.2%; Pred. No. 1.9e-09;  
RESULT 1055  
ID ADP99004 standard; protein; 1096 AA.  
DE C. albicans specific gene, CayMR047C, protein sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 11.8%; Score 279; DB 8; Length 1096;  
Best Local Similarity 27.4%; Pred. No. 5.9e-09;  
RESULT 1056  
ID AAM78355 standard; protein; 526 AA.  
DE Human protein SEQ ID NO 1017.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.8%; Score 278.5; DB 4; Length 526;  
Best Local Similarity 27.7%; Pred. No. 3.1e-09;  
RESULT 1057  
ID AEG95081 standard; protein; 526 AA.  
DE Human translocation (12; 16)(q13; p11) protein #2.  
PN WO200269900-A2.

PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1067  
ID ADD45604 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 11270.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1068  
ID ADE59687 standard; protein; 1372 AA.  
DE Rat Protein P02466, SEQ ID NO 5583.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1069  
ID ADD47529 standard; protein; 1372 AA.  
DE Rat Protein AAD41775, SEQ ID NO 13225.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 11.7%; Score 276.5; DB 7; Length 1372;  
Best Local Similarity 30.4%; Pred. No. 1e-08;  
RESULT 1070  
ID AAY84548 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP92586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 8.6e-09;  
RESULT 1071  
ID AAY84547 standard; protein; 1040 AA.  
DE A human collagen 1 (alpha2) protein helical region.  
PN EP92586-A2.  
PD 12-APR-2000.  
PA (USSU ) US SURGICAL CORP.  
Query Match 11.7%; Score 276; DB 3; Length 1040;  
Best Local Similarity 29.8%; Pred. No. 8.6e-09;  
RESULT 1072  
ID AAY96125 standard; peptide; 1078 AA.  
DE Collagen type III alpha-1.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 3; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1073  
ID AAE16478 standard; protein; 1078 AA.  
DE Human collagen alpha1 (III) protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 3; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1074  
ID ABB80736 standard; protein; 1078 AA.  
DE Collagen type III-alpha1 protein.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1075  
ID ABB09628 standard; peptide; 1078 AA.  
DE Amino acid sequence of human collagen type III alpha1.  
PN US6342361-B1.  
PD 29-JAN-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1076  
ID ADF13078 standard; protein; 1078 AA.  
DE Human collagen alpha1(III) chain precursor.  
PN US2003119058-A1.  
PD 28-JUN-2003.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.7%; Score 276; DB 7; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;  
RESULT 1077  
ID AAY56801 standard; protein; 1366 AA.  
DE Human proalpha2 (I) collagen.  
PN EP967226-A2.  
PD 29-DEC-1999.  
PA (COHE-) COHESION TECHNOLOGIES INC.  
Query Match 11.7%; Score 276; DB 3; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1078  
ID ABB90751 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 234.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1079  
ID ABB90766 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 265.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1080  
ID ABB90741 standard; protein; 1366 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 214.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 5; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1081  
ID ABU54448 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 10.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1082  
ID ABU54473 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 40.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1083  
ID ABU54458 standard; protein; 1366 AA.  
DE Human tumour endothelial marker TEM 20.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1084  
ID ABB0736 standard; protein; 1078 AA.  
DE Collagen type III-alpha1 protein.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.7%; Score 276; DB 5; Length 1078;  
Best Local Similarity 27.4%; Pred. No. 8.9e-09;

ID ABR92065 standard; protein; 1366 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:38.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.7%; Score 276; DB 6; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1085  
ID ADK70437 standard; protein; 1366 AA.  
DE Respiratory disease differentially expressed protein #3.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 11.7%; Score 276; DB 8; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1086  
ID ADQ29669 standard; protein; 1366 AA.  
DE Human colorectal cancer-associated protein #24.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 11.7%; Score 276; DB 8; Length 1366;  
Best Local Similarity 29.8%; Pred. No. 1.1e-08;  
RESULT 1087  
ID ABO59421 standard; protein; 208 AA.  
DE Human genome derived single exon protein #5655.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 11.6%; Score 275; DB 8; Length 208;  
Best Local Similarity 32.1%; Pred. No. 2.1e-09;  
RESULT 1088  
ID ABE95084 standard; protein; 525 AA.  
DE Human translocation (12; 16)(q13; p11) protein #5.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Query Match 11.6%; Score 275; DB 5; Length 525;  
Best Local Similarity 27.5%; Pred. No. 5.1e-09;  
RESULT 1089  
ID ADR14649 standard; protein; 525 AA.  
DE Human NF-kappaB pathway-associated protein SeqID650.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 11.6%; Score 275; DB 8; Length 525;  
Best Local Similarity 27.5%; Pred. No. 5.1e-09;  
RESULT 1090  
ID ABB61800 standard; protein; 944 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12192.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 11.6%; Score 275; DB 4; Length 944;  
Best Local Similarity 24.4%; Pred. No. 9e-09;  
RESULT 1091  
ID ADH13201 standard; protein; 593 AA.  
DE Human malignant neoplasia-related protein SeqID50.  
PN EP1365034-A2.  
PD 26-NOV-2003.  
PA (FARB ) BAYER AG.  
Query Match 11.6%; Score 274; DB 8; Length 593;  
Best Local Similarity 36.9%; Pred. No. 6.7e-09;  
RESULT 1092  
ID ADF55631 standard; protein; 600 AA.  
DE Protein (SEQ ID 1) related to oyster pearl keratin protein.  
PN JP2003012696-A.  
PD 15-JAN-2003.  
PA (MATS/) MATSUSHIRO A.  
Query Match 11.6%; Score 274; DB 7; Length 600;  
Best Local Similarity 30.3%; Pred. No. 1.8e-08;  
RESULT 1102

Best Local Similarity 24.5%; Pred. No. 6.7e-09;  
RESULT 1093  
ID AAG29582 standard; protein; 730 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35222.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 11.6%; Score 274; DB 3; Length 730;  
Best Local Similarity 28.9%; Pred. No. 8.1e-09;  
RESULT 1094  
ID AAG29581 standard; protein; 752 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35221.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 11.6%; Score 274; DB 3; Length 752;  
Best Local Similarity 28.9%; Pred. No. 8.3e-09;  
RESULT 1095  
ID ADN35279 standard; protein; 1313 AA.  
DE Synthetic collagen used as sealant tissue protein.  
PN WO2004028404-A2.  
PD 08-APR-2004.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.6%; Score 274; DB 8; Length 1313;  
Best Local Similarity 27.2%; Pred. No. 1.4e-08;  
RESULT 1096  
ID AAU31850 standard; protein; 2367 AA.  
DE Novel human secreted protein #2341.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.6%; Score 273; DB 4; Length 2367;  
Best Local Similarity 27.0%; Pred. No. 2.9e-08;  
RESULT 1097  
ID AAW49739 standard; protein; 479 AA.  
DE Protein polymer adhesive substrate PPAS2-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 479;  
Best Local Similarity 26.2%; Pred. No. 6.7e-09;  
RESULT 1098  
ID ABO77606 standard; protein; 619 AA.  
DE Pseudomonas aeruginosa polypeptide #9781.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 11.5%; Score 272.5; DB 7; Length 619;  
Best Local Similarity 25.2%; Pred. No. 8.6e-09;  
RESULT 1099  
ID ADK51953 standard; protein; 696 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 21.  
PN WO2003099465-A1.  
PD 04-DEC-2003.  
PA (DOWO ) DOW CORNING CORP.  
PA (GEMV ) GENENCOR INT INC.  
Query Match 11.5%; Score 272.5; DB 8; Length 696;  
Best Local Similarity 28.6%; Pred. No. 9.6e-09;  
RESULT 1100  
ID AAW09214 standard; protein; 1065 AA.  
DE CLP6 polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 272.5; DB 2; Length 1065;  
Best Local Similarity 27.7%; Pred. No. 1.4e-08;  
RESULT 1101  
ID ABB57364 standard; protein; 1373 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1029.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 11.5%; Score 272.5; DB 5; Length 1373;  
Best Local Similarity 30.3%; Pred. No. 1.8e-08;  
RESULT 1102



ID AAB82608 standard; protein; 291 AA.  
DE Spider recombinant silk protein pQE (sp1)7.  
PN W020015333-A1.  
PD 26-JUL-2001.  
PA (WELL/) MELLO C M.  
PA (ARCI/) ARCI DIACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Query Match 11.5%; Score 272; DB 4; Length 291;  
Best Local Similarity 28.1%; Pred. No. 4.5e-09;  
RESULT 1103  
ID ARG20586 standard; protein; 671 AA.  
DE Novel human diagnostic protein #20577.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 272; DB 4; Length 671;  
Best Local Similarity 30.2%; Pred. No. 9.9e-09;  
RESULT 1104  
ID ABP53470 standard; peptide; 696 AA.  
DE SELP9K related amino acid sequence #1.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.5%; Score 272; DB 5; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1e-08;  
RESULT 1105  
ID ABP53482 standard; protein; 696 AA.  
DE Protein polymer SELP9K polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J.  
PA (STED/) STEDRONSKY E R.  
Query Match 11.5%; Score 272; DB 5; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1e-08;  
RESULT 1106  
ID ADK51955 standard; protein; 696 AA.  
DE Repeat protein polymer repeat sequence, SEQ ID 23.  
PN W02003099465-A1.  
PD 04-DEC-2003.  
PA (DOMO) DOW CORNING CORP.  
PA (GEMV) GENENCOR INT INC.  
Query Match 11.5%; Score 272; DB 8; Length 696;  
Best Local Similarity 27.9%; Pred. No. 1e-08;  
RESULT 1107  
ID ABU36642 standard; protein; 370 AA.  
DE Protein encoded by Prokaryotic essential gene #22169.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 11.5%; Score 271.5; DB 6; Length 370;  
Best Local Similarity 29.0%; Pred. No. 6e-09;  
RESULT 1108  
ID AAM79339 standard; protein; 569 AA.  
DE Human protein SEQ ID NO 2985.  
PN W0200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 271.5; DB 4; Length 569;  
Best Local Similarity 27.0%; Pred. No. 9.1e-09;  
RESULT 1109  
ID AAM79340 standard; protein; 569 AA.  
DE Human protein SEQ ID NO 2986.  
PN W0200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 11.5%; Score 271.5; DB 4; Length 569;  
Best Local Similarity 27.0%; Pred. No. 9.1e-09;  
RESULT 1110  
ID AAR80324 standard; protein; 762 AA.  
DE Protein polymeric adhesion substrate 1-A.  
PN W09523611-A1.

PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.3e-08;  
RESULT 1111  
ID RAM57666 standard; peptide; 762 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.3e-08;  
RESULT 1112  
ID AAW53535 standard; protein; 762 AA.  
DE Amino acid sequence of the plasmid encoding fibrin gamma PPAS1-A.  
PN W09810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.3e-08;  
RESULT 1113  
ID AAW49713 standard; protein; 762 AA.  
DE Protein polymer adhesive substrate PPAS1-A.  
PN US5773257-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.5%; Score 271; DB 2; Length 762;  
Best Local Similarity 27.7%; Pred. No. 1.3e-08;  
RESULT 1114  
ID ABO58348 standard; protein; 2338 AA.  
DE Human genome derived single exon protein #4582.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 11.5%; Score 271; DB 8; Length 2338;  
Best Local Similarity 27.6%; Pred. No. 3.8e-08;  
RESULT 1115  
ID ADR16801 standard; protein; 1366 AA.  
DE Human collagen I alpha2 (I) chain protein.  
PN US2004151731-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 2.4e-08;  
RESULT 1116  
ID ADR16426 standard; protein; 1366 AA.  
DE Human collagen I alpha2 (I) chain protein.  
PN US2004151732-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
PA (PELU/) PELUSE S.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 2.4e-08;  
RESULT 1117  
ID ADR99147 standard; protein; 1366 AA.  
DE Collagen, type 1, alpha 2, COL1A2, SEQ ID 153.  
PN W02004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 11.4%; Score 270.5; DB 8; Length 1366;  
Best Local Similarity 30.0%; Pred. No. 2.4e-08;  
RESULT 1118  
ID ADC87061 standard; protein; 920 AA.  
DE Human GPCR protein SEQ ID NO:1514.  
PN EF1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 11.4%; Score 270; DB 7; Length 920;  
Best Local Similarity 33.5%; Pred. No. 1.8e-08;  
RESULT 1119

ID AAR28916 standard; protein; 1196 AA.  
DE Type III procollagen (prior art).  
PN W09219754-A1.  
PD 12-NOV-1992.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Query Match 11.4%; Score 270; DB 2; Length 1196;  
Best Local Similarity 29.0%; Pred. No. 2.3e-08;  
RESULT 1120  
ID AAE02537 standard; protein; 1466 AA.  
DE Porcine alpha1(III) collagen.  
PN W0200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 11.4%; Score 270; DB 4; Length 1466;  
Best Local Similarity 29.0%; Pred. No. 2.8e-08;  
RESULT 1121  
ID AAE36870 standard; protein; 360 AA.  
DE Latrodectus geometricus major ampullate spideroin 1 (Maspl) protein.  
PN W02003020916-A2.  
PD 13-MAR-2003.  
PA (UWY-) UNIV WYOMING.  
Query Match 11.4%; Score 269.5; DB 6; Length 360;  
Best Local Similarity 25.1%; Pred. No. 7.8e-09;  
RESULT 1122  
ID ADP31413 standard; protein; 951 AA.  
DE Human secreted protein SEQ ID #2180.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269.5; DB 8; Length 951;  
Best Local Similarity 25.8%; Pred. No. 2e-08;  
RESULT 1123  
ID AG31413 standard; protein; 1065 AA.  
DE CLP6 polymer encoded by plasmid pPT0246.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.4%; Score 269.5; DB 5; Length 1065;  
Best Local Similarity 26.7%; Pred. No. 2.2e-08;  
RESULT 1124  
ID ABB70198 standard; protein; 272 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37386.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 11.4%; Score 269; DB 4; Length 272;  
Best Local Similarity 29.9%; Pred. No. 6.4e-09;  
RESULT 1125  
ID ADC35284 standard; protein; 410 AA.  
DE ADP-4 silk protein.  
PN W0200305727-A1.  
PD 17-JUL-2003.  
PA (NEXI-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 11.4%; Score 269; DB 7; Length 410;  
Best Local Similarity 27.1%; Pred. No. 9.5e-09;  
RESULT 1126  
ID ADP31157 standard; protein; 474 AA.  
DE Human secreted protein SEQ ID #1924.  
PN W02004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 11.4%; Score 269; DB 8; Length 474;  
Best Local Similarity 28.9%; Pred. No. 1.1e-08;  
RESULT 1127  
ID AAB70184 standard; peptide; 248 AA.  
DE Peptide dendrimer carrier #9.  
PN W0200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 11.4%; Score 268.5; DB 4; Length 248;  
Best Local Similarity 31.2%; Pred. No. 6.3e-09;  
RESULT 1128  
ID ADL92144 standard; protein; 1027 AA.

DE Collagen protein sequence.  
PN W02003099862-A1.  
PD 04-DEC-2003.  
PA (NANO-) APPLIED NANOSYSTEMS BV.  
Query Match 11.4%; Score 268.5; DB 8; Length 1027;  
Best Local Similarity 27.7%; Pred. No. 2.4e-08;  
RESULT 1129  
ID AAR80327 standard; protein; 762 AA.  
DE Protein polymeric adhesion substrate 1-B.  
PN W09523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1130  
ID AAW57668 standard; peptide; 762 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1131  
ID RAW49715 standard; protein; 762 AA.  
DE Protein polymer adhesive substrate PPAS1-B.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 11.3%; Score 268; DB 2; Length 762;  
Best Local Similarity 27.9%; Pred. No. 2e-08;  
RESULT 1132  
ID AAR71702 standard; protein; 1366 AA.  
DE Collagen alpha 2 (I) chain precursor.  
PN W09508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 2; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1133  
ID AAY96123 standard; peptide; 1366 AA.  
DE Collagen type I alpha-2.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 3; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1134  
ID ABB50293 standard; protein; 1366 AA.  
DE Collagen type I alpha-2 ovarian tumour marker protein, SEQ ID NO:76.  
PN W0200175177-A2.  
PD 11-OCT-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 11.3%; Score 267.5; DB 4; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1135  
ID AAE16476 standard; protein; 1366 AA.  
DE Human collagen alpha 2-type I protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1136  
ID ABB80734 standard; protein; 1366 AA.  
DE Protein sequence related to human collagen.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTEOMETER BIOTECH AS.  
Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
RESULT 1137  
ID ABB09626 standard; peptide; 1366 AA.  
DE Amino acid sequence of human collagen type I alpha2.

PN USC342361-B1.  
 PD 29-JAN-2002.  
 PA. (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 11.3%; Score 267.5; DB 5; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
 RESULT 1138  
 ID ADF13076 standard; protein; 1366 AA.  
 DE Human procollagen alpha2(I) chain precursor.  
 PN US2003119058-A1.  
 PD 26-JUN-2003.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 11.3%; Score 267.5; DB 7; Length 1366;  
 Best Local Similarity 30.3%; Pred. No. 3.7e-08;  
 RESULT 1139  
 ID ADF31438 standard; protein; 675 AA.  
 DE Human secreted protein SEQ ID #2205.  
 PN W02004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 11.3%; Score 266.5; DB 8; Length 675;  
 Best Local Similarity 26.6%; Pred. No. 2.2e-08;  
 RESULT 1140  
 ID ABB64222 standard; protein; 317 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 19458.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 11.3%; Score 266; DB 4; Length 317;  
 Best Local Similarity 32.0%; Pred. No. 1.1e-08;  
 RESULT 1141  
 ID ADA07853 standard; protein; 568 AA.  
 DE Pinctada maxima nacline.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG F F.  
 PA (LIHH/) LI H.  
 PA (HSIE/) HSIEH-LI H M.  
 Query Match 11.2%; Score 265.5; DB 6; Length 568;  
 Best Local Similarity 23.0%; Pred. No. 2.1e-08;  
 RESULT 1142  
 ID AAE02536 standard; protein; 1366 AA.  
 DE Porcine alpha2(I) collagen.  
 PN W0200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.2%; Score 265.5; DB 4; Length 1366;  
 Best Local Similarity 29.0%; Pred. No. 4.9e-08;  
 RESULT 1143  
 ID AAU79907 standard; protein; 343 AA.  
 DE Fragment for resistance against dehydration stress, protein #5.  
 PN W0200226800-A1.  
 PD 04-APR-2002.  
 PA (SEIR-) SEIREN CO LTD.  
 Query Match 11.2%; Score 265; DB 5; Length 343;  
 Best Local Similarity 29.4%; Pred. No. 1.4e-08;  
 RESULT 1144  
 ID ABG28641 standard; protein; 399 AA.  
 DE Novel human diagnostic protein #28632.  
 PN W0200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 11.2%; Score 264.5; DB 4; Length 399;  
 Best Local Similarity 33.5%; Pred. No. 1.7e-08;  
 RESULT 1145  
 ID AAU79272 standard; protein; 536 AA.  
 DE Phenolic acid esterase amino acid sequence.  
 PN GB2324302-A.  
 PD 21-OCT-1998.  
 PA (BYNE-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.  
 PA (TYNE-) UNIV NEWCASTLE-UPON-TYNE.  
 Query Match 11.2%; Score 264.5; DB 2; Length 536;  
 Best Local Similarity 29.8%; Pred. No. 2.3e-08;  
 RESULT 1146

ID ADK51954 standard; protein; 1008 AA.  
 DE Repeat protein polymer repeat sequence, SEQ ID 22.  
 PN W0200309465-A1.  
 PD 04-DEC-2003.  
 PA (DOMO ) DOM CORNING CORP.  
 PA (GEMV ) GENENCOR INT INC.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1008;  
 Best Local Similarity 27.5%; Pred. No. 4.2e-08;  
 RESULT 1147  
 ID ADR70477 standard; protein; 1063 AA.  
 DE Collagen-like protein.  
 PN US2004180027-A1.  
 PD 16-SEP-2004.  
 PA (KUMA/) KOMAR M.  
 PA (CUEV/) CUEVAS W A.  
 Query Match 11.2%; Score 264.5; DB 8; Length 1063;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1148  
 ID AAR37748 standard; protein; 1065 AA.  
 DE Collagen-like polymer DCP6 encoded by clone pPT 0246.  
 PN W09310154-A1.  
 PD 27-MAY-1993.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1149  
 ID AAR93259 standard; protein; 1065 AA.  
 DE Collagen-like polymer sequence D gene 6 polymer protein (pPT0246).  
 PN US5496712-A.  
 PD 03-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1150  
 ID AAU57656 standard; peptide; 1065 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 2; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1151  
 ID AAY51883 standard; protein; 1065 AA.  
 DE Plasmid pPT0246 protein fragment containing CLP6 polymer units.  
 PN US6033654-A.  
 PD 07-MAR-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 3; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1152  
 ID ABW01629 standard; protein; 1065 AA.  
 DE Plasmid pPT0246 CLP6 polymer protein.  
 PN US2003104589-A1.  
 PD 05-JUN-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 11.2%; Score 264.5; DB 7; Length 1065;  
 Best Local Similarity 27.5%; Pred. No. 4.5e-08;  
 RESULT 1153  
 ID AAE02534 standard; protein; 1466 AA.  
 DE Bovine alpha1(III) collagen #2.  
 PN W0200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 8e-08;  
 RESULT 1154  
 ID AAE02533 standard; protein; 1466 AA.  
 DE Bovine alpha1(III) collagen #1.  
 PN W0200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Query Match 11.1%; Score 262.5; DB 4; Length 1466;  
 Best Local Similarity 26.3%; Pred. No. 8e-08;

## RESULT 1155

ID ADP69307 standard; protein; 553 AA.  
DE Human lung specific protein sequence SEQ ID NO:64.  
PN WO2003102137-A2.  
PD 11-DEC-2003.  
PA (DIAD-) DIADEXUS INC.

Query Match 11.1%; Score 262; DB 8; Length 553;  
Best Local Similarity 26.1%; Pred. No. 3.4e-08;

## RESULT 1156

ID ABB58985 standard; protein; 1937 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3747.  
PN WO200171042-A2.  
PD 27-SEP-2001.

PA (PEKE ) PE CORP NY.  
Query Match 11.1%; Score 261.5; DB 4; Length 1937;  
Best Local Similarity 24.9%; Pred. No. 1.2e-07;

## RESULT 1157

ID ADR86371 standard; protein; 1049 AA.  
DE Aspergillus fumigatus essential gene protein #421.  
PN WO2004067709-A2.  
PD 12-AUG-2004.

PA (ELIT-) ELITRA PHARM INC.

PA (ELIT-) ELITRA PHARM INC.

Query Match 11.0%; Score 261; DB 8; Length 1049;  
Best Local Similarity 23.7%; Pred. No. 7.2e-08;

## RESULT 1158

ID ABB63141 standard; protein; 828 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16215.  
PN WO200171042-A2.  
PD 27-SEP-2001.

PA (PEKE ) PE CORP NY.  
Query Match 11.0%; Score 260.5; DB 4; Length 828;  
Best Local Similarity 26.5%; Pred. No. 6.2e-08;

## RESULT 1159

ID ADQ08606 standard; protein; 1104 AA.  
DE Ciona intestinalis nervous system associated protein SeqID8.  
PN JP2004057127-A.  
PD 26-FEB-2004.

PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.

Query Match 11.0%; Score 260.5; DB 8; Length 1104;  
Best Local Similarity 28.6%; Pred. No. 8.1e-08;

## RESULT 1160

ID AAE36880 standard; protein; 399 AA.  
DE Latrodectus geometricus major ampullate spidroin 2 (MaSp2) protein #2.  
PN WO2003020916-A2.

PD 13-MAR-2003.

PA (UYWY-) UNIV WYOMING.

Query Match 11.0%; Score 259.5; DB 6; Length 399;  
Best Local Similarity 27.3%; Pred. No. 3.5e-08;

## RESULT 1161

ID ADP31162 standard; protein; 537 AA.  
DE Human secreted protein SEQ ID #1929.  
PN WO2004035732-A2.

PD 29-APR-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 11.0%; Score 259; DB 8; Length 537;  
Best Local Similarity 25.9%; Pred. No. 5e-08;

## RESULT 1162

ID ABG95083 standard; protein; 462 AA.  
DE Human translocation (12; 16) (q13; p11) protein #4.  
PN WO200269900-A2.  
PD 12-SEP-2002.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

Query Match 10.9%; Score 258.5; DB 5; Length 462;  
Best Local Similarity 32.7%; Pred. No. 4.7e-08;

## RESULT 1163

ID ADP31163 standard; protein; 594 AA.  
DE Human secreted protein SEQ ID #1930.  
PN WO2004035732-A2.  
PD 29-APR-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 10.9%; Score 258; DB 8; Length 594;  
Best Local Similarity 26.2%; Pred. No. 6.4e-08;

## RESULT 1164

ID AAR37751 standard; protein; 1077 AA.  
DE CLP 3.1 monomer containing peptide.  
PN WO9310154-A1.

PD 27-MAY-1993.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 258; DB 2; Length 1077;  
Best Local Similarity 28.7%; Pred. No. 1.1e-07;

## RESULT 1165

ID ADI26113 standard; protein; 518 AA.  
DE Human protein that promotes STAT6 activation #39.  
PN WO2003104277-A2.  
PD 18-DEC-2003.

PA (ASAH ) ASAHI KASEI KK.

Query Match 10.9%; Score 257.5; DB 8; Length 518;  
Best Local Similarity 26.2%; Pred. No. 6e-08;

## RESULT 1166

ID ABB71788 standard; protein; 385 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42156.  
PN WO200171042-A2.  
PD 27-SEP-2001.

PA (PEKE ) PE CORP NY.

Query Match 10.9%; Score 257; DB 4; Length 385;  
Best Local Similarity 35.4%; Pred. No. 4.9e-08;

## RESULT 1167

ID ADP31164 standard; protein; 534 AA.  
DE Human secreted protein SEQ ID #1931.  
PN WO2004035732-A2.  
PD 29-APR-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match 10.9%; Score 257; DB 8; Length 534;  
Best Local Similarity 26.0%; Pred. No. 6.7e-08;

## RESULT 1168

ID AAR37746 standard; protein; 633 AA.  
DE Collagen-like polymer DCP5 encoded by clone pPT 0232.  
PN WO9310154-A1.

PD 27-MAY-1993.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1169

ID AAR93257 standard; protein; 633 AA.  
DE Collagen-like polymer sequence D gene 5 polymer protein (pPT0232).  
PN US5496712-A.

PD 05-MAR-1996.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1170

ID AAW57655 standard; peptide; 633 AA.  
DE Collagen-like polymer.  
PN US5773249-A.

PD 30-JUN-1998.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 633;  
Best Local Similarity 30.4%; Pred. No. 7.8e-08;

## RESULT 1171

ID ABU17075 standard; protein; 974 AA.  
DE Protein encoded by prokaryotic essential gene #2602.  
PN WO200277183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 10.9%; Score 257; DB 6; Length 974;  
Best Local Similarity 24.1%; Pred. No. 1.2e-07;

## RESULT 1172

ID AAR37745 standard; protein; 1065 AA.  
DE Collagen-like polymer DCP4 encoded by clone pPT 0249.  
PN WO9310154-A1.  
PD 27-MAY-1993.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 10.9%; Score 257; DB 2; Length 1065;  
Best Local Similarity 28.0%; Pred. No. 1.3e-07;

## RESULT 1173

ID AAR93256 standard; protein; 1065 AA.  
 DE Collagen-like polymer sequence D gene 4 polymer protein (pPT0249).  
 PN US5496712-A.  
 PD 05-MAR-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.9%; Score 257; DB 2; Length 1065;  
 Best Local Similarity 28.0%; Pred. No. 1.3e-07;  
 RESULT 1174  
 ID AAW57654 standard; peptide; 1065 AA.  
 DE Collagen-like polymer.  
 PN US5773249-A.  
 PD 30-JUN-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.9%; Score 257; DB 2; Length 1065;  
 Best Local Similarity 28.0%; Pred. No. 1.3e-07;  
 RESULT 1175  
 ID AAM50035 standard; protein; 230 AA.  
 DE N. clavipes spideroin synthetic homologue SE1 protein.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 10.8%; Score 255.5; DB 5; Length 230;  
 Best Local Similarity 30.0%; Pred. No. 3.7e-08;  
 RESULT 1176  
 ID ADI26207 standard; protein; 589 AA.  
 DE Human protein that promotes STAT6 activation #86.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH) ASAHI KASEI KK.  
 Query Match 10.8%; Score 255.5; DB 8; Length 589;  
 Best Local Similarity 26.0%; Pred. No. 9e-08;  
 RESULT 1177  
 ID ABO53050 standard; protein; 592 AA.  
 DE Human putative spliceosome associated protein (SAP) #26.  
 PN US2003068803-A1.  
 PD 10-APR-2003.  
 PA (REED/) REED R.  
 PA (ZHOU/) ZHOU Z.  
 Query Match 10.8%; Score 255.5; DB 6; Length 592;  
 Best Local Similarity 26.0%; Pred. No. 9.1e-08;  
 RESULT 1178  
 ID ADI26209 standard; protein; 592 AA.  
 DE Human protein that promotes STAT6 activation #87.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH) ASAHI KASEI KK.  
 Query Match 10.8%; Score 255.5; DB 8; Length 592;  
 Best Local Similarity 26.0%; Pred. No. 9.1e-08;  
 RESULT 1179  
 ID ABB66654 standard; protein; 499 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 26754.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 10.8%; Score 254.5; DB 4; Length 499;  
 Best Local Similarity 26.3%; Pred. No. 8.9e-08;  
 RESULT 1180  
 ID ADN99871 standard; protein; 632 AA.  
 DE Novel human protein sequence #687.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 632;  
 Best Local Similarity 34.2%; Pred. No. 1.2e-07;  
 RESULT 1181  
 ID ABP53478 standard; protein; 1040 AA.  
 DE Protein polymer SELP6 polymer block amino acid sequence.  
 PN US2002045567-A1.  
 PD 18-APR-2002.  
 PA (CAPF/) CAPPELLO J.  
 PA (STED/) STEDRONSKY E R.  
 Query Match 10.7%; Score 254; DB 5; Length 1040;  
 Best Local Similarity 22.9%; Pred. No. 1.9e-07;  
 RESULT 1182  
 ID ABM83560 standard; protein; 1417 AA.  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3809.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 10.7%; Score 254; DB 8; Length 1417;  
 Best Local Similarity 27.4%; Pred. No. 2.6e-07;  
 RESULT 1183  
 ID ADE55694 standard; protein; 1419 AA.  
 DE Rat Protein AAA79780, SEQ ID NO 1513.  
 PN WO2003036475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 10.7%; Score 254; DB 7; Length 1419;  
 Best Local Similarity 26.4%; Pred. No. 2.6e-07;  
 RESULT 1184  
 ID ABG61861 standard; protein; 1487 AA.  
 DE Prostate cancer-associated protein #62.  
 PN WO200230268-A2.  
 PD 18-APR-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 10.7%; Score 254; DB 5; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 2.7e-07;  
 RESULT 1185  
 ID ABP56769 standard; protein; 1487 AA.  
 DE Collagen IIA protein.  
 PN WO2002100426-A1.  
 PD 19-DEC-2002.  
 PA (SMIN) SMITH & NEPHEW PLC.  
 Query Match 10.7%; Score 254; DB 6; Length 1487;  
 Best Local Similarity 27.4%; Pred. No. 2.7e-07;  
 RESULT 1186  
 ID AAG77793 standard; protein; 1745 AA.  
 DE Human pro-alpha-3(V) fibrillar procollagen polypeptide.  
 PN WO200164871-A2.  
 PD 07-SEP-2001.  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 Query Match 10.7%; Score 254; DB 4; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1187  
 ID ABB97234 standard; protein; 1745 AA.  
 DE Novel human protein SEQ ID NO: 502.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 10.7%; Score 254; DB 5; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1188  
 ID ADQ19841 standard; protein; 1745 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2660.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 10.7%; Score 254; DB 8; Length 1745;  
 Best Local Similarity 27.6%; Pred. No. 3.2e-07;  
 RESULT 1189  
 ID AAM50048 standard; protein; 264 AA.  
 DE N. clavipes spideroin synthetic homologue FA2 protein #2.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Query Match 10.7%; Score 253; DB 5; Length 264;  
 Best Local Similarity 30.7%; Pred. No. 6e-08;  
 RESULT 1190  
 ID ADK51957 standard; protein; 780 AA.  
 DE Repeat-protein polymer repeat sequence, SEQ ID 25.  
 PN WO2003099465-A1.  
 PD 04-DEC-2003.  
 PA (DOWO) DOW CORNING CORP.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 10.7%; Score 253; DB 8; Length 780;

Best Local Similarity 29.2%; Pred. No. 1.7e-07;  
RESULT 1191  
ID ADC21544 standard; protein; 1014 AA.  
DE Human type II collagen protein sequence.  
PN WO2003006603-A2.  
PD 23-JAN-2003.  
PA (AREX-) AREXIS AB.  
Query Match 10.7%; Score 253; DB 7; Length 1014;  
Best Local Similarity 27.4%; Pred. No. 2.2e-07;  
RESULT 1192  
ID AAB18321 standard; protein; 1020 AA.  
DE Collagen like protein, CLP3.1.  
PN WO200200016-A1.  
PD 03-JAN-2002.  
PA (LUMI-) LUMINIS PTY LTD.  
PA (SAUR-) SOUTH AUSTRALIAN RES & DEV INST.  
Query Match 10.7%; Score 253; DB 5; Length 1020;  
Best Local Similarity 29.2%; Pred. No. 2.2e-07;  
RESULT 1193  
ID AAR93261 standard; protein; 1077 AA.  
DE CLP 3.1 polymer sequence (pPT0297).  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.7%; Score 253; DB 2; Length 1077;  
Best Local Similarity 29.2%; Pred. No. 2.3e-07;  
RESULT 1194  
ID AAW57657 standard; peptide; 1077 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.7%; Score 253; DB 2; Length 1077;  
Best Local Similarity 29.2%; Pred. No. 2.3e-07;  
RESULT 1195  
ID ABP60377 standard; peptide; 1217 AA.  
DE Bombyx mori sericin SEQ ID NO 2.  
PN WO200286133-A1.  
PD 31-OCT-2002.  
PA (SEIR-) SEIREN CO LTD.  
Query Match 10.7%; Score 253; DB 6; Length 1217;  
Best Local Similarity 27.0%; Pred. No. 2.6e-07;  
RESULT 1196  
ID AAR59751 standard; protein; 1418 AA.  
DE Type II collagen.  
PN WO9414070-A1.  
PD 23-JUN-1994.  
PA (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.  
Query Match 10.7%; Score 253; DB 2; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1197  
ID AAR71703 standard; protein; 1418 AA.  
DE Collagen alpha 1 (II) chain precursor.  
PN WO9508115-A1.  
PD 23-MAR-1995.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.7%; Score 253; DB 2; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1198  
ID AAY96124 standard; peptide; 1418 AA.  
DE Collagen type II alpha-1.  
PN US6110689-A.  
PD 29-AUG-2000.  
PA (OSTE-) OSTEOMETER AS.  
Query Match 10.7%; Score 253; DB 3; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1199  
ID AAB35624 standard; protein; 1418 AA.  
DE Human type II collagen.  
PN US6132976-A.  
PD 17-OCT-2000.  
PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.  
Query Match 10.7%; Score 253; DB 4; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1200  
ID AAE16477 standard; protein; 1418 AA.  
DE Human collagen alpha (II) protein.  
PN US6323314-B1.  
PD 27-NOV-2001.  
PA (OSTE-) OSTROMETER AS.  
Query Match 10.7%; Score 253; DB 5; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1201  
ID ABB0735 standard; protein; 1418 AA.  
DE Collagen type II-alpha protein.  
PN US6355442-B1.  
PD 12-MAR-2002.  
PA (OSTE-) OSTROMETER BIOTECH AS.  
Query Match 10.7%; Score 253; DB 5; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1202  
ID ARG93927 standard; protein; 1418 AA.  
DE Human polypeptide orthologous to DACC-2.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY) UNIV SYDNEY.  
Query Match 10.7%; Score 253; DB 5; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1203  
ID ABB09627 standard; peptide; 1418 AA.  
DE Amino acid sequence of human collagen type II alpha1.  
PN US6342361-B1.  
PD 29-JAN-2002.  
PA (OSTE-) OSTROMETER BIOTECH AS.  
Query Match 10.7%; Score 253; DB 5; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1204  
ID ADF13077 standard; protein; 1418 AA.  
DE Human collagen alpha(II) chain precursor.  
PN US2003119058-A1.  
PD 26-JUN-2003.  
PA (OSTE-) OSTROMETER AS.  
Query Match 10.7%; Score 253; DB 7; Length 1418;  
Best Local Similarity 27.1%; Pred. No. 3e-07;  
RESULT 1205  
ID ADP31446 standard; protein; 1755 AA.  
DE Human secreted protein SEQ ID #2213.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.7%; Score 252.5; DB 8; Length 1755;  
Best Local Similarity 24.2%; Pred. No. 3.9e-07;  
RESULT 1206  
ID AAO16498 standard; protein; 227 AA.  
DE Argiope trifasciata spider silk protein #2.  
PN WO200299082-A2.  
PD 12-DEC-2002.  
PA (UYWY-) UNIV WYOMING.  
Query Match 10.7%; Score 252; DB 6; Length 227;  
Best Local Similarity 29.2%; Pred. No. 6e-08;  
RESULT 1207  
ID RAP90064 standard; protein; 429 AA.  
DE Antigenic protein for malaria vaccination.  
PN USN7238746-N.  
PD 21-MAR-1989.  
PA (USSH) NAT INST OF HEALTH.  
Query Match 10.7%; Score 252; DB 1; Length 429;  
Best Local Similarity 19.9%; Pred. No. 1.1e-07;  
RESULT 1208  
ID AAW61562 standard; protein; 1487 AA.  
DE Human type II collagen alpha-chain protein.  
PN WO9835235-A1.  
PD 13-AUG-1998.  
PA (UYSH-) UNIV SHEFFIELD.  
Query Match 10.7%; Score 252; DB 2; Length 1487;

Best Local Similarity 27.1%; Pred. No. 3.6e-07;  
RESULT 1209  
ID ABG93945 standard; protein; 1497 AA.  
DE Mouse polypeptide orthologous to DACC-10.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY-) UNIV SYDNEY.  
Query Match 10.6%; Score 252; DB 5; Length 1497;  
Best Local Similarity 26.0%; Pred. No. 3.6e-07;  
RESULT 1210  
ID ADE77159 standard; protein; 462 AA.  
DE Human protein expressed in a liver disorder #83.  
PN US2003108871-A1.  
PD 12-JUN-2003.  
PA (KASE/) KASER M R.  
Query Match 10.6%; Score 251.5; DB 8; Length 462;  
Best Local Similarity 29.9%; Pred. No. 1.3e-07;  
RESULT 1211  
ID ADP31648 standard; protein; 889 AA.  
DE Human secreted protein SEQ ID #2415.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.6%; Score 251.5; DB 8; Length 889;  
Best Local Similarity 26.6%; Pred. No. 2.4e-07;  
RESULT 1212  
ID AAP70709 standard; protein; 402 AA.  
DE Plasmodium cynomolgi sporozoite circumsporozoite protein.  
PN WO8700533-A.  
PD 29-JAN-1987.  
PA (UUNY-) UNIV NEW YORK STATE.  
PA (ARNO/) ARNOT D E.  
Query Match 10.6%; Score 251; DB 1; Length 402;  
Best Local Similarity 25.5%; Pred. No. 1.2e-07;  
RESULT 1213  
ID ADD45053 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10485.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1214  
ID ADD45057 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10489.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1215  
ID ADD48341 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14041.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1216  
ID ADD45049 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 10481.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1217  
ID ADD48337 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14037.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1218  
ID ADD48345 standard; protein; 1453 AA.  
DE Rat Protein CAB01633, SEQ ID NO 14045.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match 10.6%; Score 251; DB 7; Length 1453;  
Best Local Similarity 27.7%; Pred. No. 4.1e-07;  
RESULT 1219  
ID AAM50040 standard; protein; 219 AA.  
DE N. clavipes spidroin synthetic homologue PA2 protein.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Query Match 10.6%; Score 250.5; DB 5; Length 219;  
Best Local Similarity 32.8%; Pred. No. 7.1e-08;  
RESULT 1220  
ID ADC35282 standard; protein; 360 AA.  
DE ADF-1 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match 10.6%; Score 250.5; DB 7; Length 360;  
Best Local Similarity 25.7%; Pred. No. 1.1e-07;  
RESULT 1221  
ID AAG92278 standard; protein; 585 AA.  
DE C glutamicum protein fragment SEQ ID NO: 6032.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KYOW-) KYOWA HAKKO KOGYO KK.  
Query Match 10.6%; Score 250.5; DB 4; Length 585;  
Best Local Similarity 24.9%; Pred. No. 1.8e-07;  
RESULT 1222  
ID AAG28100 standard; protein; 274 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33192.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.6%; Score 250; DB 3; Length 274;  
Best Local Similarity 30.2%; Pred. No. 9.5e-08;  
RESULT 1223  
ID AAU08231 standard; protein; 597 AA.  
DE Polypeptide encoded by Mycobacterium tuberculosis clone mTCC#3.  
PN WO200162893-A2.  
PD 30-AUG-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.6%; Score 250; DB 4; Length 597;  
Best Local Similarity 26.7%; Pred. No. 2e-07;  
RESULT 1224  
ID ABU25538 standard; protein; 669 AA.  
DE Protein encoded by Prokaryotic essential gene #11065.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (SLIT-) ELITRA PHARM INC.  
Query Match 10.6%; Score 249.5; DB 6; Length 669;  
Best Local Similarity 43.6%; Pred. No. 2.4e-07;  
RESULT 1225  
ID ADJ67574 standard; protein; 702 AA.  
DE Human ovarian specific polypeptide SEQ ID NO:288.  
PN WO2004013311-A2.  
PD 12-FEB-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.6%; Score 249.5; DB 8; Length 702;  
Best Local Similarity 27.8%; Pred. No. 2.5e-07;  
RESULT 1226  
ID ABB60516 standard; protein; 1190 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 8340.  
 PN W0200171042-A2.  
 PD 27-SEP-2001  
 PA (PEKE ) PE CORP NY.  
 Query Match 10.5%; Score 249; DB 4; Length 1190;  
 Best Local Similarity 29.1%; Pred. No. 4.4e-07;  
 RESULT 1227  
 ID AAR79480 standard; protein; 1442 AA.  
 DE Rat type II collagen.  
 PN W09522611-A2.  
 PD 24-AUG-1995.  
 PA (UNMI ) UNIV MICHIGAN.  
 Query Match 10.5%; Score 248.5; DB 2; Length 1442;  
 Best Local Similarity 24.9%; Pred. No. 5.7e-07;  
 RESULT 1228  
 ID AAU79906 standard; protein; 267 AA.  
 DE Fragment for resistance against dehydration stress, protein #4.  
 PN W0200226800-A1.  
 PD 04-APR-2002.  
 PA (SEIR-) SEIREN CO LTD.  
 Query Match 10.5%; Score 247.5; DB 5; Length 267;  
 Best Local Similarity 33.6%; Pred. No. 1.3e-07;  
 RESULT 1229  
 ID ABB60010 standard; protein; 399 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 6822.  
 PN W0200171042-A2.  
 PD 27-SEP-2001  
 PA (PEKE ) PE CORP NY.  
 Query Match 10.5%; Score 247.5; DB 4; Length 399;  
 Best Local Similarity 25.0%; Pred. No. 1.9e-07;  
 RESULT 1230  
 ID AAY50936 standard; protein; 590 AA.  
 DE Human adult skin cDNA clone vdl\_1 derived protein #1.  
 PN W09585721-A1.  
 PD 04-NOV-1999.  
 PA (ALPH-) ALPHAGENE INC.  
 Query Match 10.5%; Score 247.5; DB 3; Length 590;  
 Best Local Similarity 24.3%; Pred. No. 2.8e-07;  
 RESULT 1231  
 ID ABF7534 standard; protein; 601 AA.  
 DE Human secretory polypeptide SPTM SEQ ID NO 718.  
 PN W0200283876-A2.  
 PD 24-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 10.5%; Score 247.5; DB 6; Length 601;  
 Best Local Similarity 24.3%; Pred. No. 2.9e-07;  
 RESULT 1232  
 ID AAG77792 standard; protein; 1739 AA.  
 DE Murine pro-alpha-3(V) fibrillar procollagen polypeptide.  
 PN W0200164871-A2.  
 PD 07-SEP-2001  
 PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
 Query Match 10.5%; Score 247.5; DB 4; Length 1739;  
 Best Local Similarity 26.6%; Pred. No. 7.9e-07;  
 RESULT 1233  
 ID ABU36445 standard; protein; 3300 AA.  
 DE Protein encoded by Prokaryotic essential gene #21972.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 10.5%; Score 247.5; DB 6; Length 3300;  
 Best Local Similarity 24.0%; Pred. No. 1.5e-06;  
 RESULT 1234  
 ID ADA33477 standard; protein; 975 AA.  
 DE Acinetobacter baumannii protein #638.  
 PN US6562958-B1.  
 PD 13-MAY-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 10.5%; Score 247; DB 6; Length 975;  
 Best Local Similarity 24.3%; Pred. No. 4.9e-07;  
 RESULT 1235  
 ID ADO08789 standard; protein; 338 AA.  
 DE Novel surgical dressing-related protein SeqID76.

PN JP2004049921-A.  
 PD 19-FEB-2004.  
 PA (SANN ) SANYO CHEM IND LTD.  
 PA (ALCA-) ALCARE KK.  
 Query Match 10.4%; Score 246.5; DB 8; Length 338;  
 Best Local Similarity 28.5%; Pred. No. 1.9e-07;  
 RESULT 1236  
 ID AAY06239 standard; protein; 595 AA.  
 DE Mouse recombinant type I collagen COL1A1-2.  
 PN EP928543-A1.  
 PD 30-JUN-1999.  
 PA (FUJF ) FUJII PHOTO FILM BV.  
 Query Match 10.4%; Score 246.5; DB 2; Length 595;  
 Best Local Similarity 28.6%; Pred. No. 3.3e-07;  
 RESULT 1237  
 ID AAY06240 standard; protein; 822 AA.  
 DE Mouse recombinant type I collagen COL1A1-3.  
 PN EP928543-A1.  
 PD 30-JUN-1999.  
 PA (FUJF ) FUJII PHOTO FILM BV.  
 Query Match 10.4%; Score 246.5; DB 2; Length 822;  
 Best Local Similarity 28.6%; Pred. No. 4.4e-07;  
 RESULT 1238  
 ID AAR71701 standard; protein; 1341 AA.  
 DE Collagen alpha 1 (I) chain precursor.  
 PN W09508115-A1.  
 PD 23-MAR-1995.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.4%; Score 246.5; DB 2; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1239  
 ID AAY96122 standard; peptide; 1341 AA.  
 DE Collagen type I alpha-1.  
 PN US6110689-A.  
 PD 29-AUG-2000.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.4%; Score 246.5; DB 3; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1240  
 ID AAE16475 standard; protein; 1341 AA.  
 DE Human collagen alpha 1 (I) protein.  
 PN US6323314-B1.  
 PD 27-NOV-2001.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1241  
 ID ABB80733 standard; protein; 1341 AA.  
 DE Collagen type I-alpha protein.  
 PN US6355442-B1.  
 PD 12-MAR-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1242  
 ID ABB09625 standard; peptide; 1341 AA.  
 DE Amino acid sequence of human collagen type I alpha1.  
 PN US6342361-B1.  
 PD 29-JAN-2002.  
 PA (OSTE-) OSTEOMETER BIOTECH AS.  
 Query Match 10.4%; Score 246.5; DB 5; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1243  
 ID ADF13075 standard; protein; 1341 AA.  
 DE Human collagen alpha 1 (I) chain precursor.  
 PN US2003119058-A1.  
 PD 26-JUN-2003.  
 PA (OSTE-) OSTEOMETER AS.  
 Query Match 10.4%; Score 246.5; DB 7; Length 1341;  
 Best Local Similarity 27.8%; Pred. No. 7.1e-07;  
 RESULT 1244  
 ID ABG93948 standard; protein; 1453 AA.  
 DE Mouse polypeptide orthologous to DACC-11.



PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY ) UNIV SYDNEY. 10.4%; Score 246.5; DB 5; Length 1453;  
Best Local Similarity 28.6%; Pred. No. 7.7e-07;  
Query Match  
RESULT 1245  
ID AAR60620 standard; protein; 1958 AA.  
DE Protein from ORF2 of Pseudorabies virus large latency transcript.  
PN US5352596-A.  
PD 04-OCT-1994.  
PA (USDA ) US SEC OF AGRIC. 10.4%; Score 246.5; DB 2; Length 1958;  
Best Local Similarity 23.7%; Pred. No. 1e-06;  
Query Match  
RESULT 1246  
ID ABO23520 standard; protein; 354 AA.  
DE Mycobacterium tuberculosis outlier protein #4.  
PN US2003039963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
PA (NAND/) NANDI T.  
PA. (BHIM/) BHIMARAO C. 10.4%; Score 245.5; DB 7; Length 354;  
Best Local Similarity 26.0%; Pred. No. 2.3e-07;  
Query Match  
RESULT 1247  
ID ADC21591 standard; protein; 1014 AA.  
DE Mouse type II collagen protein sequence.  
PN WO2003006603-A2.  
PD 23-JAN-2003.  
PA (AREX-) AREXIS AB. 10.4%; Score 245.5; DB 7; Length 1014;  
Best Local Similarity 24.9%; Pred. No. 6.3e-07;  
Query Match  
RESULT 1248  
ID AAE02535 standard; protein; 1449 AA.  
DE Porcine alpha(I) collagen.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC. 10.4%; Score 245.5; DB 4; Length 1449;  
Best Local Similarity 28.9%; Pred. No. 8.8e-07;  
Query Match  
RESULT 1249  
ID ABG93928 standard; protein; 1487 AA.  
DE Mouse polypeptide orthologous to DACC-2.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY ) UNIV SYDNEY. 10.4%; Score 245.5; DB 5; Length 1487;  
Best Local Similarity 24.9%; Pred. No. 9e-07;  
Query Match  
RESULT 1250  
ID AAG28101 standard; protein; 267 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33193.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 30.2%; Pred. No. 1.9e-07;  
RESULT 1251  
ID AAB35148 standard; protein; 894 AA.  
DE Human NFAR-2 SEQ ID NO: 4.  
PN WO200077205-A1.  
PD 21-DEC-2000.  
PA (BARB/) BARBER G N.  
PA (SAUN/) SAUNDERS L.  
PA (PERK/) PERKINS D J. 10.4%; Score 245; DB 4; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
Query Match  
RESULT 1252  
ID ADA03105 standard; protein; 894 AA.  
DE Nucleotide therapy testing protein #11.  
PN WO200302031-A1.  
PD 20-MAR-2003.  
PA (NNSH ) NIPPON SHINYAKU CO LTD.

Query Match 10.4%; Score 245; DB 6; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
RESULT 1253  
ID ADJ66639 standard; protein; 894 AA.  
DE Interleukin enhancer binding factor 3 for anti-cancer protein complex.  
PN WO2004009622-A2.  
PD 29-JAN-2004.  
PA (CELL-) CELLZONE AG. 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
Query Match  
RESULT 1254  
ID ADL56761 standard; protein; 894 AA.  
DE Human cell derived viral RNA binding protein 110.  
PN WO2004029199-A2.  
PD 08-APR-2004.  
PA (SMIK ) SMITHKLINE BEECHAM CORP. 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
Query Match  
RESULT 1255  
ID ADQ20794 standard; protein; 894 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID NO 242.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC. 10.4%; Score 245; DB 8; Length 894;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
Query Match  
RESULT 1256  
ID ADE31110 standard; protein; 906 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 242.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC. 10.4%; Score 245; DB 7; Length 906;  
Best Local Similarity 28.3%; Pred. No. 6e-07;  
Query Match  
RESULT 1257  
ID AAG41604 standard; protein; 1424 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51784.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 32.9%; Pred. No. 9.3e-07;  
RESULT 1258  
ID AAG41603 standard; protein; 1457 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51783.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 32.9%; Pred. No. 9.5e-07;  
RESULT 1259  
ID AAG30466 standard; protein; 1598 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36428.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 32.9%; Pred. No. 1e-06;  
RESULT 1260  
ID AAG30465 standard; protein; 1599 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36427.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 32.9%; Pred. No. 1e-06;  
RESULT 1261  
ID AAG41602 standard; protein; 1637 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51782.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
RESULT 1262  
ID AAG30464 standard; protein; 1684 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36426.  
PN EP1033405-A2.

PD 06-SEP-2000.  
 Query Match 10.4%; Score 245; DB 3; Length 1684;  
 Best Local Similarity 32.9%; Pred. No. 1.1e-06;  
 RESULT 1263  
 ID ADJ69005 standard; protein; 1684 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID811.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 10.4%; Score 245; DB 7; Length 1684;  
 Best Local Similarity 32.9%; Pred. No. 1.1e-06;  
 RESULT 1264  
 ID ADE87052 standard; protein; 886 AA.  
 DE Human pancreatic cell protein sequence SeqID512.  
 PN WO2003060145-A2.  
 PD 24-JUL-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 10.3%; Score 244.5; DB 7; Length 886;  
 Best Local Similarity 27.8%; Pred. No. 6.3e-07;  
 RESULT 1265  
 ID AAW09218 standard; protein; 1002 AA.  
 DE SELPOK polymer.  
 PN WO9634618-A1.  
 PD 07-NOV-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.3%; Score 244.5; DB 2; Length 1002;  
 Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
 RESULT 1266  
 ID AAW53544 standard; protein; 1002 AA.  
 DE Amino acid sequence of SELPOK peptide 2.  
 PN WO9810063-A1.  
 PD 12-MAR-1998.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.3%; Score 244.5; DB 2; Length 1002;  
 Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
 RESULT 1267  
 ID RAY51888 standard; protein; 1002 AA.  
 DE Plasmid pPT0364 protein fragment containing SELPOK polymer units.  
 PN US6033654-A.  
 PD 07-MAR-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1002;  
 Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
 RESULT 1268  
 ID AG31418 standard; protein; 1002 AA.  
 DE SELPOK protein encoded by plasmid pPT0364.  
 PN US6423333-B1.  
 PD 23-JUL-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.3%; Score 244.5; DB 5; Length 1002;  
 Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
 RESULT 1269  
 ID ABW01634 standard; protein; 1002 AA.  
 DE Plasmid pPT0364 SELPOK polymer protein.  
 PN US2003104589-A1.  
 PD 05-JUN-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 10.3%; Score 244.5; DB 7; Length 1002;  
 Best Local Similarity 29.2%; Pred. No. 7.1e-07;  
 RESULT 1270  
 ID RAY84544 standard; protein; 1057 AA.  
 DE A human collagen 1 (alpha) protein helical region.  
 PN EP992586-A2.  
 PD 12-APR-2000.  
 PA (USU) US SURGICAL CORP.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1057;  
 Best Local Similarity 27.8%; Pred. No. 7.5e-07;  
 RESULT 1271  
 ID AAY84403 standard; protein; 1058 AA.  
 DE Amino acid sequence of human type 1 (alpha) collagen polypeptide.  
 PN WO200014201-A1.  
 PD 16-MAR-2000.

PA (USU) US SURGICAL CORP.  
 PA (PAOL/) PAOLELLA D N.  
 PA (GRUS/) GRUSKIN E A.  
 PA (BUEC/) BUECHTER D D.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1058;  
 Best Local Similarity 27.8%; Pred. No. 7.5e-07;  
 RESULT 1272  
 ID RAY84540 standard; protein; 1107 AA.  
 DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.  
 PN EP992586-A2.  
 PD 12-APR-2000.  
 PA (USU) US SURGICAL CORP.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1107;  
 Best Local Similarity 27.8%; Pred. No. 7.8e-07;  
 RESULT 1273  
 ID ADE87050 standard; protein; 1161 AA.  
 DE Human pancreatic cell protein sequence SeqID510.  
 PN WO2003060145-A2.  
 PD 24-JUL-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 10.3%; Score 244.5; DB 7; Length 1161;  
 Best Local Similarity 27.8%; Pred. No. 8.2e-07;  
 RESULT 1274  
 ID RAY84538 standard; protein; 1171 AA.  
 DE A chimeric collagen 1 (alpha)/TGF-beta1 protein.  
 PN EP992586-A2.  
 PD 12-APR-2000.  
 PA (USU) US SURGICAL CORP.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1171;  
 Best Local Similarity 27.8%; Pred. No. 8.3e-07;  
 RESULT 1275  
 ID ADE87057 standard; protein; 1211 AA.  
 DE Human pancreatic cell protein sequence SeqID517.  
 PN WO2003060145-A2.  
 PD 24-JUL-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 10.3%; Score 244.5; DB 7; Length 1211;  
 Best Local Similarity 27.8%; Pred. No. 8.5e-07;  
 RESULT 1276  
 ID ADE87062 standard; protein; 1226 AA.  
 DE Human pancreatic cell protein sequence SeqID522.  
 PN WO2003060145-A2.  
 PD 24-JUL-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Query Match 10.3%; Score 244.5; DB 7; Length 1226;  
 Best Local Similarity 27.8%; Pred. No. 8.6e-07;  
 RESULT 1277  
 ID RAY84539 standard; protein; 1388 AA.  
 DE Amino acid sequence of a chimeric collagen 1 (alpha)/decorin protein.  
 PN EP992586-A2.  
 PD 12-APR-2000.  
 PA (USU) US SURGICAL CORP.  
 Query Match 10.3%; Score 244.5; DB 3; Length 1388;  
 Best Local Similarity 27.8%; Pred. No. 9.7e-07;  
 RESULT 1278  
 ID ABG93947 standard; protein; 1461 AA.  
 DE Human polypeptide orthologous to DACC-11.  
 PN WO200264623-A1.  
 PD 22-AUG-2002.  
 PA (ADPP-) ADP PHARM PTY LTD.  
 PA (UNSY) UNIV SYDNEY.  
 Query Match 10.3%; Score 244.5; DB 5; Length 1461;  
 Best Local Similarity 27.8%; Pred. No. 1e-06;  
 RESULT 1279  
 ID AAW68485 standard; protein; 1464 AA.  
 DE Human recombinant collagen protein.  
 PN WO9827202-A1.  
 PD 25-JUN-1998.  
 PA (BIOC-) BIOCEM SA.  
 Query Match 10.3%; Score 244.5; DB 2; Length 1464;  
 Best Local Similarity 27.8%; Pred. No. 1e-06;  
 RESULT 1280  
 ID AAU14136 standard; protein; 1464 AA.

DE Human novel protein #7.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.3%; Score 244.5; DB 4; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1281  
ID ADD45059 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10491.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1282  
ID ADD45055 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10487.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1283  
ID ADD45051 standard; protein; 1464 AA.  
DE Human Protein P02452, SEQ ID NO 10483.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1284  
ID ADE87048 standard; protein; 1464 AA.  
DE Human pancreatic cell protein sequence SeqID508.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1285  
ID ADR16800 standard; protein; 1464 AA.  
DE Human collagen I alpha1 (I) chain protein.  
PN US2004151731-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1286  
ID ADR16425 standard; protein; 1464 AA.  
DE Human collagen I alpha1 (I) chain protein.  
PN US2004151732-A1.  
PD 05-AUG-2004.  
PA (JICH/) JICHA D L.  
PA (PELU/) PELUSE S.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1287  
ID ADR99144 standard; protein; 1464 AA.  
DE Collagen, type I, alpha 1, COL1A1, SEQ ID 150.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 10.3%; Score 244.5; DB 8; Length 1464;  
Best Local Similarity 27.8%; Pred. No. 1e-06;  
RESULT 1288  
ID ABG22679 standard; protein; 1518 AA.  
DE Novel human diagnostic protein #22670.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.3%; Score 244.5; DB 4; Length 1518;  
Best Local Similarity 22.9%; Pred. No. 1.2e-06;

Best Local Similarity 26.1%; Pred. No. 1.1e-06;  
RESULT 1289  
ID ADE87051 standard; protein; 1536 AA.  
DE Human pancreatic cell protein sequence SeqID511.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.3%; Score 244.5; DB 7; Length 1536;  
Best Local Similarity 27.8%; Pred. No. 1.1e-06;  
RESULT 1290  
ID ABO53065 standard; protein; 441 AA.  
DE Human putative spliceosome associated protein (SAP) #42.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 10.3%; Score 244; DB 6; Length 441;  
Best Local Similarity 28.3%; Pred. No. 3.5e-07;  
RESULT 1291  
ID ADA03117 standard; protein; 591 AA.  
DE Nucleotide therapy testing protein #23.  
PN WO2003023031-A1.  
PD 20-MAR-2003.  
PA (NNSH) NIPPON SHINYAKU CO LTD.  
Query Match 10.3%; Score 244; DB 6; Length 591;  
Best Local Similarity 29.0%; Pred. No. 4.6e-07;  
RESULT 1292  
ID ADO08795 standard; protein; 316 AA.  
DE Novel surgical dressing-related protein SeqID82.  
PN JP2004049921-A.  
PD 19-FEB-2004.  
PA (SANN) SANYO CHEM IND LTD.  
PA (ALCA-) ALCARE KK.  
Query Match 10.3%; Score 243.5; DB 8; Length 316;  
Best Local Similarity 25.3%; Pred. No. 2.7e-07;  
RESULT 1293  
ID AAE36862 standard; protein; 714 AA.  
DE Human collagen type II protein.  
PN WO2003021226-A2.  
PD 13-MAR-2003.  
PA (PHAA) PHARMACIA CORP.  
Query Match 10.3%; Score 243; DB 6; Length 714;  
Best Local Similarity 27.1%; Pred. No. 6.4e-07;  
RESULT 1294  
ID ADI33185 standard; protein; 714 AA.  
DE Human collagen type II-related protein.  
PN US2003219843-A1.  
PD 27-NOV-2003.  
PA (WELS/) WELSCH D J.  
PA (DUFF/) DUFFIN K L.  
PA (NEMI/) NEMIROVSKIY O V.  
PA (DUFF/) DUFFIELD D R.  
PA (SUNY/) SUNYER T.  
PA (HOWA/) HOWARD C P.  
PA (ABRA/) ABRAMS M.  
Query Match 10.3%; Score 243; DB 8; Length 714;  
Best Local Similarity 27.1%; Pred. No. 6.4e-07;  
RESULT 1295  
ID ADP31573 standard; protein; 906 AA.  
DE Human secreted protein SEQ ID #2340.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.3%; Score 243; DB 8; Length 906;  
Best Local Similarity 25.6%; Pred. No. 8e-07;  
RESULT 1296  
ID ABB70775 standard; protein; 1357 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39117.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.3%; Score 243; DB 4; Length 1357;  
Best Local Similarity 22.9%; Pred. No. 1.2e-06;

RESULT 1297  
ID AAU28194 standard; protein; 940 AA.  
DE Novel human secretory protein, Seq ID No 363.  
PN WO200166689-A2.  
PD 13-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.3%; Score 242.5; DB 4; Length 940;  
Best Local Similarity 27.0%; Pred. No. 8.9e-07;  
RESULT 1298  
ID ABG93944 standard; protein; 1496 AA.  
DE Human polypeptide orthologous to DAC-10.  
PN WO200264625-A1.  
PD 22-AUG-2002.  
PA (ADPP-) ADP PHARM PTY LTD.  
PA (UNSY) UNIV SYDNEY.  
Query Match 10.3%; Score 242.5; DB 5; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1299  
ID ABR47419 standard; protein; 1496 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:70.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 10.3%; Score 242.5; DB 6; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1300  
ID ADB70382 standard; protein; 1496 AA.  
DE Procollagen alpha 2(V) SEQ ID NO:74.  
PN WO2003021229-A2.  
PD 13-MAR-2003.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1301  
ID ADE61180 standard; protein; 1496 AA.  
DE Human Protein NP\_000384, SEQ ID NO 7098.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1302  
ID ADP65253 standard; protein; 1496 AA.  
DE Human alpha 2 type V collagen preproprotein, collagen V, alpha-2.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.3%; Score 242.5; DB 7; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1303  
ID ADJ37161 standard; protein; 1496 AA.  
DE Human malignant pleural mesothelioma (MPM) protein #33.  
PN US2003219760-A1.  
PD 27-NOV-2003.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.3%; Score 242.5; DB 8; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1304  
ID ADR9242 standard; protein; 1496 AA.  
DE Collagen, type V, alpha 2, COL5A2, SEQ ID 248.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Query Match 10.3%; Score 242.5; DB 8; Length 1496;  
Best Local Similarity 26.8%; Pred. No. 1.4e-06;  
RESULT 1305  
ID ABB60207 standard; protein; 1779 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7413.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.3%; Score 242.5; DB 4; Length 1779;  
Best Local Similarity 25.1%; Pred. No. 1.6e-06;  
RESULT 1306  
ID ABU34499 standard; protein; 319 AA.  
DE Protein encoded by Prokaryotic essential gene #20026.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (SLIT-) ELITRA PHARM INC.  
Query Match 10.2%; Score 242; DB 6; Length 319;  
Best Local Similarity 28.9%; Pred. No. 3.4e-07;  
RESULT 1307  
ID AAU28382 standard; protein; 968 AA.  
DE Novel human secretory protein, Seq ID No 739.  
PN WO200166689-A2.  
PD 13-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 241.5; DB 4; Length 968;  
Best Local Similarity 27.6%; Pred. No. 1.1e-06;  
RESULT 1308  
ID AAY56800 standard; protein; 1411 AA.  
DE Human preproalpha 1 (I) collagen.  
PN EP967226-A2.  
PD 29-DEC-1999.  
PA (COHE-) COHESION TECHNOLOGIES INC.  
Query Match 10.2%; Score 241.5; DB 3; Length 1411;  
Best Local Similarity 27.4%; Pred. No. 1.5e-06;  
RESULT 1309  
ID AAE36878 standard; protein; 342 AA.  
DE Gastracantha mammosa major ampullate spidroin 2 (MasP2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 10.2%; Score 241; DB 6; Length 342;  
Best Local Similarity 28.5%; Pred. No. 4.2e-07;  
RESULT 1310  
ID ADN23179 standard; protein; 1744 AA.  
DE Bacterial polypeptide #5832.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 10.2%; Score 241; DB 8; Length 1744;  
Best Local Similarity 30.4%; Pred. No. 2e-06;  
RESULT 1311  
ID AAW64378 standard; protein; 943 AA.  
DE Mycobacterium tuberculosis antigen DIF2-1.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1312  
ID RAW81745 standard; protein; 943 AA.  
DE M. tuberculosis immunogenic polypeptide DIF2-1.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1313  
ID AAY39032 standard; protein; 943 AA.  
DE M. tuberculosis recombinant antigen protein DIF2-1.  
PN WO942118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1314  
ID AAY39175 standard; protein; 943 AA.  
DE M. tuberculosis antigen DIF2-1 amino acid sequence.  
PN WO942076-A2.

PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 943;  
Best Local Similarity 24.5%; Pred. No. 1.2e-06;  
RESULT 1315  
ID AAR89472 standard; protein; 1107 AA.  
DE Collagen/decorin(aa46-93) fusion protein.  
PN CA2151547-A.  
PD 11-DEC-1995.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 1107;  
Best Local Similarity 27.6%; Pred. No. 1.4e-06;  
RESULT 1316  
ID AAR89469 standard; protein; 1169 AA.  
DE Collagen/BMP-2B fusion protein.  
PN CA2151547-A.  
PD 11-DEC-1995.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 1169;  
Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
RESULT 1317  
ID AAY84537 standard; protein; 1169 AA.  
DE Amino acid sequence of a chimeric collagen 1 (alpha1)/BMP-2B protein.  
PN EF992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.2%; Score 240.5; DB 3; Length 1169;  
Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
RESULT 1318  
ID AAR89470 standard; protein; 1171 AA.  
DE Collagen/TGF-beta-1 fusion protein.  
PN CA2151547-A.  
PD 11-DEC-1995.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 1171;  
Best Local Similarity 27.6%; Pred. No. 1.5e-06;  
RESULT 1319  
ID AAR89471 standard; protein; 1388 AA.  
DE Collagen/decorin fusion protein.  
PN CA2151547-A.  
PD 11-DEC-1995.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.2%; Score 240.5; DB 2; Length 1388;  
Best Local Similarity 27.6%; Pred. No. 1.7e-06;  
RESULT 1320  
ID AAO16358 standard; protein; 7339 AA.  
DE Human translocated promoter region (TPR) protein, SEQ ID NO 6.  
PN WO200299050-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.2%; Score 240.5; DB 6; Length 7339;  
Best Local Similarity 24.3%; Pred. No. 8.4e-06;  
RESULT 1321  
ID AAR80350 standard; protein; 338 AA.  
DE Protein polymeric adhesion substrate 2-F.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.2%; Score 240; DB-2; Length 338;  
Best Local Similarity 29.6%; Pred. No. 4.8e-07;  
RESULT 1322  
ID ABU36649 standard; protein; 678 AA.  
DE Protein encoded by Prokaryotic essential gene #22176.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.2%; Score 240; DB 6; Length 678;  
Best Local Similarity 27.5%; Pred. No. 9.3e-07;  
RESULT 1323  
ID ADD89022 standard; protein; 1212 AA.  
DE TAT262.  
PN WO2003057160-A2.  
PD 17-JUL-2003.

PA (GETH) GENENTECH INC.  
Query Match 10.2%; Score 240; DB 7; Length 1212;  
Best Local Similarity 26.2%; Pred. No. 1.6e-06;  
RESULT 1324  
ID AAM40863 standard; protein; 1669 AA.  
DE Human polypeptide SEQ ID NO 5794.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 240; DB 4; Length 1669;  
Best Local Similarity 26.2%; Pred. No. 2.2e-06;  
RESULT 1325  
ID AAB70178 standard; peptide; 183 AA.  
DE Peptide dendrimer carrier #3.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 10.1%; Score 239.5; DB 4; Length 183;  
Best Local Similarity 29.7%; Pred. No. 2.8e-07;  
RESULT 1326  
ID ADP31574 standard; protein; 366 AA.  
DE Human secreted protein SEQ ID #2341.  
PN WO2004035732-A2.  
PD 23-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.1%; Score 239.5; DB 8; Length 366;  
Best Local Similarity 26.3%; Pred. No. 5.5e-07;  
RESULT 1327  
ID ADP31575 standard; protein; 384 AA.  
DE Human secreted protein SEQ ID #2342.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.1%; Score 239.5; DB 8; Length 384;  
Best Local Similarity 26.3%; Pred. No. 5.8e-07;  
RESULT 1328  
ID ABU17351 standard; protein; 469 AA.  
DE Protein encoded by Prokaryotic essential gene #2878.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.1%; Score 239.5; DB 6; Length 469;  
Best Local Similarity 28.2%; Pred. No. 7e-07;  
RESULT 1329  
ID AAY84541 standard; protein; 1057 AA.  
DE Amino acid sequence of a human collagen 1 (alpha1) protein.  
PN EF992586-A2.  
PD 12-APR-2000.  
PA (USSU) US SURGICAL CORP.  
Query Match 10.1%; Score 239.5; DB 3; Length 1057;  
Best Local Similarity 26.7%; Pred. No. 1.5e-06;  
RESULT 1330  
ID AAB82454 standard; protein; 1464 AA.  
DE Human pro-alpha-1 chain of type I procollagen.  
PN WO200144455-A2.  
PD 21-JUN-2001.  
PA (ASTR) ASTRAZENECA AB.  
Query Match 10.1%; Score 239.5; DB 4; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1331  
ID ABB90764 standard; protein; 1464 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 261.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Query Match 10.1%; Score 239.5; DB 5; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1332  
ID ABP68610 standard; protein; 1464 AA.  
DE Human pancreatic cancer expressed protein SEQ ID NO 159.  
PN WO200260317-A2.  
PD 08-AUG-2002.

PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239.5; DB 5; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1333  
ID ABUS4471 standard; protein; 1464 AA.  
DE Human tumour endothelial marker TEM 38.  
PN WO20023874-A2.  
PD 24-OCT-2002.  
PA (UYUJ) UNIV JOHNS HOPKINS.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1334  
ID ABR47417 standard; protein; 1464 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:65.  
PN WO2003004989-A2.  
PD 18-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1335  
ID ABR92064 standard; protein; 1464 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:36.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 239.5; DB 6; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1336  
ID ADD14142 standard; protein; 1464 AA.  
DE Human src biomarker polypeptide SEQ ID NO:331.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.1%; Score 239.5; DB 7; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1337  
ID ADP65246 standard; protein; 1464 AA.  
DE Human alpha 1 type I collagen preproprotein, Collagen I, alpha-1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 239.5; DB 7; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1338  
ID ADQ19470 standard; protein; 1464 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2289.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.1%; Score 239.5; DB 8; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1339  
ID ADQ29653 standard; protein; 1464 AA.  
DE Human colorectal cancer-associated protein #8.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
Query Match 10.1%; Score 239.5; DB 8; Length 1464;  
Best Local Similarity 26.7%; Pred. No. 2.1e-06;  
RESULT 1340  
ID ADP65203 standard; protein; 1629 AA.  
DE Human alpha 2 type XI collagen, isoform 3 preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 239.5; DB 7; Length 1629;  
Best Local Similarity 25.7%; Pred. No. 2.3e-06;  
RESULT 1341  
ID ABB57334 standard; protein; 1669 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:933.  
PN WO200188188-A2.  
PD 22-NOV-2001.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 10.1%; Score 239.5; DB 5; Length 1669;  
Best Local Similarity 27.7%; Pred. No. 2.4e-06;  
RESULT 1342  
ID ABU22680 standard; protein; 584 AA.  
DE Protein encoded by Prokaryotic essential gene #8207.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 10.1%; Score 239; DB 6; Length 584;  
Best Local Similarity 26.2%; Pred. No. 9.3e-07;  
RESULT 1343  
ID AAB68072 standard; protein; 662 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1344  
ID AAE02718 standard; protein; 662 AA.  
DE Human alpha (I) type I collagen helical domain (residues 531-1192).  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1345  
ID ADB84306 standard; protein; 662 AA.  
DE Recombinant gelatin #18.  
PN US2003064074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 10.1%; Score 239; DB 7; Length 662;  
Best Local Similarity 27.6%; Pred. No. 1e-06;  
RESULT 1346  
ID AAE02532 standard; protein; 1463 AA.  
DE Bovine alpha (I) collagen.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 239; DB 4; Length 1463;  
Best Local Similarity 27.7%; Pred. No. 2.2e-06;  
RESULT 1347  
ID AAU84266 standard; protein; 1806 AA.  
DE Human endometrial cancer related protein, COL11A1.  
PN WO200209573-A2.  
PD 07-FEB-2002.  
PA (IGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 10.1%; Score 239; DB 5; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1348  
ID ABJ05596 standard; protein; 1806 AA.  
DE Breast cancer-associated protein 61.  
PN WO200259377-A2.  
PD 01-AUG-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.1%; Score 239; DB 5; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1349  
ID ABR58545 standard; protein; 1806 AA.  
DE Human cancer related protein SEQ ID NO:202.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.1%; Score 239; DB 6; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1350  
ID ABUS6581 standard; protein; 1806 AA.

DE Lung cancer-associated polypeptide #174.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.1%; Score 239; DB 6; Length 1806;  
Best Local Similarity 24.7%; Pred. No. 2.7e-06;  
RESULT 1351  
ID ADP31114 standard; protein; 1288 AA.  
DE Human secreted protein SEQ ID #1881.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 10.1%; Score 238.5; DB 8; Length 1288;  
Best Local Similarity 24.5%; Pred. No. 2.1e-06;  
RESULT 1352  
ID ADP49530 standard; protein; 1420 AA.  
DE Full-length chicken type II collagen.  
PN WO2004052910-A1.  
PD 24-JUN-2004.  
PA (AFFI-) AFFILIATED HOSPITAL ACAD MILITARY SCI PL.  
Query Match 10.1%; Score 238.5; DB 8; Length 1420;  
Best Local Similarity 26.2%; Pred. No. 2.3e-06;  
RESULT 1353  
ID AAB68062 standard; protein; 500 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 238; DB 4; Length 500;  
Best Local Similarity 25.6%; Pred. No. 9.2e-07;  
RESULT 1354  
ID AAE02708 standard; protein; 500 AA.  
DE Human alpha (I) type I collagen helical domain (residues 531-1030).  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 10.1%; Score 238; DB 4; Length 500;  
Best Local Similarity 25.6%; Pred. No. 9.2e-07;  
RESULT 1355  
ID ADB84295 standard; protein; 500 AA.  
DE Recombinant gelatin #8.  
PN US2003064074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 10.1%; Score 238; DB 7; Length 500;  
Best Local Similarity 25.6%; Pred. No. 9.2e-07;  
RESULT 1356  
ID ADE87059 standard; protein; 614 AA.  
DE Human pancreatic cell protein sequence SeqID519.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.1%; Score 238; DB 7; Length 614;  
Best Local Similarity 27.5%; Pred. No. 1.1e-06;  
RESULT 1357  
ID ADE87063 standard; protein; 615 AA.  
DE Human pancreatic cell protein sequence SeqID523.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.1%; Score 238; DB 7; Length 615;  
Best Local Similarity 27.5%; Pred. No. 1.1e-06;  
RESULT 1358  
ID ADE87058 standard; protein; 691 AA.  
DE Human pancreatic cell protein sequence SeqID518.  
PN WO2003060145-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.1%; Score 238; DB 7; Length 691;  
Best Local Similarity 27.5%; Pred. No. 1.1e-06;  
RESULT 1359  
ID AAE36875 standard; protein; 349 AA.  
DE Argiope aurantia major ampullate epidroin 2 (MaSp2) protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 10.1%; Score 237.5; DB 6; Length 349;  
Best Local Similarity 23.5%; Pred. No. 7e-07;  
RESULT 1360  
ID AAR80330 standard; protein; 682 AA.  
DE Protein polymeric adhesion substrate 1-C.  
PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.1%; Score 237.5; DB 2; Length 682;  
Best Local Similarity 28.1%; Pred. No. 1.3e-06;  
RESULT 1361  
ID AAW57670 standard; peptide; 682 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.1%; Score 237.5; DB 2; Length 682;  
Best Local Similarity 28.1%; Pred. No. 1.3e-06;  
RESULT 1362  
ID AAW49717 standard; protein; 682 AA.  
DE Protein polymer adhesive substrate PPAS1-C.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.1%; Score 237.5; DB 2; Length 682;  
Best Local Similarity 28.1%; Pred. No. 1.3e-06;  
RESULT 1363  
ID AAG36619 standard; protein; 273 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44903.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.0%; Score 237; DB 3; Length 273;  
Best Local Similarity 32.9%; Pred. No. 5.9e-07;  
RESULT 1364  
ID AAG36618 standard; protein; 309 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44902.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 10.0%; Score 237; DB 3; Length 309;  
Best Local Similarity 32.9%; Pred. No. 6.7e-07;  
RESULT 1365  
ID ABR40002 standard; protein; 1606 AA.  
DE Human collagen XXII alternatively spliced variant protein.  
PN WO2003012121-A2.  
PD 13-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 10.0%; Score 237; DB 6; Length 1606;  
Best Local Similarity 22.3%; Pred. No. 3.2e-06;  
RESULT 1366  
ID AAW53519 standard; protein; 1412 AA.  
DE Amino acid sequence of the EBSI protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 2; Length 1412;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1367  
ID AAP82957 standard; protein; 1413 AA.  
DE EBSI protein comprising gagags of silk fibroin and gvgvp of elastin.  
PN WO8803533-A.  
PD 19-MAY-1988.  
PA (SYTR-) SYNTRO CORP.  
Query Match 10.0%; Score 236.5; DB 1; Length 1413;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1368  
ID AAR41008 standard; protein; 1413 AA.

DE EBSI multimeric protein.  
PN US5243038-A.  
PD 07-SEP-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 2; Length 1413;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1369  
ID AAW26343 standard; protein; 1413 AA.  
DE EBSI synthetic elastomeric protein.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 2; Length 1413;  
Best Local Similarity 28.0%; Pred. No. 3.1e-06;  
RESULT 1370  
ID AAY78278 standard; protein; 1464 AA.  
DE EBSI protein sequence SEQ ID NO:74.  
PN US6018030-A.  
PD 25-JAN-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 3; Length 1464;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1371  
ID ABG69268 standard; protein; 1465 AA.  
DE Elastin-like protein EBSI (not defined).  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 5; Length 1465;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1372  
ID ABE44969 standard; protein; 1465 AA.  
DE Recombinant structural protein EBS1 protein seq id 74.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 10.0%; Score 236.5; DB 7; Length 1465;  
Best Local Similarity 28.0%; Pred. No. 3.2e-06;  
RESULT 1373  
ID AG74869 standard; protein; 643 AA.  
DE Human cytokeraatin-1 protein.  
PN WO2003002600-A1.  
PD 09-JAN-2003.  
PA (BRAH-) BRAHMS AG.  
Query Match 10.0%; Score 235.5; DB 6; Length 643;  
Best Local Similarity 39.8%; Pred. No. 1.7e-06;  
RESULT 1374  
ID ADQ17549 standard; protein; 644 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 366.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.0%; Score 235.5; DB 8; Length 644;  
Best Local Similarity 39.8%; Pred. No. 1.7e-06;  
RESULT 1375  
ID ABB65175 standard; protein; 1180 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 22317.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 10.0%; Score 235.5; DB 4; Length 1180;  
Best Local Similarity 26.1%; Pred. No. 3e-06;  
RESULT 1376  
ID AAM39077 standard; protein; 1672 AA.  
DE Human polypeptide SEQ ID NO 2222.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSB-) HYSEQ INC.  
Query Match 10.0%; Score 235.5; DB 4; Length 1672;  
Best Local Similarity 26.0%; Pred. No. 4.2e-06;  
RESULT 1377  
ID AAB70107 standard; protein; 936 AA.  
DE Gelatin protein.

PN JP2000325095-A.  
PD 28-NOV-2000.  
PA (MIYA-) MIYAGI KAGAKU KOGYO KK.  
PA (DAII-) DAIICHI KAKAGU YAKUHIN KK.  
Query Match 9.9%; Score 235; DB 4; Length 936;  
Best Local Similarity 23.9%; Pred. No. 2.6e-06;  
RESULT 1378  
ID ABP56960 standard; protein; 2189 AA.  
DE E. maxima 250 kDa antigen homologous protein sequence SEQ ID NO:7.  
PN WO2003004684-A2.  
PD 16-JAN-2003.  
PA (WITC/) WITCOMBE D.  
PA (SMIT/) SMITH N C.  
PA (WALL/) WALLACH M.  
Query Match 9.9%; Score 235; DB 6; Length 2189;  
Best Local Similarity 27.6%; Pred. No. 5.8e-06;  
RESULT 1379  
ID AAB68066 standard; protein; 510 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.9%; Score 234.5; DB 4; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1380  
ID AAE02712 standard; protein; 510 AA.  
DE Recombinant human gelatin #1.  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.9%; Score 234.5; DB 4; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1381  
ID ADB84299 standard; protein; 510 AA.  
DE Recombinant gelatin #12.  
PN US2003064074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.9%; Score 234.5; DB 7; Length 510;  
Best Local Similarity 26.9%; Pred. No. 1.5e-06;  
RESULT 1382  
ID AAR80251 standard; peptide; 936 AA.  
DE Polymer SELP0.  
PN WO9524478-A1.  
PD 14-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.9%; Score 234.5; DB 2; Length 936;  
Best Local Similarity 28.5%; Pred. No. 2.7e-06;  
RESULT 1383  
ID ABP53472 standard; protein; 936 AA.  
DE Protein polymer SELP0 polymer block amino acid sequence.  
PN US2002045567-A1.  
PD 18-APR-2002.  
PA (CAPP/) CAPPELLO J. R.  
PA (STED/) STEDRONSKY E R.  
Query Match 9.9%; Score 234.5; DB 5; Length 936;  
Best Local Similarity 28.5%; Pred. No. 2.7e-06;  
RESULT 1384  
ID ABU56436 standard; protein; 2944 AA.  
DE Lung cancer-associated polypeptide #29.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 9.9%; Score 234.5; DB 6; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1385  
ID ADQ18966 standard; protein; 2944 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1785.  
PN WO2004048938-A2.



PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 234.5; DB 8; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1386  
ID ADQ39966 standard; protein; 2944 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1629.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 234.5; DB 8; Length 2944;  
Best Local Similarity 26.2%; Pred. No. 8.2e-06;  
RESULT 1387  
ID ADN23131 standard; protein; 3507 AA.  
DE Bacterial polypeptide #5784.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOX/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.9%; Score 234.5; DB 8; Length 3507;  
Best Local Similarity 22.6%; Pred. No. 9.7e-06;  
RESULT 1388  
ID ABR40001 standard; protein; 1626 AA.  
DE Human collagen XXII.  
PN WO2003012121-A2.  
PD 13-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.9%; Score 234; DB 6; Length 1626;  
Best Local Similarity 26.1%; Pred. No. 5e-06;  
RESULT 1389  
ID AAG36620 standard; protein; 263 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44904.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.9%; Score 233.5; DB 3; Length 263;  
Best Local Similarity 34.9%; Pred. No. 9.4e-07;  
RESULT 1390  
ID AAG51723 standard; protein; 258 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65674.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 9.9%; Score 233; DB 3; Length 258;  
Best Local Similarity 30.0%; Pred. No. 9.9e-07;  
RESULT 1391  
ID AAE36929 standard; protein; 387 AA.  
DE Nephila clavipes flagelliform (flag) consensus protein.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 9.9%; Score 233; DB 6; Length 387;  
Best Local Similarity 27.1%; Pred. No. 1.5e-06;  
RESULT 1392  
ID AAB70182 standard; peptide; 564 AA.  
DE Peptide dendrimer carrier #7.  
PN WO200107469-A2.  
PD 01-FEB-2001.  
PA (VERD/) VERDINI A.  
Query Match 9.9%; Score 233; DB 4; Length 564;  
Best Local Similarity 22.9%; Pred. No. 2.1e-06;  
RESULT 1393  
ID ADE56670 standard; protein; 864 AA.  
DE Rat Protein Q99372, SEQ ID NO 2524.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 9.9%; Score 233; DB 7; Length 864;  
Best Local Similarity 26.0%; Pred. No. 3.1e-06;  
RESULT 1394  
ID AAB68065 standard; protein; 416 AA.

DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232.5; DB 4; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1395  
ID AAE02711 standard; protein; 416 AA.  
DE Human alpha1(I) type I collagen helical domain (residues 615-1030).  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232.5; DB 4; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1396  
ID ADB84298 standard; protein; 416 AA.  
DE Recombinant gelatin #11.  
PN US2003084074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.8%; Score 232.5; DB 7; Length 416;  
Best Local Similarity 28.3%; Pred. No. 1.7e-06;  
RESULT 1397  
ID ADP31594 standard; protein; 2542 AA.  
DE Human secreted protein SEQ ID #2361.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.8%; Score 232.5; DB 8; Length 2542;  
Best Local Similarity 25.1%; Pred. No. 9.5e-06;  
RESULT 1398  
ID AAB68057 standard; protein; 501 AA.  
DE Amino acid sequence of a recombinant human gelatin.  
PN WO200134801-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232; DB 4; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1399  
ID AAE02703 standard; protein; 501 AA.  
DE Human alpha1(I) type I collagen helical domain (residues 179-679).  
PN WO200134646-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Query Match 9.8%; Score 232; DB 4; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1400  
ID ADB84290 standard; protein; 501 AA.  
DE Recombinant gelatin #3.  
PN US2003084074-A1.  
PD 03-APR-2003.  
PA (CHAN/) CHANG R C.  
PA (KIVI/) KIVIRIKKO K I.  
PA (NEFF/) NEFF T B.  
PA (OLSE/) OLSEN D R.  
PA (POLA/) POLAREK J W.  
Query Match 9.8%; Score 232; DB 7; Length 501;  
Best Local Similarity 29.7%; Pred. No. 2.2e-06;  
RESULT 1401  
ID ADQ39813 standard; protein; 1767 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1476.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.8%; Score 232; DB 8; Length 1767;  
Best Local Similarity 24.5%; Pred. No. 7.2e-06;  
RESULT 1402  
ID ADQ39817 standard; protein; 1767 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1480.

PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1767;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.2e-06;  
RESULT 1403  
ID ADP65251 standard; protein; 1806 AA.  
DE Human alpha 1 type XI collagen, isoform A preproprotein.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1404  
ID AQ39816 standard; protein; 1806 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1479.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1405  
ID AQ39815 standard; protein; 1806 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1478.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1806;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.3e-06;  
RESULT 1406  
ID AQ39812 standard; protein; 1818 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1475.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;  
RESULT 1407  
ID AQ39814 standard; protein; 1818 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1477.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 232; DB 8; Length 1818;  
Query Match Best Local Similarity 24.5%; Pred. No. 7.4e-06;  
RESULT 1408  
ID ADJ72165 standard; protein; 562 AA.  
DE Elastic polypeptide copolymer sequence #11.  
PN WO200309835-A1.  
PD 04-DEC-2003.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 562;  
RESULT 1409  
ID ADO08545 standard; protein; 562 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 33.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 562;  
RESULT 1410  
ID ADJ72166 standard; protein; 730 AA.  
DE Elastic polypeptide copolymer sequence #12.  
PN WO200309835-A1.  
PD 04-DEC-2003.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 730;  
RESULT 1411  
ID ADO08547 standard; protein; 730 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 35.  
PN EP1422242-A1.

PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 730;  
RESULT 1412  
ID ADO08572 standard; protein; 1382 AA.  
DE Multi-block copolymer PHP comprising elastic & plastic peptides SeqID 60.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 1382;  
RESULT 1413  
ID ADO08566 standard; protein; 1550 AA.  
DE Multi-block copolymer comprising elastomeric and plastic peptides Seq 54.  
PN EP1422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY.  
Query Match Best Local Similarity 29.8%; Score 231.5; DB 8; Length 1550;  
RESULT 1414  
ID ABG30822 standard; protein; 378 AA.  
DE Chicken hmrNPAL protein.  
PN US2002068321-A1.  
PD 06-JUN-2002.  
PA (NEWM/) NEWMAN S A.  
PA (BRON/) BRONSTEIN N B.  
Query Match Best Local Similarity 33.5%; Score 230.5; DB 5; Length 378;  
RESULT 1415  
ID AAW09221 standard; protein; 936 AA.  
DE SELPOK-CS1 polymer.  
PN WO9634618-A1.  
PD 07-NOV-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match Best Local Similarity 27.5%; Score 230.5; DB 2; Length 936;  
RESULT 1416  
ID RAY51891 standard; protein; 936 AA.  
DE Plasmid pPTO370 protein fragment containing SELPOK-CS1 polymer units.  
PN US6033654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match Best Local Similarity 27.5%; Score 230.5; DB 3; Length 936;  
RESULT 1417  
ID ABG31421 standard; protein; 936 AA.  
DE SELPOK-CS1 protein encoded by plasmid pPTO370.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match Best Local Similarity 27.5%; Score 230.5; DB 5; Length 936;  
RESULT 1418  
ID ABW01637 standard; protein; 936 AA.  
DE Plasmid pPTO370 SELPOK-CS1 polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match Best Local Similarity 27.5%; Score 230.5; DB 7; Length 936;  
RESULT 1419  
ID RAW53547 standard; protein; 937 AA.  
DE Amino acid sequence of SELPOK-CS1 protein.  
PN WO9810063-A1.  
PD 12-MAR-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match Best Local Similarity 27.5%; Score 230.5; DB 2; Length 937;  
RESULT 1420  
ID AA636928 standard; protein; 200 AA.  
DE Araneus diadematus minor ampullate spidroin 1 consensus protein.  
PN WO2003020916-A2.

PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING. 9.7%; Score 230; DB 6; Length 200;  
Query Match  
Best Local Similarity 29.2%; Pred. No. 1.2e-06;  
RESULT 1421  
ID ADP31572 standard; protein; 279 AA.  
DE Human secreted protein SEQ ID #2339.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 26.1%; Score 229.5; DB 8; Length 279;  
RESULT 1422  
ID ADC35283 standard; protein; 294 AA.  
DE ADF-2 silk protein.  
PN WO2003057727-A1.  
PD 17-JUL-2003.  
PA (NEXT-) NEXIA BIOTECHNOLOGIES INC.  
Query Match  
Best Local Similarity 27.5%; Score 229.5; DB 7; Length 294;  
RESULT 1423  
ID ABU19388 standard; protein; 827 AA.  
DE Protein encoded by Prokaryotic essential gene #4915.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 28.7%; Score 229.5; DB 6; Length 827;  
RESULT 1424  
ID AAY3680 standard; protein; 1574 AA.  
DE Splice variant ZAP-1A protein of the human tumor suppressor gene ZAP-1.  
PN WO9946276-A1.  
PD 16-SEP-1999.  
PA (GENO-) GENOS BIOSCIENCES INC.  
Query Match  
Best Local Similarity 27.9%; Score 229.5; DB 2; Length 1574;  
RESULT 1425  
ID ADL18527 standard; protein; 391 AA.  
DE Wheat dehydrin protein SEQ ID NO:36.  
PN WO2003027249-A2.  
PD 03-APR-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 26.8%; Score 229; DB 7; Length 391;  
RESULT 1426  
ID ADP31595 standard; protein; 3036 AA.  
DE Human secreted protein SEQ ID #2362.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 24.1%; Score 229; DB 8; Length 3036;  
RESULT 1427  
ID AEG93178 standard; protein; 430 AA.  
DE S. cerevisiae BAX-associated protein fragment SEQ ID 314.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC) JANSSEN PHARM NV.  
Query Match  
Best Local Similarity 22.8%; Score 228.5; DB 5; Length 430;  
RESULT 1428  
ID ABU69145 standard; protein; 733 AA.  
DE Human NOVX polypeptide #20.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 27.0%; Score 228.5; DB 6; Length 733;  
RESULT 1429  
ID ABB63723 standard; protein; 5002 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 17961.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 27.3%; Score 228.5; DB 4; Length 5002;  
RESULT 1430  
ID AAG84989 standard; protein; 1389 AA.  
DE Shrimp white spot Bacilliform virus (WSBV) protein 80.  
PN WO200138351-A2.  
PD 31-MAY-2001.  
PA (PENY-) PE CORP NY.  
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.  
PA (SINO-) SINOGENOMAX CO LTD.  
Query Match  
Best Local Similarity 25.9%; Score 228; DB 4; Length 1389;  
RESULT 1431  
ID AAW65462 standard; protein; 485 AA.  
DE Neocallimastix patriciarum endo-xylanase.  
PN CA2190194-A.  
PD 13-MAY-1998.  
PA (LIUJ/) LIU J H.  
PA (SELI/) SELINGER L B.  
PA (MOLO/) MOLONEY M M.  
PA (FORS/) FORSBERG C W.  
PA (CHEN/) CHENG K.  
PA (HUYI/) HU Y.  
Query Match  
Best Local Similarity 28.4%; Score 227.5; DB 2; Length 485;  
RESULT 1432  
ID AAY27283 standard; protein; 485 AA.  
DE N. patriciarum xylanase.  
PN US5948667-A.  
PD 07-SEP-1999.  
PA (MIAC) CANADA DEPT AGRICULTURE.  
Query Match  
Best Local Similarity 28.4%; Score 227.5; DB 2; Length 485;  
RESULT 1433  
ID AAB35588 standard; protein; 485 AA.  
DE N. patriciarum endo-xylanase xynC.  
PN US6137032-A.  
PD 24-OCT-2000.  
PA (MIAC) CANADA DEPT AGRICULTURE.  
Query Match  
Best Local Similarity 29.7%; Score 227.5; DB 8; Length 528;  
RESULT 1434  
ID ADJ72170 standard; protein; 528 AA.  
DE Elastic polypeptide copolymer sequence #16.  
PN WO2003099835-A1.  
PD 04-DEC-2003.  
PA (UYEM-) UNIV EMORY.  
Query Match  
Best Local Similarity 29.7%; Score 227.5; DB 8; Length 528;  
RESULT 1435  
ID ADO08555 standard; protein; 528 AA.  
DE Elastomeric hydrophilic middle block protein SeqID 43.  
PN EPI422242-A1.  
PD 26-MAY-2004.  
PA (UYEM-) UNIV EMORY.  
Query Match  
Best Local Similarity 29.7%; Score 227.5; DB 8; Length 528;  
RESULT 1436  
ID ABP9315 standard; protein; 703 AA.  
DE Human collagen protein SEQ ID NO:4.  
PN WO2003016481-A2.  
PD 27-FEB-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match  
Best Local Similarity 26.8%; Score 227; DB 6; Length 703;  
RESULT 1437  
ID ABP9314 standard; protein; 717 AA.  
DE Human collagen protein SEQ ID NO:2.  
PN WO2003016481-A2.  
PD 27-FEB-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match  
Best Local Similarity 26.8%; Score 227; DB 6; Length 717;

Best Local Similarity 26.8%; Pred. No. 6.2e-06;  
RESULT 1438  
ID ADP22968 standard; protein; 1181 AA.  
DE PRO polypeptide SEQ ID NO:62.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 227; DB 8; Length 1181;  
Best Local Similarity 26.8%; Pred. No. 9.9e-06;  
RESULT 1439  
ID ABP43711 standard; protein; 1497 AA.  
DE Bullous pemphigoid autoantigen BP180 gene.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.6%; Score 227; DB 5; Length 1497;  
Best Local Similarity 26.4%; Pred. No. 1.2e-05;  
RESULT 1440  
ID ADN24379 standard; protein; 1759 AA.  
DE Bacterial polypeptide #7032.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.6%; Score 227; DB 8; Length 1759;  
Best Local Similarity 27.9%; Pred. No. 1.5e-05;  
RESULT 1441  
ID ADQ39964 standard; protein; 2502 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1627.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.6%; Score 227; DB 8; Length 2502;  
Best Local Similarity 26.8%; Pred. No. 2e-05;  
RESULT 1442  
ID ABB69041 standard; protein; 294 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33915.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.6%; Score 226.5; DB 4; Length 294;  
Best Local Similarity 29.2%; Pred. No. 2.8e-06;  
RESULT 1443  
ID ADM16778 standard; protein; 448 AA.  
DE N. patriciarum xylanase #1.  
PN US2004053238-A1.  
PD 18-MAR-2004.  
PA (HSEU/) HSEU R.  
PA (HUAN/) HUANG Y.  
Query Match 9.6%; Score 226.5; DB 8; Length 448;  
Best Local Similarity 28.5%; Pred. No. 4.2e-06;  
RESULT 1444  
ID AAB68959 standard; protein; 192 AA.  
DE Zea mays root cap specific protein.  
PN JF2000325081-A.  
PD 28-NOV-2000.  
PA (MITA ) MITSUI CHEM INC.  
Query Match 9.6%; Score 226; DB 4; Length 192;  
Best Local Similarity 30.2%; Pred. No. 2e-06;  
RESULT 1445  
ID ABO52977 standard; protein; 379 AA.  
DE Human spliceosome associated protein (SAP) #95.  
PN US2003068803-A1.  
PD 10-APR-2003.  
PA (REED/) REED R.  
PA (ZHOU/) ZHOU Z.  
Query Match 9.6%; Score 226; DB 6; Length 379;  
Best Local Similarity 31.1%; Pred. No. 3.9e-06;  
RESULT 1446  
ID ADE61159 standard; protein; 379 AA.  
DE Human Protein P51991, SEQ ID NO 7077.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 9.6%; Score 226; DB 7; Length 379;  
Best Local Similarity 31.1%; Pred. No. 3.9e-06;  
RESULT 1447  
ID ABB60000 standard; protein; 945 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6792.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.6%; Score 226; DB 4; Length 945;  
Best Local Similarity 22.1%; Pred. No. 9.2e-06;  
RESULT 1448  
ID ABB90760 standard; protein; 1669 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 252.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.6%; Score 226; DB 5; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1449  
ID ABU54467 standard; protein; 1669 AA.  
DE Human tumour endothelial marker TEM 31.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 9.6%; Score 226; DB 6; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1450  
ID ADF90900 standard; protein; 1669 AA.  
DE Human hepatic-fibrosis disease marker protein SEQ ID 362.  
PN JF2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 9.6%; Score 226; DB 7; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1451  
ID ADR87604 standard; protein; 1669 AA.  
DE Human Type IV collagen alpha 1, SEQ ID 8.  
PN WO2004075835-A2.  
PD 10-SEP-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 226; DB 8; Length 1669;  
Best Local Similarity 26.0%; Pred. No. 1.6e-05;  
RESULT 1452  
ID ADQ21326 standard; protein; 1678 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4146.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.6%; Score 226; DB 8; Length 1678;  
Best Local Similarity 25.7%; Pred. No. 1.6e-05;  
RESULT 1453  
ID AAR05222 standard; protein; 2189 AA.  
DE Antigen GX5401FL encoded by Eimeria tenella genomic DNA.  
PN WO9000403-A.  
PD 25-JAN-1990.  
PA (GEMX ) GENEX CORP.  
Query Match 9.6%; Score 226; DB 2; Length 2189;  
Best Local Similarity 27.0%; Pred. No. 2.1e-05;  
RESULT 1454  
ID ABR53293 standard; protein; 1113 AA.  
DE Protein sequence #SEQ ID 1451.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 9.5%; Score 225.5; DB 6; Length 1113;  
Best Local Similarity 23.7%; Pred. No. 1.2e-05;  
RESULT 1455  
ID ADK63560 standard; protein; 1113 AA.

PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 9.5%; Score 224; DB 4; Length 2309;  
 Best Local Similarity 23.8%; Pred. No. 2.9e-05;  
 RESULT 1465  
 ID ABO84587 standard; protein; 1475 AA.  
 DE Human cancer-associated protein HP17-008.2.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 9.5%; Score 223.5; DB 8; Length 1475;  
 Best Local Similarity 25.5%; Pred. No. 2e-05;  
 RESULT 1466  
 ID AAW09219 standard; protein; 378 AA.  
 DE SELPOK polymer.  
 PN WO9634618-A1.  
 PD 07-NOV-1996.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.4%; Score 223; DB 2; Length 378;  
 Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
 RESULT 1467  
 ID AAY51889 standard; protein; 378 AA.  
 DE Plasmid pPT0375 protein fragment containing SELPOK polymer units.  
 PN US6033654-A.  
 PD 07-MAR-2000.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.4%; Score 223; DB 3; Length 378;  
 Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
 RESULT 1468  
 ID ABG31419 standard; protein; 378 AA.  
 DE SELPOK protein encoded by plasmid pPT0375.  
 PN US6423333-B1.  
 PD 23-JUL-2002.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.4%; Score 223; DB 5; Length 378;  
 Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
 RESULT 1469  
 ID ABW01635 standard; protein; 378 AA.  
 DE Plasmid pPT0375 SELPOK polymer protein.  
 PN US2003104589-A1.  
 PD 05-JUN-2003.  
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 Query Match 9.4%; Score 223; DB 7; Length 378;  
 Best Local Similarity 28.5%; Pred. No. 5.9e-06;  
 RESULT 1470  
 ID ADR28985 standard; protein; 976 AA.  
 DE Pseudomonas syringae antifreeze related protein SEQ ID NO:2.  
 PN WO2004072283-A1.  
 PD 26-AUG-2004.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 Query Match 9.4%; Score 223; DB 8; Length 976;  
 Best Local Similarity 24.8%; Pred. No. 1.5e-05;  
 RESULT 1471  
 ID ADR28997 standard; protein; 1200 AA.  
 DE Pseudomonas syringae antifreeze related protein SEQ ID NO:14.  
 PN WO2004072283-A1.  
 PD 26-AUG-2004.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 Query Match 9.4%; Score 223; DB 8; Length 1200;  
 Best Local Similarity 24.8%; Pred. No. 1.8e-05;  
 RESULT 1472  
 ID ADH48392 standard; protein; 821 AA.  
 DE Human recombinant gelatin-like polypeptide Hu-4.  
 PN EP1398324-A1.  
 PD 17-MAR-2004.  
 PA (FUJF ) FUJII PHOTO FILM BV.  
 Query Match 9.4%; Score 222.5; DB 8; Length 821;  
 Best Local Similarity 24.3%; Pred. No. 1.3e-05;  
 RESULT 1473  
 ID AAW09223 standard; protein; 966 AA.  
 DE SELPOK-CS2 polymer.  
 PN WO9634618-A1.  
 PD 07-NOV-1996.

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 2; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1474  
ID AAY51893 standard; protein; 966 AA.  
DE Plasmid pPT0373 crosslinking protein SELPOK-CS2 polymer unit.  
PN US0333654-A.  
PD 07-MAR-2000.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 3; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1475  
ID ARG31423 standard; protein; 966 AA.  
DE SELPOK-CS2 protein encoded by plasmid pPT0373.  
PN US6423333-B1.  
PD 23-JUL-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 5; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1476  
ID ABW01639 standard; protein; 966 AA.  
DE Plasmid pPT0373 SELPOK-CS2 polymer protein.  
PN US2003104589-A1.  
PD 05-JUN-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.4%; Score 222.5; DB 7; Length 966;  
Best Local Similarity 26.3%; Pred. No. 1.5e-05;  
RESULT 1477  
ID ABB54168 standard; protein; 1063 AA.  
DE Lactococcus lactis protein yihd.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 9.4%; Score 222.5; DB 5; Length 1063;  
Best Local Similarity 24.8%; Pred. No. 1.7e-05;  
RESULT 1478  
ID ASO84590 standard; protein; 1472 AA.  
DE Human cancer-associated protein HP17-008.5.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.4%; Score 222; DB 8; Length 1472;  
Best Local Similarity 25.2%; Pred. No. 2.5e-05;  
RESULT 1479  
ID AAW40109 standard; protein; 1694 AA.  
DE Human alpha-6(IV) collagen protein.  
PN US5731192-A.  
PD 24-MAR-1998.  
PA (UYVA) UNIV YALE.  
Query Match 9.4%; Score 222; DB 2; Length 1694;  
Best Local Similarity 25.2%; Pred. No. 2.8e-05;  
RESULT 1480  
ID ABU19448 standard; protein; 979 AA.  
DE Protein encoded by Prokaryotic essential gene #4975.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 9.4%; Score 221.5; DB 6; Length 979;  
Best Local Similarity 26.3%; Pred. No. 1.8e-05;  
RESULT 1481  
ID AAB97070 standard; protein; 2058 AA.  
DE Human polypeptide #3 expressed in intraabdominal adipose tissue.  
PN JP2001008699-A.  
PD 16-JAN-2001.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 9.4%; Score 221.5; DB 4; Length 2058;  
Best Local Similarity 29.2%; Pred. No. 3.7e-05;  
RESULT 1482  
ID ABB69088 standard; protein; 181 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 34056.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.

Query Match 9.3%; Score 220.5; DB 4; Length 181;  
Best Local Similarity 32.9%; Pred. No. 4.1e-06;  
RESULT 1483  
ID ABP98825 standard; protein; 625 AA.  
DE Human structural and cytoskeletal associated protein #16.  
PN WO2003031940-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.3%; Score 220.5; DB 6; Length 625;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1484  
ID ABG77177 standard; protein; 645 AA.  
DE Prostate adenocarcinoma associated protein #12.  
PN US2002119463-A1.  
PD 29-AUG-2002.  
PA (FARI/) PARIS M.  
PA (TURN/) TURNER C M.  
Query Match 9.3%; Score 220.5; DB 5; Length 645;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1485  
ID ADN04309 standard; protein; 645 AA.  
DE Antipsoriatic protein sequence #349.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 9.3%; Score 220.5; DB 8; Length 645;  
Best Local Similarity 41.2%; Pred. No. 1.4e-05;  
RESULT 1486  
ID ABUS2683 standard; protein; 957 AA.  
DE Human cell structure and mobility-associated protein from DKFZphfbr2\_2b5.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 9.3%; Score 220; DB 4; Length 957;  
Best Local Similarity 25.8%; Pred. No. 2.2e-05;  
RESULT 1487  
ID ADP31661 standard; protein; 1365 AA.  
DE Human secreted protein SEQ ID #2428.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1365;  
Best Local Similarity 25.1%; Pred. No. 3.1e-05;  
RESULT 1488  
ID AAE37932 standard; protein; 1488 AA.  
DE Human CGDD-21 protein.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.3%; Score 220; DB 7; Length 1488;  
Best Local Similarity 23.9%; Pred. No. 3.3e-05;  
RESULT 1489  
ID ADP31664 standard; protein; 1875 AA.  
DE Human secreted protein SEQ ID #2431.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1875;  
Best Local Similarity 25.1%; Pred. No. 4.2e-05;  
RESULT 1490  
ID ADP31662 standard; protein; 1956 AA.  
DE Human secreted protein SEQ ID #2429.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 9.3%; Score 220; DB 8; Length 1956;  
Best Local Similarity 25.1%; Pred. No. 4.3e-05;  
RESULT 1491  
ID AAW26341 standard; protein; 168 AA.  
DE Silk-like protein SlpI dimer.  
PN US5641648-A.  
PD 24-JUN-1997.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Query Match 9.3%; Score 219.5; DB 2; Length 168;  
Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
RESULT 1492  
ID A8G69263 standard; protein; 168 AA.  
DE Silk-like protein encoded by DNA clone PSY708 #2.  
PN US6355776-B1.  
PD 12-MAR-2002.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 5; Length 168;  
Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
RESULT 1493  
ID ADE44947 standard; protein; 168 AA.  
DE Silk fibroin protein repeating peptide related peptide seq id 52.  
PN US2003083464-A1.  
PD 01-MAY-2003.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 7; Length 168;  
Best Local Similarity 33.8%; Pred. No. 4.4e-06;  
RESULT 1494  
ID AAW49723 standard; protein; 829 AA.  
DE Protein polymer adhesive substrate PPAS1-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 2; Length 829;  
Best Local Similarity 29.4%; Pred. No. 2e-05;  
RESULT 1499  
ID AAW49723 standard; protein; 829 AA.  
DE Protein polymer adhesive substrate PPAS1-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 2; Length 829;  
Best Local Similarity 29.4%; Pred. No. 2e-05;  
RESULT 1500  
ID ADB70380 standard; protein; 1019 AA.  
DE Collagen VI SEQ ID NO:72.  
PN WO2003021229-A2.  
PD 13-MAR-2003.  
PA (SGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 9.3%; Score 219.5; DB 7; Length 1019;  
Best Local Similarity 29.3%; Pred. No. 2.5e-05;  
RESULT 1496  
ID ADO08293 standard; protein; 733 AA.  
DE Human NOVX polypeptide #20.  
PN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CASM/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEPLEY D M.  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUFIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Query Match 9.3%; Score 219.5; DB 8; Length 733;  
Best Local Similarity 26.5%; Pred. No. 1.8e-05;  
RESULT 1497  
ID AAR80334 standard; protein; 829 AA.  
DE Protein polymeric adhesive substrate 1-F.

PN WO9523611-A1.  
PD 08-SEP-1995.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 2; Length 829;  
Best Local Similarity 29.4%; Pred. No. 2e-05;  
RESULT 1498  
ID AAW57673 standard; peptide; 829 AA.  
DE Collagen-like polymer.  
PN US5773249-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 2; Length 829;  
Best Local Similarity 29.4%; Pred. No. 2e-05;  
RESULT 1499  
ID AAW49723 standard; protein; 829 AA.  
DE Protein polymer adhesive substrate PPAS1-F.  
PN US5773577-A.  
PD 30-JUN-1998.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 9.3%; Score 219.5; DB 2; Length 829;  
Best Local Similarity 29.4%; Pred. No. 2e-05;  
RESULT 1500  
ID ADB70380 standard; protein; 1019 AA.  
DE Collagen VI SEQ ID NO:72.  
PN WO2003021229-A2.  
PD 13-MAR-2003.  
PA (SGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 9.3%; Score 219.5; DB 7; Length 1019;  
Best Local Similarity 29.3%; Pred. No. 2.5e-05;





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OM protein - protein search, using sw model

Run on: May 15, 2005, 05:30:06 ; Search time 40 Seconds  
(without alignments)  
1058.384 Million cell updates/sec

Title: US-10-063-699-52

Perfect score: 2363

Sequence: 1 MKFQGPLACLLALCLGSGE.....KLGFINWDAINDKQRSRIP 440

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450.5	19.1	1079	2 B70807	hypothetical glyci
2	439.5	18.6	1306	2 A70934	hypothetical glyci
3	423	17.9	386	2 T49109	glycine-rich prote
4	415.5	17.6	1381	2 E70806	hypothetical glyci
5	412.5	17.5	484	2 F70846	hypothetical glyci
6	406	17.2	1901	2 F70806	hypothetical glyci
7	404.5	17.1	532	2 F70580	hypothetical glyci
8	403	17.1	1489	2 D70807	hypothetical glyci
9	400.5	16.9	1538	2 H70846	hypothetical glyci
10	399.5	16.9	853	2 A70896	hypothetical glyci
11	395	16.7	714	2 A70807	hypothetical glyci
12	395	16.7	1660	2 A70869	hypothetical glyci
13	392.5	16.6	923	2 E70820	hypothetical glyci
14	392	16.6	731	2 C70974	hypothetical glyci
15	392	16.6	1329	2 E70917	hypothetical glyci
16	386	16.3	778	2 F70963	hypothetical glyci
17	383.5	16.2	767	2 F70895	hypothetical glyci
18	383	16.2	641	1 Q0BE31	nuclear antigen BB
19	381.5	16.1	741	2 G70917	hypothetical glyci
20	380.5	16.1	837	2 E70835	hypothetical glyci
21	379	16.0	465	1 S01820	glycine-rich cell
22	378	16.0	588	2 F70971	hypothetical glyci
23	376.5	15.9	749	2 A70812	hypothetical glyci
24	375	15.9	914	2 H70987	hypothetical glyci
25	373.5	15.8	584	2 G70804	hypothetical glyci
26	373.5	15.8	667	2 A70893	hypothetical glyci
27	372	15.7	694	2 F70868	hypothetical glyci
28	371	15.7	615	2 H70589	hypothetical glyci
29	371	15.7	718	2 A36068	major ampullate fi

30	370.5	15.7	491	2 D70916	hypothetical glyci
31	369.5	15.6	1428	2 T08852	lustrin A - Califo
32	366	15.5	408	2 S57483	glycin-rich protei
33	365.5	15.5	496	2 H70839	hypothetical glyci
34	365	15.4	576	2 A70900	hypothetical glyci
35	365	15.4	591	2 B70523	hypothetical glyci
36	364.5	15.4	801	2 F70824	hypothetical glyci
37	364	15.4	606	2 H70816	hypothetical glyci
38	363	15.4	481	2 A35628	loricrin - mouse
39	363	15.4	639	2 D70931	hypothetical glyci
40	360	15.2	562	2 B70953	hypothetical glyci
41	359.5	15.2	1011	2 F70620	hypothetical glyci
42	359	15.2	463	2 B70893	hypothetical glyci
43	358.5	15.2	338	1 KNMU	hypothetical glyci
44	355	15.0	291	1 S31415	glycine-rich cell
45	352.5	14.9	384	1 A26099	glycine-rich cell
46	352	14.9	274	2 T25404	hypothetical prote
47	352	14.9	603	2 A70770	hypothetical glyci
48	351	14.9	957	2 D70835	hypothetical glyci
49	350.5	14.8	461	2 F70571	hypothetical glyci
50	350	14.8	316	1 A38743	loricrin - human
51	349	14.8	618	2 A70989	hypothetical glyci
52	349	14.8	882	2 B70812	hypothetical glyci
53	345	14.6	713	1 UMMS	period clock prote
54	345	14.6	966	2 A33626	fibrinogen alpha c
55	344	14.6	525	2 D70878	hypothetical glyci
56	344	14.6	783	2 E70824	hypothetical glyci
57	342	14.5	515	2 H70663	hypothetical glyci
58	339.5	14.4	487	2 E70983	hypothetical glyci
59	339	14.3	937	2 S58135	hypally regulated
60	335	14.2	434	2 E70768	hypothetical glyci
61	334	14.1	255	2 B84777	hypothetical prote
62	334	14.1	498	2 C70720	hypothetical glyci
63	329	13.9	549	2 T20720	hypothetical prote
64	325.5	13.8	439	2 D70954	hypothetical glyci
65	322	13.6	1207	2 T23754	hypothetical prote
66	320	13.5	594	2 G70545	hypothetical glyci
67	315	13.3	302	2 C84470	hypothetical prote
68	314.5	13.3	543	2 F70726	hypothetical glyci
69	312.5	13.2	252	1 S01821	glycine-rich prote
70	308.5	13.1	2639	2 T31328	fibrin - Chinese
71	308	13.0	271	2 S34666	glycine-rich prote
72	306.5	13.0	419	1 OZQAM	circumsporozite p
73	306	12.9	284	2 T23158	hypothetical prote
74	302	12.8	592	2 E82759	endo-1,4-beta-gluc
75	301	12.7	485	2 A60610	circumsporozite p
76	300.5	12.7	622	2 I37984	keratin 9, type I
77	299.5	12.7	398	2 A43426	collagen alpha 2 f
78	298.5	12.6	210	2 JQ1060	glycine-rich prote
79	298.5	12.6	2174	2 E95965	hypothetical glyci
80	296.5	12.5	1585	2 T31611	hypothetical prote
81	296	12.5	627	2 A44112	spidroin 2, dragli
82	293.5	12.4	794	2 T10519	pre-pro-legumin -
83	293	12.4	256	2 A70514	hypothetical glyci
84	290.5	12.3	749	2 I38488	trophinin - human
85	290	12.3	543	2 S19933	glycine-rich prote
86	290	12.3	751	2 S64741	cuticle collagen -
87	289	12.2	1414	1 S23809	collagen alpha 2(I
88	288.5	12.2	528	2 G02127	fus-like protein -
89	287	12.1	13288	2 T03099	mucin submaxillar
90	286	12.1	286	2 C61615	sericin MG-2 - gre
91	283	12.0	1051	2 A35763	collagen alpha 2 c
92	282	11.9	543	2 T49892	glycine-rich prote
93	280	11.8	1466	1 CGHU7L	collagen alpha 1(I
94	278.5	11.8	526	1 S33799	RNA-binding protei
95	278	11.8	220	2 T14441	glycine-rich prote
96	278	11.8	270	2 A60830	keratin, 70k type
97	277	11.7	256	2 T03371	glycine-rich prote
98	276.5	11.7	682	2 T28899	hypothetical prote
99	275	11.6	1172	2 T32759	hypothetical prote
100	274	11.6	593	1 KBHU0	keratin 10, type I
101	274	11.6	730	2 F96559	hypothetical prote
102	274	11.6	3016	2 S77300	hypothetical prote

103	273.5	11.6	183	2	PN0109	keratin-like prote	176	240	10.2	170	2	JC2213	hypothetical 14.7K
104	272.5	11.5	1373	1	A43291	collagen alpha 2(I	177	240	10.2	678	2	A70762	probable PPE prote
105	272.5	11.5	1492	2	A40333	collagen alpha 1'(	178	239.5	10.1	812	2	S31521	collagen COLF1 - f
106	272	11.5	375	2	JS0427	S-antigen precurs	179	239.5	10.1	1669	1	CGM94B	collagen alpha 1(I
107	272	11.5	2743326	2	T43326	germline RNA helic	180	239	10.1	1806	1	CGH01E	eggshell protein 1(X
108	271.5	11.5	370	2	T70872	hypothetical glyci	181	238.5	10.1	212	2	A44994	circumsporozoite p
109	271	11.5	681	2	AB2155	hypothetical prote	182	238.5	10.1	387	2	D41156	circumsporozoite p
110	270.5	11.4	1027	2	S28774	collagen alpha cha	183	238.5	10.1	387	2	D41156	keratin, epidermal
111	270	11.4	1844	2	T51890	related to Nup98-N	184	237	10.0	570	2	S07330	eggshell protein p
112	269	11.4	361	2	T70682	hypothetical glyci	185	236.5	10.0	220	2	A44805	probable nuclear a
113	269	11.4	1366	1	CGHU3S	collagen alpha 2(I	186	236.5	10.0	1733	1	B45344	collagen alpha 1(X
114	268.5	11.4	259	2	T15126	hypothetical prote	187	236	10.0	888	2	S28791	hypothetical prote
115	268	11.3	183	1	KNR232	glycine-rich cell	188	235	9.9	839	2	F75518	eggshell protein 2
116	266	11.3	683	2	A82704	1,4-beta-cellobios	189	234.5	9.9	207	2	B44994	oleosin homolog pc
117	265.5	11.2	568	2	JC7210	molluscan shell ma	190	234.5	9.9	419	2	T14448	collagen alpha cha
118	265.5	11.2	615	2	E70663	probable PPE prote	191	234.5	9.9	438	2	S53787	aggregan precursor
119	263	11.1	435	2	T15143	hypothetical prote	192	234.5	9.9	2109	1	I50421	collagen precursor
120	263	11.1	1752	2	A45407	collagen alpha 3(I	193	234.5	9.9	2944	2	A54849	collagen alpha 1(V
121	262.5	11.1	645	2	F70825	probable PPE prote	194	234.5	9.9	3507	2	T34513	hypothetical prote
122	262.5	11.1	1049	1	CGB078	collagen alpha 1(I	195	234	9.9	227	2	B41342	circumsporozoite p
123	262.5	11.1	2038	2	A43742	female sterile hom	196	234	9.9	1655	2	T13998	gene mastermind pr
124	262	11.1	1549	2	T48103	type VII collagen	197	233.5	9.9	165	1	KNRZG1	glycine-rich cell
125	260	11.0	730	2	A36226	collagen alpha 1 c	198	233.5	9.9	171	2	H84709	probable glycine-r
126	260	11.0	1486	1	B40333	collagen alpha 1(I	199	233.5	9.9	180	2	T28938	hypothetical prote
127	258.5	10.9	462	4	S33798	FUS/CHOP mutant fu	200	233	9.9	783	2	T35389	probable serine-th
128	257.5	10.9	386	1	S22315	snRNP-associated p	201	233	9.9	864	1	EART	elastin precursor
129	257.5	10.9	581	1	KRM82	keratin, type II c	202	232.5	9.8	290	2	T23416	hypothetical prote
130	257.5	10.9	1464	2	S59856	collagen alpha 1(I	203	232.5	9.8	643	1	KRHU2	keratin 1, type II
131	255.5	10.8	589	2	S71954	RNA/ssDNA-binding	204	231.5	9.8	244	2	T49893	glycine-rich prote
132	255	10.8	632	2	S42731	collagen alpha 1 c	205	231	9.8	221	2	T04592	glycine-rich cell
133	254	10.7	1747	2	A54121	collagen alpha-4 c	206	231	9.8	413	2	E70661	probable PPE protei
134	253.5	10.7	401	1	OZ20AC	circumsporozoite p	207	231	9.8	1758	2	T29350	hypothetical prote
135	253.5	10.7	539	2	T28770	hypothetical prote	208	230.5	9.8	1300	2	T03166	probable immediate
136	253	10.7	1217	2	S52714	sericinB - silkwo	209	230.5	9.8	3157	2	B70969	probable PPE prote
137	253	10.7	1487	1	CGHU6C	collagen alpha 1(I	210	230	9.7	115	2	D61615	sericin MG-1 - gre
138	252.5	10.7	404	2	S54729	RNA-binding protei	211	230	9.7	1778	2	T50074	probable nucleopor
139	252	10.7	582	2	F70675	probable PPE prote	212	229.5	9.7	569	1	KRMSE1	keratin, 59K type
140	252	10.7	1497	2	I49607	procollagen type V	213	229	9.7	162	2	C85356	glycine-rich prote
141	251.5	10.6	490	2	T05444	hypothetical prote	214	229	9.7	391	2	T06224	COR39 protein - wh
142	251.5	10.6	860	1	EAMS	elastin precursor	215	228.5	9.7	190	2	B48571	circumsporozoite p
143	251	10.6	429	2	A54504	circumsporozoite p	216	228.5	9.7	430	1	HHBYD8	heat shock protein
144	251	10.6	671	1	CGRT1S	collagen alpha 1(I	217	228.5	9.7	555	2	S70791	vsab protein - Myc
145	249.5	10.6	395	2	A41156	circumsporozoite p	218	228.5	9.7	561	2	A31994	keratin 10, type I
146	249.5	10.6	940	2	JB0291	PB19 protein - hum	219	228	9.6	373	2	S40777	heterogeneous ribo
147	249	10.5	590	2	E70946	probable PPE prote	220	228	9.6	920	2	B34493	collagen alpha 1(I
148	248.5	10.5	1032	2	G89427	protein T08P2.3 [I	221	227.5	9.6	180	2	T49530	related to glycine
149	248	10.5	343	2	T05221	hypothetical prote	222	227	9.6	371	2	E88633	protein F56B3.1 [I
150	248	10.5	385	2	S40778	ribonucleoprotein	223	227	9.6	402	1	CGB02S	collagen alpha 2(I
151	247.5	10.5	1418	2	T45467	collagen alpha 1(I	224	227	9.6	1210	2	A25547	ice nucleation pro
152	247.5	10.5	3300	2	D70575	probable PPE prote	225	227	9.6	1759	2	T29351	collagen alpha 2(I
153	246.5	10.4	1453	2	S21626	collagen alpha 1(I	226	226.5	9.6	326	2	A41732	heterogeneous ribo
154	246.5	10.4	1464	1	CGHUIS	collagen alpha 1(I	227	226.5	9.6	469	2	T30697	dehydrin homolog W
155	246.5	10.4	1958	2	B40505	hypothetical prote	228	226.5	9.6	641	2	T30076	hypothetical prote
156	245.5	10.4	354	2	B70663	probable PPE prote	229	226.5	9.6	918	2	S23377	collagen alpha 2(V
157	245.5	10.4	636	2	S41067	collagen alpha 1(I	230	226.5	9.6	1022	2	S04111	collagen alpha 2(V
158	245	10.4	1419	2	A41182	collagen alpha 1(I	231	226	9.6	1669	1	CGHU4B	collagen alpha 1(I
159	245.5	10.4	1487	2	B41182	collagen alpha 1(I	232	225.5	9.5	1113	2	S28925	nuclear pore compl
160	245	10.4	886	2	I50694	collagen alpha 1(I	233	224	9.5	167	2	S21359	keratin, type I, c
161	245	10.4	1684	2	T02367	hypothetical prote	234	224	9.5	404	2	B84745	probable RNA-bind
162	243	10.3	424	2	T08093	oleosin homolog ST	235	224	9.5	447	2	T42987	hypothetical prote
163	243	10.3	1226	2	T24045	hypothetical prote	236	224	9.5	1532	2	A61262	collagen alpha 1(X
164	242.5	10.3	205	2	T07959	probable cell wall	237	223.5	9.5	572	2	T08509	trbl protein - Ent
165	242.5	10.3	1496	1	CGHU2V	collagen alpha 2(V	238	223	9.4	545	2	T15667	hypothetical prote
166	242.5	10.3	1775	2	A31893	collagen alpha 1(I	239	223	9.4	1200	1	SNPSO	ice nucleation pro
167	242	10.2	385	2	T20410	hypothetical prote	240	222.5	9.4	1063	2	D86731	hypothetical prote
168	242	10.2	779	1	CGB01S	collagen alpha 1(I	241	222.5	9.4	1761	2	T13990	collagen type IV a
169	241.5	10.2	608	2	T05442	glycine-rich prote	242	222.5	9.4	2523	2	F70846	probable PPE prote
170	241.5	10.2	1042	1	CGCH1S	collagen alpha 1(I	243	222	9.4	365	2	A34840	heterogeneous ribo
171	241	10.2	380	2	A48295	collagen 1 - marin	244	222	9.4	552	2	D70604	probable PPE prote
172	241	10.2	964	1	CGCH2S	collagen alpha 2(I	245	222	9.4	1691	1	CGHU6B	collagen alpha 6(I
173	241	10.2	1546	1	CGHU2B	collagen alpha 2(X	246	221.5	9.4	173	2	JQ1064	glycine-rich prote
174	241	10.2	1744	2	S40991	collagen alpha 1(I	247	221	9.4	310	2	I50696	collagen alpha 1(I
175	240.5	10.2	673	1	CGB06C	collagen alpha 1(I	248	221	9.4	575	2	T52420	dehydrin 5 limpor

249	221	9.4	575	2	S35327	protein kinase egg	322	204.5	8.7	770	2	S59623	tropoelastin - she
250	220.5	9.3	316	2	T20497	hypothetical prote	323	204.5	8.7	1019	1	A32856	collagen alpha 1(V
251	220.5	9.3	618	2	H70552	probable PPE prote	324	204	8.6	177	2	A31204	eggshell protein p
252	220.5	9.3	645	2	A44861	keratin, 67K type	325	204	8.6	228	2	S19932	glycine-rich prote
253	220	9.3	917	2	S09646	collagen alpha 2(V	326	204	8.6	547	2	A36046	collagen alpha cha
254	220	9.3	1018	1	CGH02A	collagen alpha 2(V	327	204	8.6	1146	2	A38587	collagen, cornea-s
255	219.5	9.3	207	2	T07381	glycine-rich prote	328	203	8.6	223	2	B96506	hypothetical prote
256	219.5	9.3	2248	2	A35938	profilaggrin - hum	329	203	8.6	680	2	T08080	probable myrosinas
257	218	9.2	287	2	A60643	antigen 5401 - Elm	330	203	8.6	825	2	JC4163	DNA-binding protei
258	217.5	9.2	1880	2	T18531	tractin - medicina	331	203	8.6	1034	2	JC2143	ice nucleation act
259	217	9.2	575	2	S27761	dehydrin Dhn5 - ba	332	203	8.6	2327	2	T42630	aggreccan - bovine
260	216.5	9.2	674	2	S13301	collagen alpha 1(X	333	202.5	8.6	351	2	B34840	heterogeneous ribo
261	216.5	9.2	2090	2	S26058	probable transform	334	202.5	8.6	677	2	S23296	collagen alpha 2(I
262	216	9.1	409	2	T20847	hypothetical prote	335	202.5	8.6	1028	1	CGH01A	collagen alpha 1(V
263	215.5	9.1	2132	1	A55182	aggreccan precursor	336	202.5	8.6	3176	2	CGH03A	collagen alpha 3(V
264	215	9.1	200	2	S10334	glycine-rich prote	337	202	8.5	430	2	S52700	NUP42 protein - ye
265	215	9.1	479	2	F70573	hypothetical prote	338	201.5	8.5	393	2	T20268	hypothetical prote
266	215	9.1	1029	1	S21369	collagen alpha 2(V	339	201	8.5	1712	1	CGH02B	collagen alpha 2(I
267	215	9.1	1567	2	S11672	ice nucleation pro	340	200.5	8.5	312	2	T25048	hypothetical prote
268	215	9.1	1690	1	CGH01B	collagen alpha 4(I	341	200.5	8.5	353	2	B34504	heterogeneous nucl
269	215	9.1	1838	1	CGH01V	collagen alpha 1(V	342	200.5	8.5	623	1	S33167	gene pointed prote
270	215	9.1	1843	2	S18803	collagen alpha 1(V	343	200.5	8.5	675	2	S20819	collagen alpha 3(I
271	214.5	9.1	390	2	A32249	collagen - sea urc	344	200.5	8.5	2332	2	T34434	hypothetical prote
272	214.5	9.1	388	2	T29173	hypothetical prote	345	200	8.5	1096	2	H86237	protein FlA2N23.29
273	214.5	9.1	465	2	F75524	hypothetical prote	346	200	8.5	1258	2	JQ0188	ice nucleation pro
274	214.5	9.1	1018	2	H83135	probable adhesin P	347	200	8.5	3716	2	K70969	probable PPE prote
275	214	9.1	1024	2	S18251	collagen alpha 1(X	348	199.5	8.4	214	1	KNN72S	glycine-rich prote
276	214	9.1	1275	2	T33369	hypothetical prote	349	199.5	8.4	670	2	T49510	fibroin-3 related
277	213.5	9.0	245	2	F70787	hypothetical glyci	350	199.5	8.4	707	2	A48686	probable RNA helic
278	213.5	9.0	695	2	T24950	hypothetical prote	351	199.5	8.4	1022	2	T24663	hypothetical prote
279	213.5	9.0	959	2	B44402	nuclear pore compl	352	199	8.4	825	1	EDBEXD	immediate-early pr
280	213.5	9.0	1670	1	CGH03B	collagen alpha 3(I	353	198.5	8.4	191	2	A42844	abscisic acid-and
281	213.5	9.0	2415	1	A39086	aggreccan precursor	354	198.5	8.4	380	2	T14447	oleosin homolog pc
282	213.5	9.0	1804	2	H96597	hypothetical prote	355	198.5	8.4	921	2	S04095	collagen alpha 1(I
283	212.5	9.0	2551	2	B98047	hypothetical prote	356	198.5	8.4	1433	2	A46053	bullous pemphigoid
284	212	9.0	390	2	S27766	WCS120 protein - w	357	198.5	8.4	1691	1	S22917	collagen alpha 5(I
285	212	9.0	635	2	A57131	collagen alpha 2(V	358	198	8.4	346	2	S40775	ribonucleoprotein
286	212	9.0	907	2	A45560	sporozoite surface	359	198	8.4	541	2	S51799	nucleoporin NUP57
287	211.5	9.0	488	2	A27353	collagen alpha 1(I	360	198	8.4	1213	2	S16356	ovo protein - frui
288	211	8.9	967	2	S66852	hypothetical prote	361	197.5	8.4	744	2	S15435	collagen alpha 1(V
289	210.5	8.9	471	2	T33997	hypothetical prote	362	197	8.3	361	2	T14460	oleosin homolog gb
290	210.5	8.9	3190	2	T13828	CREB-binding prote	363	197	8.3	1142	2	JX0369	collagen alpha 1(X
291	209.5	8.9	688	2	A53330	collagen alpha 2(I	364	196.5	8.3	571	1	UMEP	period clock prote
292	209.5	8.9	920	2	A45748	collagen alpha 1(V	365	196.5	8.3	754	2	A55267	collagen alpha 5(I
293	209	8.8	680	2	S31216	collagen alpha 1(X	366	196	8.3	136	2	T29282	hypothetical prote
294	209	8.8	1707	2	A33526	collagen alpha 2(I	367	196	8.3	1147	1	MWAXIB	myosin heavy chain
295	209	8.8	3137	2	A37797	collagen alpha 3(V	368	195.5	8.3	314	2	T08675	hypothetical prote
296	208.5	8.8	377	2	T08095	oleosin homolog ST	369	195.5	8.3	633	2	B40983	collagen alpha 1(X
297	208	8.8	201	2	T07099	hypothetical prote	370	195.5	8.3	698	2	JH0163	No-on-transient A
298	208	8.8	307	2	T27609	hypothetical prote	371	195.5	8.3	700	2	JH0162	No-on-transient A
299	208	8.8	457	2	H70820	hypothetical glyci	372	195.5	8.3	921	2	S42617	collagen alpha 1(I
300	208	8.8	618	2	S32436	probable tail fi	373	195.5	8.3	1560	2	T02885	peroxisome prolife
301	207.5	8.8	365	2	A26459	helix-destabilizin	374	195	8.3	358	2	S40776	ribonucleoprotein
302	207	8.8	208	2	T46896	merozoite surface	375	195	8.3	469	2	A24450	collagen alpha 2(V
303	207	8.8	313	2	T04776	hypothetical prote	376	195	8.3	1748	2	A42136	cnfB protein - Tec
304	207	8.8	405	2	T29167	hypothetical prote	377	194.5	8.2	383	2	A53053	dentin sialoprotei
305	207	8.8	645	2	D90782	probable tail fi	378	194.5	8.2	839	2	H90577	lipoprotein vaai l
306	207	8.8	645	2	H85642	probable tail fi	379	194.5	8.2	959	2	S32605	collagen alpha 3(V
307	207	8.8	680	1	CGH01D	collagen alpha 1(X	380	194	8.2	1028	2	T03516	probable outer mem
308	207	8.8	2124	2	A28452	proteoglycan core	381	194	8.2	1400	2	T31555	hypothetical prote
309	206.5	8.7	190	2	A24713	sericin - silkworm	382	194	8.2	1436	2	B70520	probable PPE prote
310	206.5	8.7	342	2	S14432	heterogeneous ribo	383	193.5	8.2	931	2	S13580	collagen alpha 1(I
311	206.5	8.7	615	2	A05269	collagen alpha 1(I	384	193.5	8.2	1096	2	T08619	probable metallopr
312	206.5	8.7	1025	2	S34839	collagen alpha 1(V	385	192	8.1	526	1	KRBOVI	keratin, 54K type
313	206	8.7	447	2	G84687	probable disease r	386	191.5	8.1	644	1	FGHUA	fibronogen alpha c
314	206	8.7	1322	2	S07053	ice nucleation pro	387	191.5	8.1	866	2	D44234	collagen alpha 1(X
315	205.5	8.7	406	2	G71404	probable ribonucle	388	191.5	8.1	1315	2	A56101	collagen alpha 1(X
316	205.5	8.7	518	2	A55840	macrophage bacteri	389	191.5	8.1	1774	2	B56101	collagen alpha 1(X
317	205	8.7	502	2	A48679	differentiated ker	390	191	8.1	323	1	T19142	hypothetical prote
318	205	8.7	775	2	A61228	collagen alpha 2(I	391	190.5	8.1	743	1	S23779	collagen alpha 1(V
319	205	8.7	1417	2	A83080	hypothetical prote	392	190.5	8.1	796	2	S57844	lethal(3)malignant
320	205	8.7	1603	2	S23810	collagen alpha 1(X	393	190.5	8.1	2329	2	T28125	hypothetical prote
321	204.5	8.7	382	2	S20375	collagen alpha 3(V	394	190	8.0	344	2	S41707	PopAI protein - Ps

395	190	8.0	963	2	B70524	probable PPE prote	468	178.5	7.6	335	2	T14449	oleosin homolog pc
396	189.5	8.0	289	2	E96770	protein RNA-bindin	469	178	7.5	300	2	T19929	hypothetical prote
397	189	8.0	301	2	B31219	collagen 2 - Caeno	470	178	7.5	333	2	S59499	cellulase egli - s
398	189	8.0	848	2	S02262	glutinin high mole	471	178	7.5	539	2	T50579	probable membrane
399	189	8.0	1176	2	C26427	period clock prote	472	178	7.5	688	2	T48796	probable ATP-depen
400	189	8.0	1218	2	A26598	period clock prote	473	177.5	7.5	314	2	T34269	hypothetical prote
401	189	8.0	1218	2	A26427	period clock prote	474	177.5	7.5	337	2	T34203	hypothetical prote
402	188.5	8.0	203	1	J01061	glycine-rich prote	475	177	7.5	176	2	S30147	glycine-rich RNA b
403	188.5	8.0	363	2	T51341	RNA helicase RH9 I	476	177	7.5	255	2	AF1857	hypothetical prote
404	188.5	8.0	423	2	A41267	collagen 13, nonfi	477	177	7.5	304	2	T26185	hypothetical prote
405	188.5	8.0	632	2	T02627	hypothetical prote	478	177	7.5	304	2	T26184	hypothetical prote
406	188	8.0	487	2	C70830	probable PPE prote	479	177	7.5	495	2	B71360	hypothetical prote
407	188	8.0	1596	2	A33106	neurogenic locus m	480	177	7.5	908	2	A33280	sarcalumenin precu
408	187.5	7.9	752	2	T34355	hypothetical prote	481	177	7.5	1199	2	A06670	nuclear envelope p
409	187.5	7.9	956	2	T08144	myosinase-binding	482	177	7.5	3759	2	A35085	trithorax protein
410	187.5	7.9	1076	2	C96620	protein T30B16.23	483	176.5	7.5	137	2	T04930	glycine-rich cell
411	187.5	7.9	1718	2	T14603	hypothetical prote	484	176.5	7.5	367	2	A32068	circumsporozoite p
412	187	7.9	586	2	T26667	hypothetical prote	485	176.5	7.5	638	2	I53169	cyclokeratin 2 - hu
413	186.5	7.9	252	2	A55047	collagen alpha 1(V	486	176.5	7.5	798	2	T21369	hypothetical prote
414	186.5	7.9	356	2	S16907	collagen alpha 1(I	487	176.5	7.5	1241	2	S01827	period clock prote
415	186.5	7.9	378	1	OZZQAB	circumsporozoite p	488	176.5	7.5	2554	2	AB3528	extracellular seri
416	186.5	7.9	398	1	OZZQAS	circumsporozoite p	489	176	7.4	325	2	T18594	hypothetical prote
417	186	7.9	671	2	A35912	homeotic protein p	490	176	7.4	747	1	EABO	elastin precursor,
418	186	7.9	1763	2	S16366	collagen alpha 2(I	491	175.5	7.4	316	2	S08169	collagen col-12 pr
419	185.5	7.9	346	1	S35500	heterogeneous ribo	492	175.5	7.4	316	2	S08170	collagen col-13 pr
420	185.5	7.9	753	2	JC2059	glutinin, high mol	493	175.5	7.4	403	2	T08471	harpin - Erwinia a
421	185.5	7.9	789	2	A30843	glutinin high mole	494	175.5	7.4	775	1	EDBE11	immediate-early pr
422	185.5	7.9	791	2	JN0690	glutinin, high-mol	495	175	7.4	201	2	F84596	glycine-rich prote
423	185	7.8	704	2	T34034	hypothetical prote	496	175	7.4	352	2	T24279	hypothetical prote
424	185	7.8	867	2	S57795	probable deoxyribo	497	175	7.4	358	2	T26281	hypothetical prote
425	185	7.8	1004	2	C82672	surface-exposed ou	498	175	7.4	363	2	T16831	hypothetical prote
426	184.5	7.8	330	2	T26604	hypothetical prote	499	175	7.4	464	2	S95513	collagen II Al pro
427	184.5	7.8	388	2	JC6164	circumsporozoite p	500	175	7.4	528	2	D46449	hypothetical prote
428	184.5	7.8	798	2	T33022	hypothetical prote	501	175	7.4	598	2	T38403	probable nucleopor
429	184.5	7.8	1063	2	A40253	acidic nuclear pro	502	174.5	7.4	340	2	T20807	hypothetical prote
430	184	7.8	333	2	T23618	hypothetical prote	503	174.5	7.4	406	2	S38170	SRP40 protein - ye
431	184	7.8	625	2	A34615	profilaggrin - rat	504	174.5	7.4	460	2	T33110	hypothetical prote
432	184	7.8	813	2	S70795	vaas protein precu	505	174.5	7.4	629	2	A29666	keratin, 65K type
433	184	7.8	1102	2	A32247	virG protein - Shi	506	174.5	7.4	672	2	I40333	tracheal colonizat
434	183.5	7.8	445	2	A27263	SOK spicule matrix	507	174	7.4	239	2	S49193	GCR 101 protein -
435	183.5	7.8	541	2	T15299	hypothetical prote	508	174	7.4	314	2	T32247	hypothetical prote
436	182.5	7.7	174	2	S18654	variant surface an	509	174	7.4	330	2	S46657	collagen alpha 1(X
437	182.5	7.7	306	2	S33538	embryogenic cell p	510	174	7.4	344	2	T40167	hypothetical prote
438	182.5	7.7	443	2	C70780	probable PPE prote	511	174	7.4	387	2	E95995	hypothetical calci
439	182.5	7.7	472	2	S28026	nuclear pore compl	512	174	7.4	448	2	T15188	hypothetical prote
440	182.5	7.7	1293	2	B40025	maleless protein,	513	174	7.4	475	2	T03170	hypothetical prote
441	182.5	7.7	2204	2	A70524	probable PPE prote	514	174	7.4	718	1	S33168	gene pointed prote
442	182	7.7	287	2	B39615	merozoite 45K surf	515	174	7.4	782	2	T32155	hypothetical prote
443	182	7.7	305	2	T20906	hypothetical prote	516	173.5	7.3	204	2	T09592	protein corA, cold
444	182	7.7	1053	2	B70987	probable PPE prote	517	173.5	7.3	424	1	Z38PFD	coat protein A pre
445	181.5	7.7	154	2	B84468	probable glycine-r	518	173.5	7.3	424	1	Z38PFD	coat protein A pre
446	181.5	7.7	1287	2	T46032	nuclear DNA helica	519	173.5	7.3	424	1	Z38PM3	coat protein A pre
447	181	7.7	256	2	T11869	protein CPD22, dr	520	173.5	7.3	542	2	T29707	hypothetical prote
448	181	7.7	356	2	T22827	hypothetical prote	521	173.5	7.3	558	2	E70756	hypothetical glyci
449	181	7.7	416	2	A32947	filaggrin - precu	522	173.5	7.3	779	2	A35006	cell surface glyco
450	181	7.7	569	2	S42886	collagen - silkwor	523	173.5	7.3	1912	2	T29088	vitellogenin I pre
451	181	7.7	614	2	T33149	hypothetical prote	524	173	7.3	258	2	S71561	drought-induced pr
452	181	7.7	1388	2	A53317	collagen alpha 1(X	525	173	7.3	281	2	C90577	lipoprotein veasA I
453	181	7.7	1533	2	A46221	abdominal segment	526	173	7.3	347	2	B99112	merozoite 45K surf
454	180.5	7.6	196	2	S49194	GCR 17 protein - f	527	173	7.3	656	1	A49358	RNA-binding protei
455	180.5	7.6	605	2	T33913	hypothetical prote	528	173	7.3	1032	2	T34433	hypothetical prote
456	180.5	7.6	744	1	A34246	collagen alpha 1(V	529	173	7.3	1043	2	T13733	FTZ-F1 protein - f
457	180.5	7.6	744	1	S23298	collagen alpha 1(V	530	172.5	7.3	864	2	A48266	protein-tyrosine k
458	180	7.6	268	2	B61615	fibroin heavy chai	531	172	7.3	446	2	T45525	WSC4 homolog [impo
459	180	7.6	434	1	Z3BPIK	coat protein A - p	532	172	7.3	1052	2	AF2959	conserved hypotet
460	180	7.6	674	2	S23297	collagen alpha 1(X	533	172	7.3	1341	2	FH8323	hypothetical prote
461	180	7.6	792	1	BAHU	elastin precursor,	534	171.5	7.3	655	1	A55726	RNA-binding protei
462	179.5	7.6	784	2	A26601	elastin precursor,	535	171.5	7.3	1127	2	A25018	circadian rhythm p
463	179.5	7.6	838	1	BEWTHM	glutinin, high mol	536	171	7.2	337	2	T23794	hypothetical prote
464	179	7.6	310	2	T29731	hypothetical prote	537	171	7.2	1176	2	T18042	ice nucleation pro
465	179	7.6	314	2	T32985	hypothetical prote	538	170.5	7.2	108	1	S01844	fibroin - silkworm
466	179	7.6	995	2	T22942	hypothetical prote	539	170.5	7.2	367	2	JC4831	adsorption prote
467	178.5	7.6	313	2	T22828	hypothetical prote	540	170.5	7.2	396	2	T29773	hypothetical prote

541	170.5	7.2	1589	2	T42233	submaxillary mucin	614	163	6.9	418	2	T15142	hypothetical prote
542	170.5	7.2	4936	2	AH2515	hypothetical prote	615	163	6.9	490	2	T09084	phosphatidylinosit
543	170	7.2	434	2	S08091	gene III protein -	616	163	6.9	633	2	F84564	probable protein k
544	170	7.2	615	2	T20839	hypothetical prote	617	162.5	6.9	262	1	TLBPM1	tail fiber protein
545	170	7.2	1208	2	S17286	period clock prote	618	162.5	6.9	289	2	T20177	hypothetical prote
546	170	7.2	3498	2	T22330	hypothetical prote	619	162.5	6.9	658	2	T41309	hypothetical threo
547	169.5	7.2	183	2	S57773	early nodulin GRP3	620	162.5	6.9	925	2	JC2033	G protein-coupled
548	169.5	7.2	661	1	S59633	endo-1,4-beta-xyla	621	162.5	6.9	1168	1	MXAXIC	myosin heavy chain
549	169.5	7.2	849	2	A96592	hypothetical prote	622	162	6.9	166	1	KRBO28	keratin, 68K type
550	169.5	7.2	924	2	F87103	initiation factor	623	162	6.9	198	2	I49558	collagen alpha 1(I
551	169.5	7.2	988	2	T08102	myosinase-binding	624	162	6.9	323	2	T24582	hypothetical prote
552	169.5	7.2	1504	2	T49896	glycine/proline-ri	625	162	6.9	167	2	S35423	protein kinase egg
553	169	7.2	290	2	T24586	hypothetical prote	626	162	6.9	1888	2	S78476	collagen alpha 1(X
554	169	7.2	304	2	T22482	hypothetical prote	627	161.5	6.8	316	2	T13288	hypothetical prote
555	169	7.2	308	2	T37286	collagen 40 - Caen	628	161.5	6.8	500	2	T20961	hypothetical prote
556	169	7.2	380	2	T28888	cuticle collagen d	629	161.5	6.8	707	2	S52390	D-hordein precursor
557	168.5	7.1	640	2	A54502	S antigen precursor	630	161.5	6.8	800	2	I51653	dsRNA-binding prot
558	168	7.1	234	2	G95989	hypothetical glyci	631	161.5	6.8	978	2	D81411	probable lipoprote
559	168	7.1	252	2	T03160	capsid protein - a	632	161.5	6.8	1441	2	B86807	hypothetical prote
560	168	7.1	633	2	A25473	chorion E2 protein	633	161	6.8	284	2	T29528	hypothetical prote
561	168	7.1	673	2	T00328	hypothetical prote	634	161	6.8	290	2	T24590	hypothetical prote
562	168	7.1	684	2	A50328	collagen alpha 1(X	635	161	6.8	591	2	A45135	profilaggrin - hum
563	167.5	7.1	183	2	S57772	early nodulin GRP3	636	161	6.8	650	2	G87572	calcium-binding pr
564	167.5	7.1	276	2	T33525	hypothetical prote	637	161	6.8	805	2	T25795	hypothetical prote
565	167.5	7.1	286	2	B45632	merozoite surface	638	161	6.8	925	2	T19361	hypothetical prote
566	167.5	7.1	629	2	S42629	keratin K3 - rabbi	639	161	6.8	1701	2	T43213	ENBPI protein - ba
567	167.5	7.1	786	2	T16509	hypothetical prote	640	161	6.8	1852	1	VJCH2	vitellogenin II pr
568	167.5	7.1	1075	2	T48805	hypothetical prote	641	160.5	6.8	212	2	E86179	hypothetical prote
569	167.5	7.1	1366	2	T35985	probable large Pro	642	160.5	6.8	281	2	C88638	protein F58P6.1 [i
570	167.5	7.1	1747	2	A35974	collagen alpha 1(X	643	160.5	6.8	323	2	T27450	hypothetical prote
571	167.5	7.1	1857	2	S31212	collagen alpha 1(X	644	160.5	6.8	327	2	S25421	nucleolar protein
572	167	7.1	106	2	F84797	hypothetical prote	645	160.5	6.8	1516	2	T01055	hypothetical prote
573	167	7.1	166	2	T10463	glycine-rich prote	646	160.5	6.8	2020	2	C48399	ABC-type transport
574	167	7.1	303	2	T19289	hypothetical prote	647	160	6.8	169	2	T10465	glycine-rich prote
575	167	7.1	325	2	T32248	hypothetical prote	648	160	6.8	262	2	S00275	tail fiber protein
576	167	7.1	389	2	F96788	hypothetical prote	649	160	6.8	266	2	T22706	hypothetical prote
577	167	7.1	407	2	T21956	protein f4012.22 l	650	160	6.8	299	2	T22705	hypothetical prote
578	167	7.1	1221	2	T13283	probable transcrip	651	160	6.8	320	1	DDRT	helix-destabilizin
579	167	7.1	1237	2	D71850	probable outer mem	652	160	6.8	320	1	A44485	heterogeneous ribo
580	167	7.1	1772	2	T36105	probable large gly	653	160	6.8	320	2	S04617	heterogeneous ribo
581	166.5	7.0	313	2	A28444	filaggrin precursor	654	160	6.8	320	2	S02061	heterogeneous ribo
582	166.5	7.0	416	2	T32458	hypothetical prote	655	160	6.8	378	1	OZZQAL	circumsporozoite p
583	166.5	7.0	522	2	T36501	probable serine/th	656	160	6.8	582	2	S10099	transcription fact
584	166.5	7.0	556	2	AH1981	hypothetical prote	657	160	6.8	671	2	A38109	autolysin - Entero
585	166.5	7.0	634	2	T08145	myosinase-binding	658	160	6.8	987	2	E70808	probable PPE prote
586	166.5	7.0	738	2	E87627	hypothetical prote	659	160	6.8	1296	2	T13936	collar protein iso
587	166.5	7.0	1120	2	H88449	protein F54D8.1 [i	660	160	6.8	1325	2	T13386	hypothetical prote
588	166	7.0	291	2	T26576	hypothetical prote	661	160	6.8	1499	2	C88822	hypothetical prote
589	166	7.0	617	2	T49444	lustrin A related	662	159.5	6.7	186	2	S28021	rab18 protein - Ar
590	166	7.0	1122	2	B26427	period clock prote	663	159.5	6.7	260	2	S00276	tail fiber protein
591	166	7.0	1519	2	S41525	major ring-forming	664	159.5	6.7	301	2	B84533	hypothetical prote
592	165.5	7.0	220	2	A23990	conserved hypothet	665	159.5	6.7	336	2	T20348	hypothetical prote
593	165.5	7.0	220	2	E98293	hypothetical prote	666	159.5	6.7	654	2	A34734	transcription fact
594	165.5	7.0	389	2	D26995	homeotic protein U	667	159.5	6.7	742	4	C34734	transcription fact
595	165	7.0	291	2	T20083	hypothetical prote	668	159.5	6.7	825	4	B34734	transcription fact
596	165	7.0	319	2	T22250	hypothetical prote	669	159.5	6.7	1534	2	A56734	ribosome receptor,
597	165	7.0	433	2	S20963	homeotic protein H	670	159	6.7	299	2	T19564	hypothetical prote
598	165	7.0	823	2	S14055	nucleoskeletal-lik	671	159	6.7	302	2	T32872	hypothetical prote
599	164.5	7.0	200	2	B86181	hypothetical prote	672	159	6.7	494	2	T15502	hypothetical prote
600	164.5	7.0	600	2	S07638	spore coat protein	673	159	6.7	516	2	C44479	collagen alpha 1(X
601	164.5	7.0	819	2	T08745	probable RNA helic	674	159	6.7	1711	1	A47392	chromodomain-helic
602	164.5	7.0	1446	1	A45344	immediate-early pr	675	158.5	6.7	307	2	T16842	hypothetical prote
603	164	6.9	237	2	A88640	protein C34H4.4 [i	676	158.5	6.7	461	2	JN0097	secreted 45K prote
604	164	6.9	368	2	H96590	probable membrane	677	158	6.7	231	2	S17367	rab15B protein - w
605	164	6.9	561	2	T16148	hypothetical prote	678	158	6.7	299	2	T25407	hypothetical prote
606	163.5	6.9	299	2	T00837	glycine-rich prote	679	158	6.7	306	2	T21938	hypothetical prote
607	163.5	6.9	414	1	I38977	TAR DNA-binding pr	680	158	6.7	1460	2	S48457	nucleoporin RA17 -
608	163.5	6.9	623	1	A51337	collagen alpha 4(I	681	158	6.7	3124	2	A40020	collagen alpha 1(X
609	163.5	6.9	666	2	A42296	lysozyme 2 (EC 3.2	682	157.5	6.7	317	2	T19143	hypothetical prote
610	163.5	6.9	668	2	C71868	hypothetical prote	683	157.5	6.7	830	2	S15720	glutenin high mole
611	163.5	6.9	729	2	S35332	hnRNA-binding prot	684	157	6.6	145	2	T08435	la coata protein -
612	163.5	6.9	928	2	C81265	probable lipoprote	685	157	6.6	225	2	S05546	dehydrin 18 - barl
613	163	6.9	254	2	A31488	filaggrin - mouse	686	157	6.6	249	2	B33144	homeotic protein U

687	157	6.6	299	2	T24833	hypothetical prote	760	151.5	6.4	486	1	KRXL	keratin 3, type I,
688	157	6.6	363	1	OZZOAK	circumsporozite p	761	151.5	6.4	797	2	A36811	hypothetical prote
689	157	6.6	366	1	S11449	collagen short cha	762	151.5	6.4	901	2	JC6093	dead ringer nuclea
690	157	6.6	623	2	A45571	surface antigen 2,	763	151.5	6.4	1076	1	A35622	nuclear pore prote
691	157	6.6	624	2	A55576	collagen alpha 2(X	764	151	6.4	161	2	S71453	glycine-rich RNA-b
692	157	6.6	806	2	T13690	hypothetical prote	765	151	6.4	333	2	E48423	homeotic protein e
693	157	6.6	1829	2	B81086	iron-regulated pro	766	151	6.4	339	2	T22607	hypothetical prote
694	157	6.6	1910	2	AF0394	probable adhesin h	767	151	6.4	387	2	T34507	cutical collagen 6
695	156.5	6.6	173	2	S53050	RNA binding protei	768	151	6.4	405	2	S19355	hypothetical prote
696	156.5	6.6	273	2	T40618	probable cell wall	769	151	6.4	537	2	B33485	spore coat protein
697	156.5	6.6	387	2	H86445	probable G-Box bin	770	150.5	6.4	387	2	E95933	probable calcium-b
698	156.5	6.6	471	2	A39024	collagen alpha 3(I	771	150.5	6.4	461	2	T51044	related to spore c
699	156.5	6.6	758	2	T48815	mixed-linked glucu	772	150.5	6.4	524	2	A82580	polyvinylalcohol d
700	156.5	6.6	1217	2	T25894	hypothetical prote	773	150	6.3	234	2	T49448	hypothetical prote
701	156.5	6.6	1777	2	T34369	hypothetical prote	774	150	6.3	234	2	T06811	dehydrin 2 - garde
702	156.5	6.6	3295	2	AE0074	probable adhesin Y	775	150	6.3	283	2	T19732	hypothetical prote
703	156	6.6	169	2	S30148	glycine-rich prote	776	150	6.3	327	2	T29031	hypothetical prote
704	156	6.6	259	1	S46286	RNA-binding protei	777	150	6.3	359	2	T22774	hypothetical prote
705	156	6.6	291	2	T34494	hypothetical prote	778	150	6.3	423	2	A55797	collagen precursor
706	156	6.6	320	2	S30192	heterogeneous ribo	779	150	6.3	1072	2	G95851	probable hemolysin
707	156	6.6	431	1	WTHU2G	homeotic protein H	780	150	6.3	1390	2	T18883	hypothetical prote
708	156	6.6	571	2	T43456	hypothetical prote	781	149.5	6.3	148	2	T09527	glycine-rich prote
709	156	6.6	1665	2	T29008	hypothetical prote	782	149.5	6.3	287	2	T22637	hypothetical prote
710	155.5	6.6	163	2	T23076	hypothetical prote	783	149.5	6.3	317	2	T29960	hypothetical prote
711	155.5	6.6	169	1	S38331	glycine-rich RNA-b	784	149.5	6.3	325	2	S02170	collagen alpha 1(I
712	155.5	6.6	298	2	T23271	hypothetical prote	785	149.5	6.3	385	2	D41732	heterogeneous nucl
713	155	6.6	419	1	KRXL2B	keratin, 64K type	786	149.5	6.3	419	2	T04886	DAG protein homolo
714	155	6.6	1487	1	EDBE81	immediate-early pr	787	149.5	6.3	473	2	I50629	collagen - chicken
715	154.5	6.5	270	2	A36034	fibronogen alpha c	788	149.5	6.3	573	2	C86266	F3F19.21 protein -
716	154.5	6.5	304	2	T22602	hypothetical prote	789	149.5	6.3	1028	2	A56038	DNA-binding protei
717	154.5	6.5	343	2	T29547	hypothetical prote	790	149	6.3	264	2	S37137	prion protein - gr
718	154.5	6.5	433	1	QOBEV2	UL44 protein - hum	791	149	6.3	318	2	S27977	cuticle collagen d
719	154.5	6.5	705	2	S18733	glutenin high mole	792	149	6.3	329	2	JS0167	collagen col-6 - C
720	154.5	6.5	3436	2	S55659	tegument protein 6	793	149	6.3	345	1	B41732	heterogeneous nucl
721	154	6.5	205	2	T05713	hypothetical prote	794	149	6.3	371	1	JN0450	conglutinin precur
722	154	6.5	297	2	T27525	eyelid - fruit fly	795	149	6.3	896	2	T45878	conglutinin - bovi
723	154	6.5	2715	2	T13049	variant surface an	796	149	6.3	963	2	T48707	related to regulat
724	153.5	6.5	135	2	T01322	protein W09G12.6 [	797	149	6.3	1112	2	H95964	probable outer mem
725	153.5	6.5	178	2	E88637	hypothetical prote	799	148.5	6.3	107	2	B85356	glycine-rich prote
726	153.5	6.5	289	2	T34241	hypothetical prote	800	148.5	6.3	283	2	T29980	hypothetical prote
727	153.5	6.5	304	2	T23801	hypothetical prote	801	148.5	6.3	302	2	T21257	hypothetical prote
728	153.5	6.5	309	2	T19389	hypothetical prote	802	148.5	6.3	364	2	S43574	C0585.3 protein (c
729	153.5	6.5	311	2	S08110	salivary protein 1	803	148.5	6.3	454	2	T35380	probable membrane
730	153.5	6.5	333	2	T20436	hypothetical prote	804	148.5	6.3	456	2	E86903	hypothetical prote
731	153.5	6.5	401	2	C88571	protein C05B5.3 [i	805	148.5	6.3	660	2	A24266	glutenin high mole
732	153.5	6.5	437	2	S15144	hypothetical prote	806	148	6.3	289	2	T27708	hypothetical prote
733	153.5	6.5	437	2	T02345	hypothetical prote	807	148	6.3	298	2	E95286	hypothetical prote
734	153.5	6.5	1791	2	T02345	cytotoxin RTX homo	808	148	6.3	299	2	T20605	hypothetical prote
735	153.5	6.5	1829	2	S35027	glycine-rich prote	809	148	6.3	306	2	T21939	hypothetical prote
736	153	6.5	132	2	S14977	rab16B protein - r	810	148	6.3	447	2	T18447	HrpW protein - Erw
737	153	6.5	164	2	S11846	dehydrin DHN3 - ga	811	148	6.3	549	2	B86264	hypothetical prote
738	153	6.5	222	2	S18139	hypothetical prote	812	148	6.3	661	2	A58768	ATP-dependent RNA
739	153	6.5	285	2	T29982	hypothetical prote	813	148	6.3	892	2	T27005	hypothetical prote
740	153	6.5	349	2	A41349	histone-specific t	814	148	6.3	1305	2	T00670	probable inositol
741	153	6.5	349	2	S77570	transcription fact	815	147.5	6.2	235	2	G01226	leukophysin - huma
742	153	6.5	483	1	TVRTKA	protein kinase (EC	816	147.5	6.2	300	2	T24482	hypothetical prote
743	153	6.5	629	2	T34726	probable dehydroge	817	147.5	6.2	482	2	B31795	collagen alpha 1(X
744	153	6.5	1487	1	EDBEF6	155K transcription	818	147.5	6.2	589	2	T25299	hypothetical prote
745	152.5	6.5	257	2	C84533	hypothetical prote	819	147.5	6.2	1329	2	T29074	hypothetical prote
746	152.5	6.5	279	2	T26125	hypothetical prote	820	147.5	6.2	1584	2	T18276	protein-tyrosine k
747	152.5	6.5	299	2	T29956	hypothetical prote	821	147	6.2	226	2	S27759	maturatation-associ
748	152.5	6.5	316	2	T19291	hypothetical prote	822	147	6.2	264	2	A54330	major prion protei
749	152.5	6.5	420	2	D83556	probable coat prot	823	147	6.2	282	2	JS0168	collagen col-8 - C
750	152.5	6.5	584	2	E70825	hypothetical glyci	824	147	6.2	283	2	T19731	hypothetical prote
751	152.5	6.5	1198	2	T49726	hypothetical prote	825	147	6.2	374	1	A42046	surfactant protein
752	152	6.4	258	2	A29259	Ubx protein - fruit	826	147	6.2	578	2	S55102	PSP2 protein - yea
753	152	6.4	474	2	T26421	shufflon A - Esche	827	147	6.2	684	2	T36771	probable integral
754	152	6.4	735	2	T35778	probable fusidic a	828	147	6.2	760	2	A45174	eye cell developme
755	152	6.4	815	2	B30843	glutenin high mole	829	147	6.2	762	2	S08207	sialoglycoprotein
756	152	6.4	828	2	C88402	Protein H05C05.1 [	830	147	6.2	1317	2	A54831	nuclear pore compl
757	151.5	6.4	182	2	A36686	ultra-high-sulfur	831	147	6.2	1594	2	T43072	hemolysin A - Edwa
758	151.5	6.4	294	2	T21668	hypothetical prote	832	146.5	6.2	166	2	T18691	hypothetical prote
759	151.5	6.4	367	2	JC6087	helix-loop-helix t							

833	146.5	6.2	294	2	T22639	hypothetical prote	906	142	6.0	449	1	S30205	transcription fact
834	146.5	6.2	310	2	T22641	hypothetical prote	907	142	6.0	475	2	C86863	N-acetylglucosyl-L
835	146.5	6.2	368	2	G84769	hypothetical prote	908	142	6.0	1166	2	T13958	syngap-b1 protein
836	146.5	6.2	377	2	A47380	RING finger-contai	909	142	6.0	1249	2	T14270	Ras-GTPase activat
837	146.5	6.2	533	2	A48459	S antigen, heat st	910	142	6.0	1286	2	T28634	adhesin AIDA-I pre
838	146.5	6.2	704	2	S21311	BKcore-NS-23 prote	911	142	6.0	1293	2	T14259	ras GTPase-activat
839	146	6.2	258	2	T13591	tail fiber adhesin	912	142	6.0	1588	2	A86036	probable adhesin Z
840	146	6.2	281	2	T32765	hypothetical prote	913	142	6.0	1588	2	H91188	probable adhesin Z
841	146	6.2	283	2	JS0170	collagen col-19 -	914	142	6.0	2535	2	AC0304	probable hemolysin
842	146	6.2	295	2	T22833	hypothetical prote	915	141.5	6.0	255	2	AS3026	filaggrin A - mous
843	146	6.2	412	2	A84455	hypothetical prote	916	141.5	6.0	474	2	I38240	transcription fact
844	146	6.2	467	2	I50476	keratin type I - g	917	141.5	6.0	788	2	J80747	regulatory protein
845	146	6.2	712	2	A45638	immunodominant mic	918	141.5	6.0	1398	2	T13741	hypothetical prote
846	146	6.2	1215	2	T32734	myosin-IA - Acanth	919	141.5	6.0	3535	2	E83641	probable hemagglut
847	146	6.2	1340	2	A39808	proteoglycan core	920	141.5	6.0	3968	2	A44265	trithorax homolog
848	145.5	6.2	215	2	T17207	hypothetical prote	921	141	6.0	191	2	I46412	keratin KAP5.4 - s
849	145.5	6.2	313	2	T26465	hypothetical prote	922	141	6.0	253	2	A33144	homeotic protein U
850	145.5	6.2	461	2	A43782	keratin, type II -	923	141	6.0	511	2	S10527	endoglucanase B pr
851	145.5	6.2	561	1	CDECP3	cloacin DFJ3 prote	924	141	6.0	684	2	A56154	Abl substrate ena
852	145.5	6.2	643	2	T03518	hypothetical prote	925	140.5	5.9	148	2	B71419	hypothetical prote
853	145.5	6.2	658	2	AH0110	probable surface p	926	140.5	5.9	309	2	T28708	hypothetical prote
854	145.5	6.2	815	2	JN0689	glutinin, high-mol	927	140.5	5.9	317	2	T39869	probable lysophosp
855	145.5	6.2	1467	2	A75564	conserved hypotet	928	140.5	5.9	431	2	S09824	hypothetical prote
856	145	6.1	150	2	C86224	hypothetical prote	929	140.5	5.9	484	2	S66713	hypothetical prote
857	145	6.1	154	2	T03018	glycine-rich prote	930	140.5	5.9	561	2	T22917	probable ATP-depen
858	145	6.1	170	2	S34637	glycine-rich prote	931	140.5	5.9	579	2	T37248	probable matrix me
859	145	6.1	375	1	A45225	pulmonary surfacta	932	140.5	5.9	1690	2	T35694	ATP dependent DNA
860	145	6.1	380	1	GNVSMB	genome polyprotein	933	140	5.9	111	2	T29295	hypothetical prote
861	145	6.1	431	1	A40168	transcription fact	934	140	5.9	296	2	T21070	hypothetical prote
862	145	6.1	539	2	G95405	hypothetical prote	935	140	5.9	327	2	S38342	hypothetical prote
863	145	6.1	556	2	T36502	serine/threonine p	936	140	5.9	360	2	T37285	fibrillarin - mous
864	145	6.1	633	2	T02673	heterogeneous nucl	937	140	5.9	425	1	KRXL2A	collagen dpv-2 - C
865	145	6.1	919	2	A39248	hypothetical prote	938	140	5.9	669	2	A97443	keratin, 64K type
866	145	6.1	3345	2	T13423	androgen receptor	939	140	5.9	669	2	AC2661	hypothetical prote
867	144.5	6.1	156	2	S52246	transposable retro	940	140	5.9	710	2	S28014	outp protein - Erw
868	144.5	6.1	453	2	A41640	vestigial protein	941	140	5.9	888	2	I58378	tyrosine kinase -
869	144.5	6.1	512	2	S70644	annexin VII - Afri	942	140	5.9	1788	2	T31095	vitellogenin precu
870	144.5	6.1	937	2	A56517	nucleoporin Nup98	943	140	5.9	5627	2	C83339	hypothetical prote
871	144.5	6.1	2761	2	T21064	hypothetical prote	944	139.5	5.9	104	2	JC4190	holotricin 3 precu
872	144	6.1	208	2	T21689	hypothetical prote	945	139.5	5.9	543	2	A32693	steroid receptor p
873	144	6.1	283	2	T29837	hypothetical prote	946	139.5	5.9	576	2	S69214	deformed epidermal
874	144	6.1	294	2	T29839	hypothetical prote	947	139.5	5.9	591	2	AC3528	extracellular seri
875	144	6.1	381	2	T27806	hypothetical prote	948	139.5	5.9	653	2	T34356	hypothetical prote
876	144	6.1	492	2	A87471	hypothetical prote	949	139.5	5.9	746	2	B32693	steroid receptor p
877	144	6.1	1475	2	S42718	nuclear pore compl	950	139.5	5.9	845	2	D96799	hypothetical prote
878	143.5	6.1	168	1	S12312	glycine-rich RNA-b	951	139.5	5.9	900	2	B70694	probable INF8 - My
879	143.5	6.1	228	2	A44982	collagen UCOL1 - P	952	139.5	5.9	914	2	T08081	probable myrosinas
880	143.5	6.1	341	2	B75374	conserved hypotet	953	139	5.9	282	2	T16036	cuticle collagen c
881	143.5	6.1	527	2	B70700	hypothetical prote	954	139	5.9	294	2	T35892	hypothetical prote
882	143.5	6.1	608	2	T32923	hypothetical prote	955	139	5.9	298	2	T27644	hypothetical prote
883	143.5	6.1	660	1	Q0B83	BHLFI protein - hu	956	139	5.9	328	2	G88499	protein K04G7.10 [
884	143.5	6.1	709	2	T28712	hypothetical prote	957	139	5.9	524	2	T27043	hypothetical prote
885	143.5	6.1	720	1	A55160	Trg protein - frui	958	139	5.9	860	2	S43846	xylanase B - rumen
886	143.5	6.1	1268	2	B99789	hemagglutinin/hemo	959	139	5.9	1209	2	T13153	brachma associated
887	143.5	6.1	1270	2	B85649	hypothetical prote	960	139	5.9	1279	2	A47363	RNA helicase A - h
888	143.5	6.1	1666	2	T43169	hypothetical prote	961	139	5.9	1839	2	S77626	mannuronan C-5-epi
889	143	6.1	182	2	A02947	keratin, 60K type	962	138.5	5.9	152	2	G96010	hypothetical expor
890	143	6.1	284	2	T29838	hypothetical prote	963	138.5	5.9	239	2	T05494	glycine-rich prote
891	143	6.1	556	2	T42100	serine/threonine p	964	138.5	5.9	469	2	T36097	probable ATP-bindi
892	142.5	6.0	197	2	I46413	keratin KAP5.5 - s	965	138.5	5.9	576	1	S22453	colicin E7 [EC 3.1
893	142.5	6.0	329	2	T32783	hypothetical prote	966	138.5	5.9	735	2	T45059	hypothetical prote
894	142.5	6.0	590	2	A26638	homeotic protein D	967	138.5	5.9	859	2	D96502	hypothetical prote
895	142.5	6.0	648	2	S04832	glutinin high mole	968	138.5	5.9	949	2	D90803	Aida-I adhesin-lik
896	142.5	6.0	693	2	T33251	hypothetical prote	969	138.5	5.9	1005	2	H85611	probable adhesin Z
897	142	6.0	159	2	C49773	ecdysone-dependent	970	138.5	5.9	1111	2	T29070	hypothetical prote
898	142	6.0	164	2	S11847	rab16c protein - r	971	138.5	5.9	1411	2	T48529	hypothetical prote
899	142	6.0	167	2	T17179	glycine-rich RNA-b	972	138.5	5.9	2441	2	D71623	erythrocyte membra
900	142	6.0	266	1	TLBP2X	tail fiber protein	973	138	5.8	283	2	T19141	hypothetical prote
901	142	6.0	269	2	S48444	probable temperatu	974	138	5.8	532	2	T35119	probable aminotran
902	142	6.0	272	2	T75548	hypothetical prote	975	138	5.8	640	2	T08179	LRG5 protein - Chl
903	142	6.0	324	2	T28032	hypothetical prote	976	138	5.8	1087	2	T30844	serine-repeat anti
904	142	6.0	351	1	OZZQKU	circumsporozoite p	977	137.5	5.8	165	2	T03583	glycine-rich RNA-b
905	142	6.0	387	2	S00867	colicin N - Escher	978	137.5	5.8	448	1	A56018	transcription fact

979	137.5	5.8	598	2	T32166	hypothetical prote	1052	134.5	5.7	297	2	T18638	hypothetical prote
980	137.5	5.8	676	2	S41022	hypothetical prote	1053	134.5	5.7	326	2	T29810	hypothetical prote
981	137.5	5.8	1192	2	T18611	probable serine/th	1054	134.5	5.7	326	2	J50169	collagen col-14 -
982	137.5	5.8	1219	2	T14578	nucleoporin Nup153	1055	134.5	5.7	380	2	T24786	hypothetical prote
983	137.5	5.8	1468	2	A44345	nucleoporin - rat	1056	134.5	5.7	398	2	T34947	hypothetical prote
984	137.5	5.8	1608	2	A28182	hemolysin A - Serr	1057	134.5	5.7	767	2	A35645	major surface prot
985	137.5	5.8	1770	2	A71517	hypothetical prote	1058	134.5	5.7	1199	2	S20969	Na+/Ca2+,K+-exchan
986	137.5	5.8	1805	2	A34736	nestin - rat	1059	134.5	5.7	1938	2	A37361	probable integral
987	137	5.8	179	1	GZRT0	secretory granule	1060	134	5.7	142	2	S12311	glycine-rich RNA-b
988	137	5.8	197	2	S25088	dehydrin DHN1 - ga	1061	134	5.7	162	2	T10479	glycine-rich RNA-b
989	137	5.8	232	2	S18138	dehydrin DHN2 - ga	1062	134	5.7	210	2	B44984	collagen - nematod
990	137	5.8	383	2	T46707	proteophosphoglyca	1063	134	5.7	235	2	T33380	hypothetical prote
991	137	5.8	691	2	F91251	probable tape meas	1064	134	5.7	278	2	S44796	F09GS.6 protein -
992	137	5.8	858	2	JG0183	myosin Myok - Dict	1065	134	5.7	492	2	D70870	probable PE protei
993	137	5.8	1005	2	C71513	hypothetical prote	1066	134	5.7	627	2	T35608	polyketide hydroxy
994	136.5	5.8	127	2	D84469	probable glycine-r	1067	134	5.7	632	2	T00084	hypothetical prote
995	136.5	5.8	159	2	S18345	environmental stre	1068	134	5.7	803	2	C83561	probable type II s
996	136.5	5.8	222	2	A88102	protein W09G10.1 [	1069	134	5.7	1065	2	T13230	dachshund isoform
997	136.5	5.8	228	2	D86416	probable beta-1,3	1070	134	5.7	1072	2	T13232	dachshund protein
998	136.5	5.8	301	2	T23441	hypothetical prote	1071	134	5.7	1074	2	T13229	dachshund protein
999	136.5	5.8	407	2	T14909	bZIP DNA-binding p	1072	134	5.7	1081	2	T13231	dachshund protein
1000	136.5	5.8	486	2	F86911	conserved hypochet	1073	134	5.7	1174	2	A40853	potassium channel
1001	136.5	5.8	1001	2	S41603	type V adenyl cycl	1074	133.5	5.6	175	2	S54255	probable glycine r
1002	136.5	5.8	1290	2	T00018	period protein hom	1075	133.5	5.6	349	2	T41394	hypothetical serin
1003	136.5	5.8	1365	2	S14871	suppressor two of	1076	133.5	5.6	618	2	T42664	hypothetical prote
1004	136	5.8	440	2	I61183	transcription fact	1077	133.5	5.6	694	2	S71786	wingless receptor
1005	136	5.8	441	2	T49265	hypothetical prote	1078	133.5	5.6	743	2	T34853	probable fusidic a
1006	136	5.8	524	2	T08931	hypothetical prote	1079	133.5	5.6	1367	2	T33819	hypothetical prote
1007	136	5.8	635	2	T00011	ccal protein - rat	1080	133	5.6	127	2	S49195	GCR 20 protein - f
1008	136	5.8	643	1	F0LJLK	gag polyprotein -	1081	133	5.6	133	2	T09608	environmental stre
1009	136	5.8	647	2	S06450	steroid hormone re	1082	133	5.6	135	2	C82998	hypothetical prote
1010	136	5.8	924	2	B41359	potassium channel	1083	133	5.6	154	2	T01983	tumor related prote
1011	136	5.8	924	2	S12746	hypothetical prote	1084	133	5.6	195	2	S32123	glycine-rich prote
1012	136	5.8	963	2	T19140	hypothetical prote	1085	133	5.6	199	2	T36594	probable single-st
1013	136	5.8	1823	2	S28974	vitellogenin precu	1086	133	5.6	370	2	T22510	hypothetical prote
1014	135.5	5.7	206	2	S13066	gene M-twist protei	1087	133	5.6	510	2	A32380	nuclear protein fk
1015	135.5	5.7	257	2	JQ1900	major prion protei	1088	133	5.6	538	2	H86335	T20H2.2 protein -
1016	135.5	5.7	260	2	S53629	major prion protei	1089	133	5.6	611	1	S06047	endo-1,4-beta-xyla
1017	135.5	5.7	298	2	JC1448	collagen col-34 -	1090	133	5.6	622	2	G96762	hypothetical prote
1018	135.5	5.7	342	2	T45886	RNA-binding protei	1091	133	5.6	663	2	S21912	BRcore-Q1-21 prote
1019	135.5	5.7	536	2	T37544	hypothetical serin	1092	133	5.6	1077	2	A44067	serine-rich protei
1020	135.5	5.7	610	2	S05807	SAN1 protein - yea	1093	133	5.6	3828	2	T13857	trithorax protein
1021	135.5	5.7	650	2	T22002	hypothetical prote	1094	132.5	5.6	243	2	S27758	maturatation-associa
1022	135.5	5.7	716	2	D69855	conserved hypochet	1095	132.5	5.6	308	2	T19846	hypothetical prote
1023	135.5	5.7	1212	2	T13804	shs protein - frui	1096	132.5	5.6	325	2	T38308	hypothetical prote
1024	135.5	5.7	1290	2	S76853	hypothetical prote	1097	132.5	5.6	333	2	C48423	homeotic protein e
1025	135.5	5.7	1576	2	S65774	homeotic protein H	1098	132.5	5.6	547	2	F71287	probable treponema
1026	135	5.7	98	2	S08137	gene 2C protein -	1099	132.5	5.6	839	2	E84824	hypothetical prote
1027	135	5.7	129	2	T03861	glycine-rich prote	1100	132.5	5.6	1520	1	TVFFA	protein-tyrosine k
1028	135	5.7	139	2	T33968	hypothetical prote	1101	132.5	5.6	1629	2	T06461	DNA-binding protei
1029	135	5.7	142	2	S56703	glycine-rich cell	1102	132.5	5.6	2271	2	F90073	hypothetical prote
1030	135	5.7	174	2	S00273	period clock prote	1103	132	5.6	160	2	T04346	glycine-rich RNA-b
1031	135	5.7	188	2	S49192	GCR 1 protein - fr	1104	132	5.6	165	2	S59529	RNA-binding glycin
1032	135	5.7	241	2	T27929	hypothetical prote	1105	132	5.6	165	2	S41773	glycine-rich RNA-b
1033	135	5.7	302	2	A39615	merozoite 45K surf	1106	132	5.6	300	2	A39112	merozoite 45K surf
1034	135	5.7	369	2	S33603	surfactant protein	1107	132	5.6	302	2	A31921	collagen dpy-13 pr
1035	135	5.7	414	2	JN0866	nucleolar protein	1108	132	5.6	305	2	T30165	hypothetical prote
1036	135	5.7	464	2	E82865	conjugal transfer	1109	132	5.6	348	2	A34705	collagen - Caenorh
1037	135	5.7	467	2	S30839	UTR2 protein - yea	1110	132	5.6	427	2	T20800	hypothetical prote
1038	135	5.7	573	2	A33533	cell surface glyco	1111	132	5.6	428	2	T24769	hypothetical prote
1039	135	5.7	595	2	H86212	protein P24B9.20 [	1112	132	5.6	517	2	T10927	3C3.18c protein -
1040	135	5.7	888	2	T46726	secreted acid phos	1113	132	5.6	647	2	S18737	gag polyprotein -
1041	135	5.7	1302	2	C81182	iron-regulated pro	1114	132	5.6	700	2	I51235	DEAD box protein -
1042	135	5.7	1804	2	T34518	nestin - golden ha	1115	132	5.6	705	2	S32644	nucleolin - Africa
1043	135	5.7	1904	2	T13256	tail-host specific	1116	132	5.6	782	2	A10062	conserved hypochet
1044	135	5.7	2468	2	A83412	hypothetical prote	1117	132	5.6	1525	2	T14961	hypothetical prote
1045	134.5	5.7	158	2	T08957	glycine-rich prote	1118	131.5	5.6	252	2	T10697	immature seed prot
1046	134.5	5.7	197	2	T03442	glycine-rich prote	1119	131.5	5.6	322	2	G95244	hypothetical prote
1047	134.5	5.7	209	2	A41342	circumsporozoite p	1120	131.5	5.6	355	2	C39725	hypothetical prote
1048	134.5	5.7	278	2	S39310	merozoite surface	1121	131.5	5.6	386	2	A48571	circumsporozoite p
1049	134.5	5.7	289	2	S74632	hypothetical prote	1122	131.5	5.6	461	2	T10265	arabinogalactan-pr
1050	134.5	5.7	291	2	T20942	hypothetical prote	1123	131.5	5.6	463	2	T10015	hypothetical prote
1051	134.5	5.7	297	2	T18637	hypothetical prote	1124	131.5	5.6	471	2	S15035	acetylcholinestera



1125	131.5	5.6	479	2	A38307	metallopeptidase	1198	129	5.5	551	1	NRECE3	colicin E3 (EC 3.1
1126	131.5	5.6	510	2	T37541	probable glycolipid	1199	129	5.5	581	1	NDECE2	colicin E2 (EC 3.1
1127	131.5	5.6	520	2	AB1183	ATP-dependent RNA	1200	129	5.5	626	2	T01485	probable polygalac
1128	131.5	5.6	525	2	A35596	nuclear pore glyco	1201	129	5.5	632	2	T07587	probable polygalac
1129	131.5	5.6	589	2	AD2263	hypothetical prote	1202	129	5.5	670	2	F84540	hypothetical prote
1130	131.5	5.6	713	2	JC2534	RvLG protein - rat	1203	129	5.5	707	2	A46302	PTB-associated spl
1131	131.5	5.6	940	2	D89723	protein F3908.lb l	1204	129	5.5	895	2	AD0541	outer membrane flm
1132	131.5	5.6	945	2	T21998	hypothetical prote	1205	129	5.5	1442	2	T42607	transcription acti
1133	131.5	5.6	962	2	S03818	carboxymethylcellu	1206	129	5.5	1741	2	S74910	hemolysin - Synech
1134	131.5	5.6	1039	2	T35878	hypothetical prote	1207	128.5	5.4	157	1	S14857	glycine-rich prote
1135	131.5	5.6	1130	2	T30251	repetin - mouse	1208	128.5	5.4	271	2	A47156	hexamer-binding pr
1136	131.5	5.6	1704	2	T43141	vitellogenin 1 - m	1209	128.5	5.4	401	2	A48423	engrailed homeodom
1137	131.5	5.6	1732	2	T43026	probable DNA-direc	1210	128.5	5.4	427	2	A32372	female-specific do
1138	131	5.5	180	2	JG7876	prion protein homo	1211	128.5	5.4	549	2	S32372	male-specific doub
1139	131	5.5	184	1	CGRT2S	collagen alpha 2(I	1212	128.5	5.4	564	1	KRHUEB	keratin 6b, type I
1140	131	5.5	304	2	T16107	hypothetical prote	1213	128.5	5.4	564	2	T16171	keratin 6f, type I
1141	131	5.5	307	2	T37287	collagen 36 - Caen	1214	128.5	5.4	634	2	A54495	knob protein precu
1142	131	5.5	355	2	F71435	probable nuclear a	1215	128.5	5.4	710	2	T31502	hypothetical prote
1143	131	5.5	440	2	S71795	transcription fact	1216	128.5	5.4	1275	2	T45362	hypothetical prote
1144	131	5.5	485	2	B40552	bindin fertilizati	1217	128.5	5.4	1367	2	T13703	tama protein - fru
1145	131	5.5	642	2	S27806	homeotic protein B	1218	128.5	5.4	1621	2	T30200	protein-tyrosine k
1146	131	5.5	653	1	S44749	Co6G4.2 protein -	1219	128	5.4	185	2	JC4085	glycine-rich cutic
1147	131	5.5	724	2	A48569	antigen Em100 - Bi	1220	128	5.4	321	2	A38712	fibillarlin [valid
1148	131	5.5	728	2	S21913	BRcore-TNfr1-Q1-Z1	1221	128	5.4	339	2	S20880	homeotic protein H
1149	131	5.5	733	2	A27041	tyrosine kinase-re	1222	128	5.4	514	2	S21914	BRcore-2 protein -
1150	131	5.5	1053	2	T07965	reverse transcript	1223	128	5.4	547	2	H85699	partial probable a
1151	131	5.5	1148	2	A71446	hypothetical prote	1224	128	5.4	547	2	C90842	partial probable a
1152	131	5.5	1332	2	T15670	hypothetical prote	1225	128	5.4	598	2	A84616	hypothetical prote
1153	131	5.5	2703	1	A24420	notch protein - fr	1226	128	5.4	606	2	S13367	Om(1D) protein - f
1154	130.5	5.5	163	2	JC6571	cold-inducible RNA	1227	128	5.4	640	2	A41726	homeotic protein B
1155	130.5	5.5	251	2	D96010	hypothetical expor	1228	128	5.4	733	2	S10932	probable protein k
1156	130.5	5.5	286	2	S34665	collagen, cuticula	1229	128	5.4	918	2	A88188	protein Cl8H9.3 [1
1157	130.5	5.5	369	2	S11980	variable major pro	1230	128	5.4	1870	2	S37671	MHC class III hist
1158	130.5	5.5	381	2	A54415	transcription fact	1231	128	5.4	1970	1	S21054	DNA-directed RNA p
1159	130.5	5.5	473	2	F70031	cell wall-binding	1232	128	5.4	2248	1	D42088	adenylate cyclase
1160	130.5	5.5	643	2	P50339	intermediate filam	1233	127.5	5.4	290	2	B88638	protein F58P6.2 [1
1161	130.5	5.5	748	2	T04011	hypothetical prote	1234	127.5	5.4	321	2	F60110	repetitive protein
1162	130.5	5.5	1036	1	A34755	nitrogen regulator	1235	127.5	5.4	325	2	T16324	hypothetical prote
1163	130.5	5.5	2154	2	F83068	hypothetical prote	1236	127.5	5.4	373	2	S43455	hypothetical prote
1164	130.5	5.5	2440	2	S39162	transcription coac	1237	127.5	5.4	550	1	JGRTA	fibriogen alpha c
1165	130	5.5	123	2	C39777	hypothetical prote	1238	127.5	5.4	693	2	JG7925	nucleolin - common
1166	130	5.5	182	1	KRB02A	keratin, 68K type	1239	127.5	5.4	817	2	T22442	hypothetical prote
1167	130	5.5	250	2	S35026	filaggrin B - mous	1240	127.5	5.4	827	2	JC4900	transferred entry
1168	130	5.5	253	2	S53618	major prion protei	1241	127.5	5.4	1641	2	T10955	early nodulin bind
1169	130	5.5	253	2	S53619	major prion protei	1242	127.5	5.4	1872	2	S36152	MHC class III hist
1170	130	5.5	331	2	F70820	hypothetical glyci	1243	127.5	5.4	1940	2	F75393	hypothetical prote
1171	130	5.5	334	2	S53490	RNA-binding protei	1244	127	5.4	228	2	T49891	glycine-rich prote
1172	130	5.5	448	2	S05355	hypothetical prote	1245	127	5.4	241	2	S71048	major prion protei
1173	130	5.5	563	2	A36054	mucin homolog - bo	1246	127	5.4	253	1	UJHU	major prion protei
1174	130	5.5	622	2	G86371	hypothetical prote	1247	127	5.4	253	2	S53617	major prion protei
1175	130	5.5	625	2	T41603	alpha-amylase - fi	1248	127	5.4	253	2	S53635	prion protein - si
1176	130	5.5	676	2	S61977	transcription fact	1249	127	5.4	253	2	S53614	major prion protei
1177	130	5.5	1618	2	S21424	nestin - human	1250	127	5.4	253	2	I37032	major prion protei
1178	130	5.5	1872	2	T30888	vitellogenin - Ath	1251	127	5.4	253	2	I61847	major prion protei
1179	130	5.5	3705	2	AD0123	probable autotrans	1252	127	5.4	253	2	S53616	major prion protei
1180	129.5	5.5	142	2	C33910	sal homeotic prote	1253	127	5.4	298	2	A40616	34K antigen - Myco
1181	129.5	5.5	287	2	T15779	hypothetical prote	1254	127	5.4	370	1	OZZQAV	cirumporoazole p
1182	129.5	5.5	296	2	A31219	collagen 1 - Caeno	1255	127	5.4	378	1	OZZQAV	cirumporoazole p
1183	129.5	5.5	564	1	KRHUEA	keratin 6a, type I	1256	127	5.4	409	2	A70647	probable PPG prote
1184	129.5	5.5	666	2	T05432	hypothetical prote	1257	127	5.4	496	2	A54770	N-acetylglucosamin
1185	129.5	5.5	732	2	T08420	1-phosphatidylinos	1258	127	5.4	579	2	E83144	hypothetical prote
1186	129.5	5.5	900	2	B87957	protein Y106GB.7	1259	127	5.4	644	1	I40712	endo-1,4-beta-xyla
1187	129.5	5.5	948	2	T26417	hypothetical prote	1260	127	5.4	718	2	D84675	hypothetical prote
1188	129.5	5.5	1706	1	OYBRC	cyclolysin - Borde	1261	127	5.4	719	2	S61046	ARPI protein - yea
1189	129.5	5.5	4776	2	E95206	cell wall surface	1262	127	5.4	720	2	T51007	hypothetical prote
1190	129	5.5	155	2	S20846	glycine-rich prote	1263	127	5.4	748	2	S15652	cellodextrinase C
1191	129	5.5	156	2	S41771	glycine-rich RNA-b	1264	127	5.4	1145	2	G87284	adenylate cyclase
1192	129	5.5	201	2	G01204	twist protein homo	1265	127	5.4	1705	2	S51672	probable tape-meas
1193	129	5.5	256	2	JU0268	major prion protei	1266	127	5.4	1787	2	AG1360	hypothetical prote
1194	129	5.5	256	2	S37149	prion protein - go	1267	126.5	5.4	301	2	T21314	homeotic protein H
1195	129	5.5	256	2	A54281	major prion protei	1268	126.5	5.4	342	2	S18649	homeotic protein H
1196	129	5.5	323	2	S16318	homeotic protein H	1269	126.5	5.4	420	2	T14911	bZIP DNA-binding p
1197	129	5.5	456	1	KRHU5	keratin 15, type I	1270	126.5	5.4	590	2	A29904	keratin 5, type II

1271	126.5	5.4	742	2	JC7595	scavenger receptor	1344	124.5	5.3	1374	2	AE3259	extracellular seri
1272	126.5	5.4	764	2	H71607	hypothetical prote	1345	124.5	5.3	1613	2	T06678	hypothetical prote
1273	126.5	5.4	910	2	A34721	androgen receptor	1346	124.5	5.3	2960	2	A45259	desmoyokin - human
1274	126.5	5.4	911	2	B34721	androgen receptor	1347	124.5	5.3	3591	1	S21010	filamentous hemagg
1275	126.5	5.4	929	2	C96623	hypothetical prote	1348	124	5.2	285	2	A34759	prion protein - Ch
1276	126.5	5.4	989	2	D89852	fibrinogen-binding	1349	124	5.2	285	2	T31503	hypothetical prote
1277	126.5	5.4	993	2	AE1905	outer membrane sec	1350	124	5.2	437	2	E90996	probable tail fibre
1278	126.5	5.4	2059	2	D82671	surface protein XF	1351	124	5.2	452	2	I49595	cytokeatin 15 - m
1279	126.5	5.4	2142	2	B35098	MHC class III hist	1352	124	5.2	452	2	T30082	hypothetical prote
1280	126	5.3	144	2	S35716	glycine-rich prote	1353	124	5.2	459	2	T45911	hypothetical prote
1281	126	5.3	199	2	S32224	acp-22 protein - y	1354	124	5.2	486	1	A57601	transcription fact
1282	126	5.3	284	2	A35419	neutrophil protein	1355	124	5.2	562	2	T49788	related to merozoi
1283	126	5.3	302	2	T15936	hypothetical prote	1356	124	5.2	580	2	S11890	serine proteinase
1284	126	5.3	305	2	S33692	fibrillarin - fss	1357	124	5.2	784	2	AC1091	5'-nucleotidase, p
1285	126	5.3	320	2	T09555	fibrillarin - Arab	1358	124	5.2	787	2	TC00798	hypothetical prote
1286	126	5.3	324	2	A31920	collagen sqt-1 pre	1359	124	5.2	856	2	T13159	BiB-55KDa-associat
1287	126	5.3	340	2	A83402	hypothetical prote	1360	124	5.2	1325	2	A64905	ydek protein - Esc
1288	126	5.3	417	2	TC7092	paul protein - fis	1361	124	5.2	1360	2	T34302	cell polarity prot
1289	126	5.3	518	2	T23745	hypothetical prote	1362	124	5.2	1428	2	T13926	probable protein p
1290	126	5.3	622	2	AF0169	probable exported	1363	124	5.2	4550	2	T18440	hypothetical prote
1291	126	5.3	720	2	T48302	hypothetical prote	1364	124	5.2	7463	2	T36248	CDA peptidase synthe
1292	126	5.3	910	2	S68983	auxilin - bovine	1365	123.5	5.2	152	2	T07858	glycine-rich prote
1293	126	5.3	1022	2	T17406	developmental prot	1366	123.5	5.2	198	2	T06813	dehydrin 3 - garde
1294	126	5.3	1070	2	AI0484	probable autotrans	1367	123.5	5.2	260	2	S22373	proline-rich prote
1295	125.5	5.3	165	2	T03392	probable dehydrin	1368	123.5	5.2	280	2	T24454	hypothetical prote
1296	125.5	5.3	199	2	S16063	acp-22 protein - y	1369	123.5	5.2	310	2	T43147	hypothetical prote
1297	125.5	5.3	226	2	A53892	prion-related prot	1370	123.5	5.2	369	1	TVFVAF	transforming prote
1298	125.5	5.3	292	2	T23866	hypothetical prote	1371	123.5	5.2	371	2	T36871	probable pseudouri
1299	125.5	5.3	453	2	T18804	collagen alpha 4(I	1372	123.5	5.2	378	2	D88042	protein F56D12.5 (
1300	125.5	5.3	627	2	T05789	hypothetical prote	1373	123.5	5.2	646	2	H96665	protein F22C12.10
1301	125.5	5.3	634	2	A28412	histidine-rich pro	1374	123.5	5.2	651	2	S18874	nucleolin - Africa
1302	125.5	5.3	933	2	S41539	fibrinogen-binding	1375	123.5	5.2	730	2	T43317	pgl-1 protein - Ca
1303	125.5	5.3	936	2	F75822	hypothetical prote	1376	123.5	5.2	761	2	AI0074	probable autotrans
1304	125.5	5.3	960	1	A39651	discs-large tumor	1377	123.5	5.2	770	2	T51024	related to C2H2 zi
1305	125.5	5.3	1148	2	S72635	exo-poly-alpha-gal	1378	123.5	5.2	771	2	T29177	hypothetical prote
1306	125.5	5.3	1475	2	F066399	protein F17I21.22	1379	123.5	5.2	964	2	A84693	hypothetical prote
1307	125.5	5.3	1611	2	T06677	hypothetical prote	1380	123.5	5.2	1035	2	AD3203	autotransporter pr
1308	125	5.3	179	2	A85217	hypothetical prote	1381	123.5	5.2	1230	2	E64664	outer membrane pro
1309	125	5.3	254	1	UWYI17	major prion PrP-Sc	1382	123.5	5.2	1237	2	A34598	ecdysone-induced p
1310	125	5.3	254	2	B34759	prion protein - go	1383	123.5	5.2	1394	2	B34598	ecdysone-induced p
1311	125	5.3	296	2	T24827	hypothetical prote	1384	123.5	5.2	1403	2	S77624	mannuronan C-5-epi
1312	125	5.3	323	2	T51417	fibrillarin - Afri	1385	123	5.2	129	2	T06256	dormancy-associate
1313	125	5.3	333	2	T23006	hypothetical prote	1386	123	5.2	129	2	S14984	glycine-rich prote
1314	125	5.3	343	2	A29319	circumsporozoite p	1387	123	5.2	144	2	S04069	glycine-rich prote
1315	125	5.3	354	2	T06487	probable DNA-bindi	1388	123	5.2	257	2	A23545	major prion PrP27-
1316	125	5.3	425	2	T11619	probable nucleopor	1389	123	5.2	318	2	T35213	probable secreted
1317	125	5.3	438	2	D90734	probable tail fibre	1390	123	5.2	321	2	S13550	anther-specific pr
1318	125	5.3	438	2	S62453	hypothetical prote	1391	123	5.2	385	2	H89046	protein Cl0G8.8 l1
1319	125	5.3	440	2	S37303	sox-4 protein - mo	1392	123	5.2	407	2	G90907	probable tail fibre
1320	125	5.3	466	2	T35164	probable secreted	1393	123	5.2	483	2	A55033	keratin 12 - mouse
1321	125	5.3	509	2	T09572	cdc2-like protein	1394	123	5.2	511	2	S24345	Balbani ring 1 pr
1322	125	5.3	534	2	T39903	serine-rich protei	1395	123	5.2	522	2	S41819	nucleoporin p62 -
1323	125	5.3	570	2	S56132	cellulase [EC 3.2.	1396	123	5.2	559	2	G82326	MSHA biogenesis pr
1324	125	5.3	635	2	F75477	hypothetical prote	1397	123	5.2	624	2	T02289	probable polygalac
1325	125	5.3	642	1	S34416	transcription fact	1398	123	5.2	656	1	S59631	endo-1,4-beta-xyla
1326	125	5.3	712	2	B47021	pectic enzyme secr	1399	123	5.2	841	2	CH7331	ISCc2, transposase
1327	125	5.3	943	2	JC4081	sucrase/fructanase	1400	123	5.2	902	2	T26775	hypothetical prote
1328	125	5.3	955	2	G64866	probable membrane	1401	123	5.2	1070	2	S75712	cellulase [EC 3.2.
1329	125	5.3	1315	2	T05300	hypothetical prote	1402	123	5.2	1334	2	T50568	probable multi-dom
1330	124.5	5.3	177	2	S37749	collagen alpha 2(X	1403	123	5.2	1560	2	T30282	calcium-binding pr
1331	124.5	5.3	341	2	T22551	hypothetical prote	1404	122.5	5.2	160	2	T26289	hypothetical prote
1332	124.5	5.3	355	2	A33821	chromosomal protei	1405	122.5	5.2	296	2	B39581	GRESAG protein 9u
1333	124.5	5.3	360	2	G85014	GBF2, G-box bindin	1406	122.5	5.2	391	2	A39645	transcription fact
1334	124.5	5.3	458	2	T31631	hypothetical prote	1407	122.5	5.2	437	2	A55682	keratin l3, type I
1335	124.5	5.3	481	2	A26483	bindin precursor -	1408	122.5	5.2	532	2	B35621	spore germination
1336	124.5	5.3	516	2	AC1540	ATP-dependent RNA	1409	122.5	5.2	626	2	F85295	hypothetical prote
1337	124.5	5.3	682	2	JC7670	cathepsin B mRNA 3	1410	122.5	5.2	685	2	JC6331	rho-type guanine e
1338	124.5	5.3	687	2	F83671	hypothetical prote	1411	122.5	5.2	748	2	T51738	rRNA helicase RH3 l
1339	124.5	5.3	710	2	A31641	daughterless (da)	1412	122.5	5.2	867	2	T27136	hypothetical prote
1340	124.5	5.3	812	1	MMECO5	outer membrane ush	1413	122.5	5.2	871	2	T27135	hypothetical prote
1341	124.5	5.3	995	2	T32466	hypothetical prote	1414	122.5	5.2	930	2	D86546	polymorphic outer
1342	124.5	5.3	997	2	B71617	SERA antigen/papai	1415	122.5	5.2	930	2	D72078	polymorphic outba
1343	124.5	5.3	1262	2	T30524	protein phosphatas	1416	122.5	5.2	930	2	A81591	polymorphic membra



Db 725 GNSGTGSDGAGGGAAGTGTGGDGLTGNG 759

RESULT 2

A70934

hypothetical glycine-rich protein Rv0578c - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: A70934

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70934

A;Status: preliminary;

A;Molecule type: DNA

A;Residues: 1-1306 <COL>

A;Cross-references: UNIPROT:O53775; GB:AL021942; GB:AL123456; NID:g3242298; PIDN:CAAL1744

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv0578c

C;Superfamily: collagen alpha 1(IV) chain

Query Match 18.6%; Score 439.5; DB 2; Length 1306;

Best Local Similarity 30.9%; Pred. No. 8e-16;

Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSGEAGPLOSGBESTGTN--IGBALHGLGDLALSGVGKAIGK-----EAGGAAGSKV 67

Db 567 GHGAAGNL-----GVNGGVGAGGHHG-GD--PGVGGAGGGGSGSTPGANGAPNTP 615

QY 68 SEA--LQQGTREAVGTGVRQVPGFGAADALGNRVGE-AAHALGNTGHE-----TGRQAEV 120

Db 616 TSGCNGCNGCRGADATGFGQTGASGGRGDPGLVNGGAGGAGNGSKGLPLGLRLGNP- 674

QY 121 IRHGADAVRSWGVPHSGAWETSQGHGIFGSGGLGGGQ-----QGNRG 166

Db 675 ---GLDGGTGGNGGAGGSGGAWAGNGGTGAGGTGGVGGTGGSGSDGVNGSSAGADHPG 731

QY 167 GLGTTPWHVPGNSAGSFGMNPQ-----APWGQGNNGPPNPGTN-----TOG 210

Db 732 GTGGVGTGKGDDGGAAPNGVAGSQCPGAGGDDGTTGVGNGGRCIDGADATAG 791

QY 211 AVAQPGYGSVRASNQNEGCTNPP-----PSGS-----GGSSNSGGSGSGSGSGSNGD 262

Db 792 ARGQDGGAGGAGGKGRGGTGGPGGAGPAGTTGSGAGNGSGSGGTGGDPDGGNGANGS 851

QY 263 --NNNGSSGSSGSSGSSGSSGSSG-----GSS-----GGSSGNSG----- 298

Db 852 VFTNNGIGGNGGNGNAGPSGAGSGSGAGSTFGATGSSSIHVNNGNGNGGNGDHALSG 911

QY 299 -GSRGDSGSSSGSSTGS--SSGNHGGG-----GNGHKPGCEKPGNEARGSGESGI 349

Db 912 NGAAGNGGNGGNSLRGSCAGCHGNGGNGVNRGWDGDTGTGAGNAGACIINGAGAGN 971

QY 350 QGFRGGVSSNMREISKGNR-----LLGSGDNYRGGSSGSGSWGSGGDGAVGV---NTVNS 402

Db 972 GGDGTTGSDGNPCAITGSGCRGGDGGVGGGQGGSVAGDGDGGRGGAGGTGTLRLGTGA 1031

QY 403 ETSFGMFN 410

Db 1032 TGATGTFD 1039

RESULT 3

T49109

Glycine-rich protein - Arabidopsis thaliana

N;Alternate names: protein AT4g22020

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C;Accession: T49109

R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; M submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25016

A;Accession: T49109

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-396 <BEV>

A;Cross-references: UNIPROT:O65450; EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22020

A;Experimental source: cultivar Columbia; BAC clone FIN20

C;Genetics:

A;Gene: ATSP:AT4g22020

A;Map position: 4

C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 17.9%; Score 423; DB 2; Length 396;

Best Local Similarity 33.2%; Pred. No. 2e-15;

Matches 133; Conservative 22; Mismatches 169; Indels 76; Gaps 14;

QY 17 GSGEAGPLOSGBESTGTNIGBALHGLGDLALSGVGKAIGKEAGGAAGSKVSEALGGTTR 76

Db 63 GGG 122

QY 77 EAVVTGV-RQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEADVIRHGADAVRGSWQGV 135

Db 123 SGAGAGVGGTGTGGVGG 164

QY 136 PHISGAWETSQGHGIFGSGGLGQGGQGNPGLGTPWVHGYPGNSAGSFGMNPQAPWQ 195

Db 165 GAGAGVGGSGGAG--GG 214

QY 196 GNGGPPNPGTNTQGAVAOPGYGSVRASNQNEGCTNPPPSGGSGSSNSGGSGSGSGSS 255

Db 215 GGGGG--GGGGGGGANGSGSHGS-----GSGAGGGVSGAAGGGGGGGGGGG 258

QY 256 GGSN---GDNNGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSS 312

Db 259 GSGSKVGGYGHGSGFGGVFGNSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 314

QY 313 STGSSGNGHGGGNGHKGCEKPGNEARGSGES-GIOGFRGGVSSNMREISKGNRL 371

Db 315 GMKGSGSGGG 356

QY 372 LGSGDNYRGQSSWCSG--GGDAVGG-----VNTVNSETSP 406

Db 357 NGCGGVGFMGLFGIGIGGGSGGGTYYQTNLTKDNKSP 396

RESULT 4

H70806

hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C;Accession: E70806

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: E70806

A;Status: preliminary;

A;Molecule type: DNA

A;Residues: 1-1381 <COL>

A;Cross-references: GB:AL020222; GB:AL123456; NID:g3261554; PIDN:CAAL17744.1; PID:g2924444

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv3507

C;Superfamily: collagen alpha 1(IV) chain

Query Match 17.6%; Score 415.5; DB 2; Length 1381;

Best Local Similarity 29.9%; Pred. No. 1.5e-14;



QY	340	EARGSGESGIQFRGQGVSSNMREISKEGNRLLGSG-DNYRGQSGSWGSGGGDAVGGVN	398
Db	713	EGGAGGNSGVCGTNGSGGAGAG--GKGCTGGAGSGADNPTGAGPAGGAGGTGGGAAG	770
QY	399	TVNSETSPG	407
Db	771	GAGGATGTG	779
RESULT 7			
F70580			
hypothetical glycine-rich protein Rv2162c - Mycobacterium tuberculosis (strain H37RV)			
C;Species: Mycobacterium tuberculosis			
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004			
C;Accession: F70580			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; MUID:98295987; PMID:9634230			
A;Accession: F70580			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-532 <COL>			
A;Cross-references: UNIPROT:O06215; GB:Z95388; GB:AL123456; NID:g3261759; PIDN:CAB08665.			
A;Experimental source: strain H37RV			
C;Genetics:			
A;Gene: Rv2162c			
C;Superfamily: uncharacterized glycine-rich protein, PE motif containing			
Query Match 17.1%; Score 404.5; DB 2; Length 532;			
Best Local Similarity 32.2%; Pred. No. 2.4e-14;			
Matches 138; Conservative 33; Mismatches 182; Indels 75; Gaps 17;			
QY	6	PLACLIALCLGSG-EAGPLQSGEESTGTNIGALHGLGLDALSEGVGKA-----ICKEA	59
Db	106	PTQTLRPLINGADGPGQNGPG-GLIYNGNGGAGDTANPNCNGSGSAGLIGNG	164
QY	60	GGAAGSKVSEALOGGTREAVGTGVRQVPGFAADALG-----NRVGEAAHALNVTGHEIG	114
Db	165	ACGAGA-----ATGAGGAGGNGWLYNGNGPGGAAGLTAGGVSPPAGGAGGAAGLWGH---	217
QY	115	ROADVIRHCAADVRSQVPGHSGAWETSGGHGIFGSGGGLGGGCGNPGGLGTPWH	174
Db	218	-----CGAGGAGGSASAPGAGGAGDGGRRGLLYGDDGAGGAG-GN-GSNGVTGVH	267
QY	175	GYPNSAGSPMNPQGAAPWQGGNGGPPNFNTN-----TQGAVAQPGYGSVRASNQEGCT	230
Db	268	GGNGGAGGAAGLIGNGAGGDDGNGGLSNTGASGAGGAGGAALIGNGDDGGHGGHG	327
QY	231	NPPPSGGGSSNSGGSG-----SQSGSGSGSGNGDNNNGSSSGSSSGSSSGSS	285
Db	328	NSGAGGAGGAGGAGGAGGCHVGLIGNGNGGAGGNGGNDN-----SSTLADAGSGGAGA	381
QY	286	SGSSSGSSNSG-GRGDSGSSSWGSSSTGS-----SSGNHGSGGGNGHK	331
Db	382	ACNGGLFYNGGVGRGGNGGSSAGTSGDGGIGGAGIGLIGSGGGGGGNGGQQA	441
QY	332	PGCEKPCNEARG--SGESGIQFRGQGVSSNMREISKEGNRLLGSGG-DNYRGQSGSWGS	388
Db	442	P---TFGNAGDGGAGGNARLIGDGGG-----GNGEGEGDGPVKGDDGGNGN	487
QY	389	GGSDAVGG	396
Db	488	GGNAVVG	495
RESULT 8			
D70807			
hypothetical glycine-rich protein Rv3514 - Mycobacterium tuberculosis (strain H37RV)			
C;Species: Mycobacterium tuberculosis			

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000			
C;Accession: D70807			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; MUID:98295987; PMID:9634230			
A;Accession: D70807			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-1489 <COL>			
A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA17751.1; PID:g2924451			
A;Experimental source: strain H37RV			
C;Genetics:			
A;Gene: RV3514			
C;Superfamily: collagen alpha 1(IV) chain			
Query Match 17.1%; Score 403; DB 2; Length 1489;			
Best Local Similarity 32.5%; Pred. No. 7.1e-14;			
Matches 137; Conservative 30; Mismatches 179; Indels 76; Gaps 19;			
QY	17	GSGEAGPLQSGEESTGTNIGALHGLGLDALSEGVGKAIKKEAGGAAGSKVSEALOGGTR	76
Db	1090	GTGGTG---GVGGTGGDCGNA-GTCAGDPGKGGTGTGTGSGCGAGSGGAGNFNGGTG	1144
QY	77	EAVGTGVRQVPGFAADALGNRVGEAA-----HALGNTGHEIGRQAEADVIRHGADAVR	129
Db	1145	GTGGTG-----GTGGKGMGGIAGDGGPGDGNAGVGKGGTNG-----NGSGGTT	1191
QY	130	GSNQGVPGHSGA-----WETSGHGI--FGSOGGLGCGGQ-----GNPGLGTDPWHG	175
Db	1192	GGTGGAGNAGAGGLANTGCTAGNAGIGDGGCGGNGGCGGDSGSLGGQPGPAGGPGGKG	1251
QY	176	YFNSAGSPMNPQGA--PWQGGNGGP-----PNFGTNTQGAVAQPGYGSVRASNON	226
Db	1252	GAGNAGTGTGTGSGAGGAGGCGGAGGAGISFNSGNSCGTGTGTGGVGGTG-GD--CGNAG	1308
QY	227	EGCTNPPPSGSG--CGSSNSGSGSGSQSGSSGSGNDNNNGSSSGSSSGSSSGSSSG	284
Db	1309	TGAGDPGKGGTGTGTGTGSGSGAGSGGAGNFNGTGTGTGTGKGWGGIAGDGGPG	1368
QY	285	SSGSSS-----GSSNGN--SGSRGDSGSESSWGSSTGSSNHGSGGNGHKPGCEKP	337
Db	1369	GDGNAGVCGKGTNGNGSGSGTGTGTGPGSGGAPTGSCTGKGGAGGDDG--DGAD--	1424
QY	338	GNEARGSGESGIQFRGQGVSSNMREISKEGNRLLG-GSGDNYRGQSGSWGSGGDAVGG	396
Db	1425	CGAATGVGGDGGNGNG-----GNGGTGVGSPGGLGAGGAGGTGGLGAGAGGG	1473
QY	397	VN	398
Db	1474	AD	1475
RESULT 9			
H70846			
hypothetical glycine-rich protein Rv3345c - Mycobacterium tuberculosis (strain H37RV)			
C;Species: Mycobacterium tuberculosis			
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000			
C;Accession: H70846			
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A;Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.			
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome			
A;Reference number: A70500; MUID:98295987; PMID:9634230			
A;Accession: H70846			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown			
A;Molecule type: DNA			
A;Residues: 1-1538 <COL>			

QY 77 EAVGTGVR-----QVPFGAADALGNRVCE--AAHALGNTGHEIGR-----Q 116  
 Db 385 GGAGGNARLWGVGGAGGAGGDCGAGGAGGKGGSLSGNANGGAGGDSGRGTTGGAGGEGG 444  
 QY 117 AEDVI-----RHGAD-----AVRGSWQGVPHSGAWETSGGHGIFGSOGLGGQ----- 160  
 Db 445 AAGLLVGTGGHGGDGGAGGAAVKGGDGGNAAGTGI-AGAGRGAGGSGSGSGDGGGGNA 503  
 QY 161 -----GQGNPGGLGTPTWVHGYPCNSAGSFCMN-POGAPWQGGNGGP-----PNF 204  
 Db 504 GPACWLFDGCGAGGNGGAAAGGAGGAGCGGCGGNGCGNGGNGGNGGNGATGCGWLYGNG 563  
 QY 205 GTNTQGA-OPGVGSVRASNQNECTN-----PPPSGGSGSSNSG----- 245  
 Db 564 GAGGQGAATAGAGGAGAGVSVTNGCGTGGNGIGTGGSGGACGNAGLLGVGGAGGHAAS 623  
 QY 246 GGSQSGSSSGS-----GSGNDNNGSSSG-GSSSGSSSGSSSGSSSGSSG----- 291  
 Db 624 GGADRGAGGTGTPTISSDGGAGDGGDGGNGGAGGTGGLLFGAGGNGPGSGSGAADI 683  
 QY 292 -GSSNGSGSGRSDGSESSWGSSTGSSNGHGGSGGN-----GHKPGCEKPGNEA- 341  
 Db 684 NGGAGNGCGTGDNGG--NGSGGGAGSGDGGGAGGNGAWLFGNGGAGGGGKGGNGAG 740  
 QY 342 --RGSRSIGQFRGQGVSSNNREISKEGNRLLLGSGDNYRGOGSSWGSGGDAVGG 396  
 Db 741 GGLGGSGFLPLNGSGDGGDGGNGAPGGVLYNGGAG--GQSGSGGIGGPGATGG 795

RESULT 11  
 A70807  
 hypothetical glycine-rich protein Rv3511 - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C:Accession: A70807  
 R;Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: A70807  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-714 <COL>  
 A:Cross-references: GB:AL022022; GB:AL123456; NID:G3261554; PIDN:CAA17748.1; PID:G292444.4  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: Rv3511  
 C:Superfamily: elastin

Query Match 16.7%; Score 395; DB 2; Length 714;  
 Best Local Similarity 29.9%; Pred. No. 9.7e-14;  
 Matches 138; Conservative 28; Mismatches 169; Indels 126; Gaps 19;

QY 17 GSGGAGPLQSGSESTGTNIGEA---LGHLGLDALSEGVKA--IGKEAGGAAGSKVSEAL 71  
 Db 164 GSGGAG---GTGAPGGNGENAGWLYGRG-----GVGGAGGIGGTTGGAGGH--AWLF 210  
 QY 72 GQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRAEDVIRHGADAVRGS 131  
 Db 211 GHGGTGGIGGG---PG-----GNGGWLNGGHH-----GGAGGIGGG 244  
 QY 132 WQGVPHSGAWETSGHGFSGSGG-----LGGQGGNPGGLG-----T 170  
 Db 245 SCGAGGNGGWLNGGIGIGAGGTGGAGGTGNAWLLGGGTGGAGGIGGNGGHGNG 304  
 QY 171 PWVHGYPCNSAGSFCMNPFQAPWQGGNGGPPNFNGTNTQGA VQAPGVGSVRASNQNECT 230  
 Db 305 GWLLNGNGN-GGLGDDGGTGGHGGNGCNFGWLLGTAGGGGNGAGSTGTAGGSGGT 363  
 QY 231 NPPPSGGSGSSNSGG-----GSGSQSGSGSGSGNDNNNGSSSGSSSGS----- 276





C;Genetics:  
A;Gene: Rv1450c  
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 16.6%; Score 392; DB 2; Length 1329;  
Best Local Similarity 28.5%; pred. No. 2.4e-13;  
Matches 141; Conservative 36; Mismatches 157; Indels 120; Gaps 21;

Qy 17 GSSEAGPLQGSESTGTNICEALCHGLGDALSEGVGKAIGKEAG-GAAGSKVSEALCGQT 75  
| | | | : |  
Db 756 GKGGAGGL--AGDGGNGANGNFATFDGNGCHGHGNGGNPFAGCGGGSGGAGSTPGAKGAHGF 814  
| | | | : |  
Qy 76 REAVG-----TGVRQVPFGAADALGNRVGEAAHALGNTGH---ETGRQAEIVRH 123  
| | | | : |  
Db 815 TPTSGDGDDGNGENSQVVGGNGDGGNGGSGSAGTGGNGRGCDGAFGMSANATNP 874  
| | | | : |  
Qy 124 GADAVRGSWGVPHGHGAWETSOGHGIFGSOGLGGQG-----QG 163  
| | | | : |  
Db 875 GENGPNGN----PFGNGGAGGAGLNGNGGAGNGGLGGFPGNGAAGANGVAVGAPG 930  
| | | | : |  
Qy 164 NPGLGTPWVHYPGNSAGSPGMNPQ-----GAPMGQGGNGPPNFGT---NTQGA 213  
| | | | : |  
Db 931 QPGGAGG---HGGAGNGGAGGNGGQGVVSDBGAGGAGGDPGPDGANGMNGQGAGA 987  
| | | | : |  
Qy 214 PQYGVSVRASN---QNEGCTNP PPSGS-----GGSSSNSGGSGSQSG 253  
| | | | : |  
Db 988 FAGGGGGRGDDGNAGNAGAGGPGGTGSTAGKAGPAGSILHDGGNGCHGHGAASGGNGG 1047  
| | | | : |  
Qy 254 SSSGSGNDNNSSSGCSSS-GSSSGSSSGSSG-----GSSSGSSGNSG-GSRGD 303  
| | | | : |  
Db 1048 PGCHGGNGNGGTGANGNGGI GG TGAGSTGAKVLGTNEGDGDDGRRGNGRGGNGG 1107  
| | | | : |  
Qy 304 SGSESSWGS-STGSSSNHG-----GSCGGNGHKPGCKPGNEARG----- 343  
| | | | : |  
Db 1108 QELTGAGENGTTGTPGNGGNGNGASGLVTSPDGGGGRRGDAGRGGDAGLGSSGP 1167  
| | | | : |  
Qy 344 -----SGESGIQGFRCQGVSSNMREITSKEGNRLLLGSGDNRYRGQGSWGSGGGDAV 394  
| | | | : |  
Db 1168 GGTFGDWMTGTTGTTGTGGQGANGL-----TGGR--GGTGGN-GGNGNTGGTGGGAGGT 1219  
| | | | : |  
Qy 395 GGVNTVNSETSPGM 408  
| | | | : |  
Db 1220 GG--TGHSQPQM 1231  
| | | | : |

Search completed: May 15, 2005, 06:09:59  
Job time : 67 secs

Search completed: May 15, 2005, 06:09:59  
Job time : 67 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 14, 2005, 06:24:18 ; Search time 45 Seconds  
(without alignments)  
729.902 Million cell updates/sec

Title: US-10-063-699-52

Perfect score: 2363

Sequence: 1 MKPQGPLACLLALCLGSGE.....KLGFINWDINKDQRSSRP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfileai.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669	28.3	230	4	US-09-673-395A-256
2	402.5	17.0	1136	3	US-08-806-029-9
3	402.5	17.0	1177	1	US-07-609-716-31
4	402.5	17.0	1177	1	US-08-175-155-29
5	402.5	17.0	1177	1	US-08-477-509B-64
6	402.5	17.0	1177	2	US-08-707-237A-35
7	402.5	17.0	1177	3	US-08-482-085B-64
8	402.5	17.0	1177	3	US-08-475-411A-31
9	402.5	17.0	1177	3	US-08-478-029A-31
10	402.5	17.0	1177	3	US-09-444-791A-64
11	399	16.9	1059	2	US-08-175-155-48
12	399	16.9	1059	2	US-08-707-237A-54
13	399	16.9	1059	3	US-08-806-029-10
14	399	16.9	1101	1	US-08-477-509B-83
15	399	16.9	1101	3	US-08-482-085B-83
16	399	16.9	1101	3	US-09-444-791A-83
17	383	16.2	641	4	US-09-249-585A-3
18	383	16.2	641	4	US-09-410-399-4
19	376.5	15.9	1038	1	US-07-609-716-36
20	376.5	15.9	1038	3	US-08-475-411A-36
21	376.5	15.9	1038	3	US-08-478-029A-36
22	373	15.8	745	2	US-09-010-928B-28
23	373	15.8	870	2	US-09-010-928B-2
24	371	15.7	651	3	US-08-556-978B-19
25	371	15.7	651	3	US-09-247-806-1
26	371	15.7	651	4	US-09-863-859-1
27	371	15.7	718	1	US-08-425-069-2
28	371	15.7	718	2	US-08-317-844B-2
29	371	15.7	747	3	US-09-034-177-3
30	367	15.5	1011	1	US-08-477-509B-94
31	367	15.5	1011	3	US-08-482-085B-94
32	367	15.5	1011	3	US-09-444-791A-94
33	367	15.5	1170	1	US-08-175-155-59
34	367	15.5	1170	2	US-08-707-237A-66
35	366	15.5	766	1	US-08-175-155-53
36	366	15.5	766	2	US-08-477-509B-88
37	366	15.5	766	2	US-08-707-237A-61
38	366	15.5	766	3	US-08-482-085B-88
39	366	15.5	766	3	US-09-444-791A-88
40	366	15.5	979	3	US-08-477-509B-89
41	366	15.5	979	3	US-08-482-085B-89
42	366	15.5	979	3	US-09-444-791A-89
43	366	15.5	1050	1	US-08-175-155-54
44	364.5	15.4	907	2	US-09-010-928B-4
45	364.5	15.4	2018	3	US-09-444-791A-80
46	364.5	15.4	2100	1	US-08-477-509B-80
47	364.5	15.4	2100	3	US-08-482-085B-80
48	364	15.4	649	1	US-07-609-716-49
49	364	15.4	649	3	US-08-475-411A-49
50	364	15.4	649	3	US-08-478-029A-49
51	364	15.4	784	1	US-07-609-716-48
52	364	15.4	784	3	US-08-475-411A-48
53	364	15.4	784	3	US-08-478-029A-48
54	364	15.4	1018	1	US-08-089-862-11
55	364	15.4	1018	1	US-08-587-333-18
56	364	15.4	1018	5	PCT-US94-07776-16
57	364	15.4	2107	1	US-08-175-155-45
58	364	15.4	2107	2	US-08-707-237A-51
59	362	15.3	604	3	US-08-556-978B-63
60	362	15.3	1332	1	US-07-609-716-41
61	362	15.3	1332	3	US-08-475-411A-41
62	362	15.3	1332	3	US-08-478-029A-41
63	358.5	15.2	2055	1	US-08-175-155-46
64	358.5	15.2	2055	1	US-08-477-509B-81
65	358.5	15.2	2055	2	US-08-707-237A-52
66	358.5	15.2	2055	3	US-08-482-085B-81
67	358.5	15.2	2055	3	US-09-444-791A-81
68	358	15.2	606	3	US-08-556-978B-21
69	358	15.2	606	3	US-08-556-978B-23
70	358	15.2	606	3	US-09-247-806-4
71	358	15.2	606	3	US-09-247-806-6
72	358	15.2	606	3	US-09-247-806-8
73	358	15.2	809	4	US-09-863-859-13
74	358	15.2	818	4	US-09-863-859-22
75	358	15.2	1617	4	US-09-863-859-14
76	358	15.2	1626	4	US-09-863-859-24
77	354	15.0	945	1	US-08-089-863-6
78	354	15.0	945	1	US-08-587-333-13
79	354	15.0	945	5	PCT-US94-07776-11
80	351.5	14.9	1056	1	US-08-212-237-6
81	351.5	14.9	1056	3	US-08-806-029-29
82	351.5	14.9	1056	5	PCT-US95-02772-6
83	350.5	14.8	2257	1	US-08-175-155-47
84	350.5	14.8	2257	1	US-08-477-509B-82
85	350.5	14.8	2257	2	US-08-707-237A-53
86	350.5	14.8	2257	3	US-08-482-085B-82
87	350.5	14.8	2257	3	US-09-444-791A-82
88	350	14.8	316	4	US-09-538-092-997
89	348.5	14.7	528	4	US-09-490-291-8
90	348	14.7	832	1	US-08-209-747-2
91	348	14.7	832	1	US-08-458-298-2
92	343	14.5	681	4	US-09-490-291-4
93	343	14.5	691	4	US-09-490-291-6
94	336	14.2	1169	3	US-08-806-029-33
95	327.5	13.9	334	3	US-09-060-756-728
96	327.5	13.9	334	4	US-09-670-314-728
97	322.5	13.6	972	1	US-08-212-237-7
98	322.5	13.6	972	3	US-08-806-029-30
99	322.5	13.6	972	5	PCT-US95-02772-7
100	319.5	13.5	318	3	US-09-060-756-727

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101	319.5	13.5	318	4	US-09-670-314-727	Sequence 727, App	174	268	11.3	762	1	US-08-397-633A-31	Sequence 31, Appl
102	317.5	13.4	988	1	US-08-212-237-5	Sequence 5, Appl	175	267.5	11.3	1024	3	US-08-931-820-2	Sequence 2, Appl
103	317.5	13.4	988	3	US-08-806-029-28	Sequence 28, Appl	176	267.5	11.3	1366	3	US-08-963-825-19	Sequence 19, Appl
104	317.5	13.4	988	5	PCT-US95-02772-5	Sequence 5, Appl	177	267.5	11.3	1366	3	US-09-500-811-19	Sequence 19, Appl
105	309.5	13.1	200	4	US-09-989-981A-13	Sequence 13, Appl	178	267.5	11.3	1366	3	US-09-570-573-19	Sequence 19, Appl
106	309	13.1	201	3	US-09-052-995-1	Sequence 1, Appl	179	267.5	11.3	1366	3	US-09-548-608-19	Sequence 8, Appl
107	309	13.1	201	3	US-09-053-003-40	Sequence 40, Appl	180	264.5	11.2	1008	3	US-09-219-849-8	Sequence 8, Appl
108	309	13.1	201	4	US-09-054-281-22	Sequence 22, Appl	181	264.5	11.2	1065	1	US-08-642-255-80	Sequence 80, Appl
109	309	13.1	201	4	US-09-478-948-6	Sequence 6, Appl	182	264.5	11.2	1065	3	US-08-642-246-16	Sequence 16, Appl
110	309	13.1	201	4	US-09-818-094-40	Sequence 40, Appl	183	264.5	11.2	1065	4	US-09-451-206-16	Sequence 16, Appl
111	309	13.1	201	4	US-09-754-947-5	Sequence 5, Appl	184	264.5	11.2	1065	5	PCT-US96-06223-16	Sequence 16, Appl
112	308	13.0	235	2	US-08-529-190B-1	Sequence 1, Appl	185	264	11.2	269	1	US-08-452-531-4	Sequence 4, Appl
113	304.5	12.9	889	3	US-08-806-029-19	Sequence 19, Appl	186	264	11.2	269	2	US-08-460-746A-4	Sequence 4, Appl
114	302	12.8	714	3	US-08-556-978B-61	Sequence 61, Appl	187	264	11.2	269	3	US-08-460-555-4	Sequence 4, Appl
115	302	12.8	714	3	US-09-247-806-10	Sequence 10, Appl	188	264	11.2	269	3	US-08-460-066-4	Sequence 4, Appl
116	300.5	12.7	768	3	US-08-806-029-35	Sequence 35, Appl	189	257	10.9	633	1	US-08-642-255-73	Sequence 73, Appl
117	300.5	12.7	884	1	US-08-397-633A-68	Sequence 68, Appl	190	257	10.9	1065	1	US-08-642-255-72	Sequence 72, Appl
118	300.5	12.7	884	2	US-08-435-641-15	Sequence 15, Appl	191	254	10.7	1040	3	US-08-806-029-32	Sequence 32, Appl
119	300.5	12.7	884	2	US-08-707-237A-96	Sequence 96, Appl	192	254	10.7	1745	4	US-09-795-061-4	Sequence 4, Appl
120	300.5	12.7	884	3	US-08-642-246-15	Sequence 15, Appl	193	253	10.7	1060	3	US-08-931-820-3	Sequence 3, Appl
121	300.5	12.7	884	4	US-09-451-206-15	Sequence 15, Appl	194	253	10.7	1077	1	US-07-972-032-82	Sequence 82, Appl
122	300.5	12.7	884	5	PCT-US96-06223-15	Sequence 15, Appl	195	253	10.7	1077	1	US-08-642-255-95	Sequence 95, Appl
123	300	12.7	738	3	US-08-864-038A-3	Sequence 3, Appl	196	253	10.7	1418	3	US-08-963-825-20	Sequence 20, Appl
124	296.5	12.5	1024	1	US-08-212-237-8	Sequence 8, Appl	197	253	10.7	1418	3	US-09-010-999-1	Sequence 1, Appl
125	296.5	12.5	1024	3	US-08-806-029-31	Sequence 31, Appl	198	253	10.7	1418	3	US-09-500-811-20	Sequence 20, Appl
126	296.5	12.5	1024	5	PCT-US95-02772-8	Sequence 8, Appl	199	253	10.7	1418	3	US-09-570-573-20	Sequence 20, Appl
127	296	12.5	595	1	US-08-425-069-4	Sequence 4, Appl	200	253	10.7	1418	3	US-09-548-608-20	Sequence 20, Appl
128	296	12.5	595	2	US-08-317-844B-4	Sequence 4, Appl	201	251.5	10.6	462	2	US-09-919-039-324	Sequence 324, App
129	294.5	12.5	832	1	US-08-212-237-4	Sequence 4, Appl	202	248.5	10.5	1442	2	US-08-316-650-12	Sequence 12, Appl
130	294.5	12.5	832	3	US-08-806-029-27	Sequence 27, Appl	203	248.5	10.5	1442	5	PCT-US95-02251-12	Sequence 12, Appl
131	294.5	12.5	832	5	PCT-US95-02772-4	Sequence 4, Appl	204	247.5	10.5	419	4	US-09-270-767-41767	Sequence 41767, A
132	294	12.4	493	3	US-08-556-978B-59	Sequence 59, Appl	205	247.5	10.5	943	4	US-09-477-135A-131	Sequence 131, App
133	294	12.4	529	3	US-09-247-806-2	Sequence 2, Appl	206	247.5	10.5	1739	4	US-09-795-061-2	Sequence 2, Appl
134	294	12.4	674	1	US-08-317-522A-3	Sequence 3, Appl	207	247	10.5	975	4	US-09-328-352-4764	Sequence 4764, Ap
135	294	12.4	674	1	US-08-439-818A-3	Sequence 3, Appl	208	246.5	10.4	448	4	US-09-248-796A-13135	Sequence 13135, A
136	294	12.4	674	2	US-08-751-965-3	Sequence 3, Appl	209	246.5	10.4	556	4	US-09-248-796A-22338	Sequence 22338, A
137	294	12.4	674	2	US-08-738-975-3	Sequence 3, Appl	210	246.5	10.4	595	3	US-09-219-849-48	Sequence 48, Appl
138	294	12.4	674	2	US-08-728-626-3	Sequence 3, Appl	211	246.5	10.4	595	3	US-09-219-849-50	Sequence 50, Appl
139	294	12.4	674	3	US-08-808-599A-3	Sequence 3, Appl	212	246.5	10.4	822	3	US-09-219-849-49	Sequence 49, Appl
140	290.5	12.3	749	1	US-08-317-522A-2	Sequence 2, Appl	213	246.5	10.4	1057	3	US-08-931-820-1	Sequence 1, Appl
141	290.5	12.3	749	1	US-08-439-818A-2	Sequence 2, Appl	214	246.5	10.4	1341	3	US-08-963-825-18	Sequence 18, Appl
142	290.5	12.3	749	1	US-08-751-965-2	Sequence 2, Appl	215	246.5	10.4	1341	3	US-09-500-811-18	Sequence 18, Appl
143	290.5	12.3	749	2	US-08-738-975-2	Sequence 2, Appl	216	246.5	10.4	1341	3	US-09-570-573-18	Sequence 18, Appl
144	290.5	12.3	749	2	US-08-728-626-2	Sequence 2, Appl	217	246.5	10.4	1341	3	US-09-548-608-18	Sequence 18, Appl
145	290.5	12.3	749	3	US-08-808-599A-2	Sequence 2, Appl	218	246.5	10.4	1958	1	US-07-945-283-2	Sequence 2, Appl
146	288.5	12.2	873	1	US-08-397-633A-54	Sequence 54, Appl	219	245	10.4	907	4	US-09-949-016-9750	Sequence 9750, Ap
147	288.5	12.2	873	3	US-08-806-029-14	Sequence 14, Appl	220	245	10.4	907	4	US-09-949-016-9751	Sequence 9751, Ap
148	283.5	12.0	401	3	US-09-219-849-34	Sequence 34, Appl	221	244.5	10.3	492	2	US-08-468-996-11	Sequence 11, Appl
149	283.5	12.0	599	4	US-09-602-459-22	Sequence 22, Appl	222	244.5	10.3	1002	2	US-08-707-237A-103	Sequence 103, App
150	283.5	12.0	599	4	US-09-602-459-23	Sequence 23, Appl	223	244.5	10.3	1002	3	US-08-642-246-25	Sequence 25, Appl
151	283	12.0	1160	3	US-08-808-599A-24	Sequence 24, Appl	224	244.5	10.3	1002	4	US-09-451-206-25	Sequence 25, Appl
152	280	11.8	1057	3	US-08-931-820-4	Sequence 4, Appl	225	244.5	10.3	1002	5	PCT-US96-06229-25	Sequence 25, Appl
153	278.5	11.8	526	4	US-09-538-092-1080	Sequence 1080, Ap	226	244.5	10.3	1464	4	US-09-331-347C-21	Sequence 21, Appl
154	276	11.7	231	4	US-09-248-796A-14281	Sequence 14281, A	227	244	10.3	492	4	US-08-468-996-12	Sequence 12, Appl
155	276	11.7	1078	3	US-08-963-825-21	Sequence 21, Appl	228	243	10.3	1017	4	US-08-468-996-10	Sequence 10, Appl
156	276	11.7	1078	3	US-09-500-811-21	Sequence 21, Appl	229	242.5	10.3	955	4	US-09-949-016-8369	Sequence 8369, Ap
157	276	11.7	1078	3	US-09-570-573-21	Sequence 21, Appl	230	241.5	10.2	1461	4	US-09-585-887-9	Sequence 9, Appl
158	276	11.7	1078	3	US-09-548-608-21	Sequence 21, Appl	231	241.5	10.2	250	4	US-09-289-578-9	Sequence 9, Appl
159	276	11.7	1366	4	US-09-585-887-10	Sequence 10, Appl	232	240.5	10.2	943	3	US-09-556-556-204	Sequence 204, App
160	276	11.7	1366	4	US-09-289-578-10	Sequence 10, Appl	233	240.5	10.2	943	3	US-09-072-596-199	Sequence 199, App
161	276	11.7	1366	4	US-09-949-016-5882	Sequence 5882, Ap	234	240.5	10.2	943	4	US-09-072-967-204	Sequence 204, App
162	274	11.6	482	4	US-09-902-540-14708	Sequence 14708, A	235	240.5	10.2	943	3	US-09-219-849-6	Sequence 6, Appl
163	274	11.6	593	4	US-09-538-092-919	Sequence 919, App	236	239	10.1	960	3	US-09-219-849-6	Sequence 6, Appl
164	273	11.6	486	1	US-08-397-633A-77	Sequence 77, App	237	239	10.1	1806	4	US-09-919-497-56	Sequence 56, Appl
165	272.5	11.5	479	1	US-08-397-633A-78	Sequence 78, Appl	238	237.5	10.1	682	1	US-08-642-255-126	Sequence 126, App
166	272.5	11.5	619	4	US-09-252-991A-26352	Sequence 26352, A	239	237.5	10.1	682	1	US-08-397-633A-36	Sequence 36, Appl
167	272	11.5	291	4	US-09-490-291-2	Sequence 2, Appl	240	236.5	10.0	1413	2	US-08-175-155-39	Sequence 39, Appl
168	272	11.5	696	3	US-08-806-029-36	Sequence 36, Appl	241	236.5	10.0	1413	2	US-08-707-237A-45	Sequence 45, Appl
169	272	11.5	750	3	US-08-806-029-25	Sequence 25, Appl	242	236.5	10.0	1464	3	US-08-477-509B-74	Sequence 74, Appl
170	271	11.5	761	2	US-08-707-237A-84	Sequence 84, Appl	243	236.5	10.0	1464	3	US-08-482-085B-74	Sequence 74, Appl
171	271	11.5	762	1	US-08-642-255-114	Sequence 114, App	244	236.5	10.0	1465	3	US-09-444-791A-74	Sequence 74, Appl
172	271	11.5	762	1	US-08-397-633A-26	Sequence 26, Appl	245	236	10.0	508	4	US-09-270-767-46233	Sequence 46233, A
173	268	11.3	762	1	US-08-642-255-120	Sequence 120, App	246	236	10.0	552	3	US-09-219-849-7	Sequence 7, Appl

247	235.5	10.0	643	4	US-09-538-092-844	Sequence 844, App	320	206	8.7	417	1	US-08-477-509B-104	Sequence 104, App
248	234.5	9.9	936	1	US-08-212-237-3	Sequence 3, Appli	321	206	8.7	417	1	US-08-642-255-102	Sequence 102, App
249	234.5	9.9	936	2	US-08-806-029-26	Sequence 26, Appl	322	206	8.7	417	1	US-08-707-237A-76	Sequence 76, Appl
250	234.5	9.9	936	5	PCT-US95-02772-3	Sequence 3, Appli	323	206	8.7	417	3	US-08-482-085B-104	Sequence 104, App
251	232.5	9.8	536	4	US-09-270-767-43766	Sequence 43766, A	324	206	8.7	417	3	US-09-444-791A-104	Sequence 104, App
252	231.5	9.8	100	4	US-09-411-067C-1	Sequence 4, Appli	325	206	8.7	837	1	US-08-175-155-68	Sequence 68, Appl
253	231.5	9.8	2088	4	US-09-548-372D-13	Sequence 13, Appl	326	206	8.7	837	1	US-08-477-509B-103	Sequence 103, App
254	231.5	9.8	2088	4	US-09-548-367D-13	Sequence 13, Appl	327	206	8.7	837	1	US-08-642-255-101	Sequence 101, App
255	231.5	9.8	2088	4	US-09-551-853D-13	Sequence 13, Appl	328	206	8.7	837	2	US-08-707-237A-75	Sequence 75, Appl
256	231.5	9.8	2088	4	US-09-548-376D-13	Sequence 13, Appl	329	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
257	231.5	9.8	2088	4	US-09-548-373D-13	Sequence 13, Appl	330	206	8.7	837	3	US-08-482-085B-103	Sequence 103, App
258	231.5	9.8	2088	4	US-09-548-366P-13	Sequence 13, Appl	331	206	8.7	897	1	US-09-444-791A-103	Sequence 103, App
259	231.5	9.8	2088	4	US-09-548-368D-13	Sequence 13, Appl	332	206	8.7	1516	4	US-08-397-633A-50	Sequence 50, Appl
260	230.5	9.8	936	3	US-08-707-237A-108	Sequence 108, App	333	205.5	8.7	489	2	US-09-349-016-8209	Sequence 8209, Ap
261	230.5	9.8	936	3	US-08-642-246-30	Sequence 30, Appl	334	205.5	8.7	489	2	US-08-794-795-7	Sequence 7, Appli
262	230.5	9.8	936	4	US-09-451-206-30	Sequence 30, Appl	335	205.5	8.7	518	1	US-09-249-200-7	Sequence 7, Appli
263	230.5	9.8	936	5	PCT-US96-06229-30	Sequence 30, Appl	336	205.5	8.7	518	3	US-08-392-367B-2	Sequence 2, Appli
264	229.5	9.7	857	4	US-09-302-540-12312	Sequence 12312, A	337	205	8.7	187	4	US-08-893-467A-2	Sequence 2, Appli
265	227.5	9.6	485	2	US-08-749-391-2	Sequence 2, Appli	338	205	8.7	228	3	US-09-680-175-4	Sequence 4, Appli
266	227.5	9.6	485	3	US-09-390-200-2	Sequence 2, Appli	339	205	8.7	1415	4	US-09-219-849-38	Sequence 38, Appl
267	224.5	9.5	748	3	US-09-219-849-10	Sequence 10, Appl	340	205	8.7	1603	4	US-09-252-991A-26438	Sequence 26438, A
268	223	9.4	378	2	US-08-707-237A-104	Sequence 104, App	341	203.5	8.6	688	4	US-09-949-016-6136	Sequence 6136, Ap
269	223	9.4	378	3	US-08-642-246-26	Sequence 26, Appl	342	203	8.6	1259	4	US-09-902-540-10297	Sequence 10297, A
270	223	9.4	378	4	US-09-451-206-26	Sequence 26, Appl	343	201.5	8.5	123	4	US-09-949-016-10366	Sequence 10366, A
271	223	9.4	378	5	PCT-US96-06229-26	Sequence 26, Appl	344	201.5	8.5	123	4	US-09-072-596-243	Sequence 243, App
272	222.5	9.4	966	3	US-08-642-246-34	Sequence 34, Appl	345	201.5	8.5	433	3	US-09-072-596-248	Sequence 248, App
273	222.5	9.4	966	4	US-09-451-206-34	Sequence 34, Appl	346	201.5	8.5	433	3	US-08-806-029-34	Sequence 34, Appl
274	222.5	9.4	966	5	PCT-US96-06229-34	Sequence 34, Appl	347	201.5	8.5	684	4	US-09-524-101D-20	Sequence 20, Appl
275	222.5	9.4	1343	4	US-09-949-016-10641	Sequence 10641, A	348	201	8.5	1712	4	US-09-949-016-8348	Sequence 8348, Ap
276	222	9.4	412	4	US-09-248-796A-26345	Sequence 26345, A	349	200.5	8.5	341	2	US-09-961-403-9	Sequence 9, Appli
277	222	9.4	637	1	US-09-949-016-8152	Sequence 8152, Ap	350	200.5	8.5	341	2	US-08-538-711A-8	Sequence 8, Appli
278	222	9.4	1694	1	US-08-494-168-2	Sequence 2, Appli	351	200.5	8.5	341	3	US-08-725-027-8	Sequence 8, Appli
279	220.5	9.3	645	3	US-09-919-172-41	Sequence 41, Appl	352	200.5	8.5	353	3	US-09-542-552-8	Sequence 8, Appli
280	219.5	9.3	168	3	US-09-444-791A-52	Sequence 52, Appl	353	200.5	8.5	353	3	US-08-538-711A-7	Sequence 7, Appli
281	219.5	9.3	829	1	US-08-642-255-132	Sequence 132, App	354	200.5	8.5	353	4	US-08-725-027-7	Sequence 7, Appli
282	219.5	9.3	829	1	US-08-397-633A-53	Sequence 53, Appl	355	200.5	8.5	353	4	US-09-542-552-7	Sequence 7, Appli
283	219	9.3	274	4	US-09-976-594-417	Sequence 417, App	356	200.5	8.5	353	4	US-09-538-092-989	Sequence 989, App
284	218.5	9.2	378	4	US-10-164-595-2	Sequence 2, Appli	357	200.5	8.5	410	4	US-09-949-016-10345	Sequence 10345, A
285	217.5	9.2	495	2	US-08-794-795-2	Sequence 2, Appli	358	199	8.4	541	4	US-09-248-796A-26119	Sequence 26119, A
286	217.5	9.2	495	3	US-09-249-200-2	Sequence 2, Appli	359	199	8.4	599	4	US-09-949-016-8890	Sequence 8890, Ap
287	217	9.2	295	4	US-09-248-796A-25715	Sequence 25715, A	360	199	8.4	825	4	US-10-210-428-1	Sequence 1, Appli
288	216.5	9.2	595	4	US-09-370-838-187	Sequence 187, App	361	199	8.4	825	4	US-10-237-551-161	Sequence 161, App
289	216.5	9.2	595	4	US-09-854-133-187	Sequence 187, App	362	199	8.4	826	4	US-09-894-998A-47	Sequence 47, Appl
290	216.5	9.2	684	1	US-08-555-669-12	Sequence 12, Appl	363	199	8.4	826	4	US-10-237-551-47	Sequence 47, Appl
291	216.5	9.2	684	3	US-09-073-663-12	Sequence 12, Appl	364	198.5	8.4	547	1	US-08-494-168-7	Sequence 7, Appli
292	216.5	9.2	2090	4	US-09-538-092-1081	Sequence 1081, Ap	365	198	8.4	541	4	US-09-538-092-347	Sequence 347, App
293	216.5	9.2	2120	4	US-09-949-016-9768	Sequence 9768, Ap	366	197.5	8.4	464	4	US-09-252-991A-24883	Sequence 24883, A
294	215.5	9.1	520	2	US-08-794-795-6	Sequence 6, Appli	367	197	8.3	1078	4	US-09-949-016-11185	Sequence 11185, A
295	215.5	9.1	520	3	US-09-249-200-6	Sequence 6, Appli	368	197	8.3	1143	4	US-09-949-016-6137	Sequence 6137, Ap
296	215	9.1	390	1	US-08-106-981-4	Sequence 4, Appli	369	195.5	8.3	279	3	US-09-010-999-2	Sequence 2, Appli
297	215	9.1	479	3	US-09-177-349-3	Sequence 3, Appli	370	195	8.3	146	1	US-07-609-716-105	Sequence 105, App
298	215	9.1	479	4	US-09-918-951-3	Sequence 3, Appli	371	195	8.3	146	3	US-08-475-411A-105	Sequence 105, App
299	215	9.1	1218	4	US-09-949-016-7065	Sequence 7065, Ap	372	195	8.3	146	3	US-08-478-029A-105	Sequence 105, App
300	215	9.1	1319	4	US-09-538-092-1291	Sequence 1291, Ap	373	195	8.3	281	1	US-08-397-633A-75	Sequence 75, Appl
301	215	9.1	1690	4	US-09-949-016-5884	Sequence 5884, Ap	374	194.5	8.2	166	4	US-09-841-334A-21	Sequence 21, Appl
302	214	9.1	406	4	US-09-949-016-9243	Sequence 9243, Ap	375	194.5	8.2	166	4	US-09-837-969A-21	Sequence 21, Appl
303	213.5	9.0	310	3	US-09-219-849-47	Sequence 47, Appl	376	194.5	8.2	442	4	US-09-248-796A-21400	Sequence 21400, A
304	213.5	9.0	1670	4	US-09-949-016-5883	Sequence 5883, Ap	377	194.5	8.2	1268	4	US-09-949-016-7487	Sequence 7487, Ap
305	213	9.0	529	4	US-08-381-656-1	Sequence 1, Appli	378	193	8.2	359	4	US-09-270-767-43751	Sequence 43751, A
306	212.5	9.0	347	4	US-09-623-497-1	Sequence 1, Appli	379	192	8.1	623	3	US-09-029-348-3	Sequence 3, Appli
307	212	9.0	100	4	US-09-411-067C-5	Sequence 5, Appli	380	192	8.1	744	4	US-09-949-016-9607	Sequence 9607, Ap
308	211	8.9	371	4	US-09-538-092-884	Sequence 884, App	381	192	8.1	1345	2	US-08-977-767-3	Sequence 3, Appli
309	210.5	8.9	262	1	US-08-397-633A-73	Sequence 73, Appl	382	191.5	8.1	160	3	US-08-542-051-18	Sequence 18, Appl
310	210	8.9	1609	4	US-09-949-016-10910	Sequence 10910, A	383	191.5	8.1	644	4	US-09-919-039-121	Sequence 121, App
311	209.5	8.9	353	2	US-08-687-702-37	Sequence 37, Appl	384	191.5	8.1	847	4	US-09-373-157-4	Sequence 4, Appli
312	209.5	8.9	1034	4	US-09-252-991A-26658	Sequence 26658, A	385	191.5	8.1	847	4	US-09-949-016-8582	Sequence 8582, Ap
313	208.5	8.8	435	4	US-09-302-540-12731	Sequence 12731, A	386	190.5	8.1	637	4	US-09-479-467A-15	Sequence 15, Appl
314	208	8.8	689	4	US-09-949-016-11276	Sequence 11276, A	387	190.5	8.1	2870	4	US-09-479-467A-15	Sequence 15, Appl
315	208	8.8	1064	1	US-08-642-255-62	Sequence 62, Appl	388	190.5	8.1	3178	4	US-09-479-467A-4	Sequence 4, Appli
316	207	8.8	680	4	US-09-949-001-15	Sequence 15, Appl	389	190	8.0	276	3	US-08-506-553C-26	Sequence 26, Appl
317	207	8.8	680	4	US-09-949-001-20	Sequence 20, Appl	390	190	8.0	344	1	US-08-891-254-7	Sequence 7, Appli
318	206.5	8.7	938	4	US-09-949-016-9992	Sequence 9992, Ap	391	190	8.0	344	2	US-08-819-539-7	Sequence 7, Appli
319	206	8.7	417	1	US-08-175-155-69	Sequence 69, Appl	392	190	8.0	344	2	US-09-030-270A-7	Sequence 7, Appli

393	190	8.0	344	3	US-08-984-207-7	Sequence 7, Appli	466	171.5	7.3	1127	3	US-09-150-460B-11	Sequence 11, Appli
394	190	8.0	344	3	US-09-013-587-7	Sequence 7, Appli	467	171.5	7.3	2211	3	US-09-738-884-1	Sequence 1, Appli
395	190	8.0	344	3	US-09-086-118-27	Sequence 27, Appli	468	171.5	7.3	2211	3	US-10-096-961A-1	Sequence 1, Appli
396	190	8.0	344	4	US-09-431-614-15	Sequence 15, Appli	469	171.5	7.2	641	4	US-09-270-767-41562	Sequence 41562, A
397	190	8.0	344	5	PCT-US96-08819-7	Sequence 7, Appli	470	170.5	7.2	591	4	US-09-949-016-10914	Sequence 10914, A
398	190	8.0	626	3	US-09-029-348-2	Sequence 2, Appli	471	170.5	7.2	591	4	US-09-949-016-10915	Sequence 10915, A
399	189.5	8.0	549	1	US-08-494-168-8	Sequence 8, Appli	472	170.5	7.2	513	4	US-09-248-796A-25078	Sequence 25078, A
400	189.5	8.0	644	1	US-08-206-176-2	Sequence 2, Appli	473	170.5	7.2	519	3	US-09-453-702B-2657	Sequence 265, App
401	189	8.0	643	2	US-08-551-356-4	Sequence 4, Appli	474	169.5	7.2	415	3	US-09-025-769B-280	Sequence 280, App
402	189	8.0	643	5	PCT-US93-12687-4	Sequence 4, Appli	475	169.5	7.2	415	4	US-09-490-070A-280	Sequence 280, App
403	189	8.0	1336	2	US-08-551-356-6	Sequence 6, Appli	476	169.5	7.2	415	4	US-09-153-280	Sequence 280, App
404	189	8.0	1336	5	PCT-US93-12687-6	Sequence 6, Appli	477	169.5	7.2	415	4	US-09-490-324-280	Sequence 280, App
405	188	8.0	287	1	US-08-397-633A-76	Sequence 76, Appli	478	168.5	7.1	208	1	US-08-212-237-9	Sequence 9, Appli
406	187.5	7.9	180	4	US-09-248-796A-22352	Sequence 22352, A	479	168.5	7.1	208	5	PCT-US95-02772-9	Sequence 9, Appli
407	187	7.9	232	1	US-08-642-255-61	Sequence 61, Appli	480	168.5	7.1	755	4	US-09-919-497-57	Sequence 57, Appli
408	186.5	7.9	532	1	US-08-494-168-9	Sequence 9, Appli	481	168	7.1	111	3	US-08-963-168C-15	Sequence 15, Appli
409	186.5	7.9	1566	4	US-09-581-472B-2	Sequence 2, Appli	482	168	7.1	131	3	US-08-963-168C-8	Sequence 8, Appli
410	186	7.9	251	1	US-08-397-633A-74	Sequence 74, Appli	483	168	7.1	136	3	US-08-963-168C-6	Sequence 6, Appli
411	186	7.9	336	4	US-09-270-767-44531	Sequence 44531, A	484	168	7.1	316	4	US-09-248-796A-26455	Sequence 26455, A
412	186	7.9	605	4	US-09-976-594-616	Sequence 616, App	485	168	7.1	345	4	US-09-657-013-112	Sequence 112, App
413	186	7.9	1581	3	US-09-110-517-2	Sequence 2, Appli	486	168	7.1	684	4	US-09-961-403-5	Sequence 5, Appli
414	185.5	7.9	673	4	US-09-107-532A-5134	Sequence 5134, Ap	487	167.5	7.1	357	1	US-07-609-716-66	Sequence 66, Appli
415	185	7.8	546	1	US-08-494-168-10	Sequence 10, Appli	488	167.5	7.1	357	1	US-08-642-255-33	Sequence 33, Appli
416	184.5	7.8	174	4	US-09-270-767-61801	Sequence 61801, A	489	167.5	7.1	357	3	US-08-475-411A-66	Sequence 66, Appli
417	184.5	7.8	216	3	US-08-506-553C-23	Sequence 23, Appli	490	167.5	7.1	357	3	US-08-478-029A-66	Sequence 9, Appli
418	184	7.8	159	1	US-07-609-716-104	Sequence 104, App	491	167.5	7.1	551	4	US-09-489-039A-9083	Sequence 9083, Ap
419	184	7.8	159	3	US-08-475-411A-104	Sequence 104, App	492	167.5	7.1	558	4	US-09-071-035-268	Sequence 268, App
420	184	7.8	159	3	US-08-478-029A-104	Sequence 104, App	493	167.5	7.1	1338	4	US-09-071-035-258	Sequence 258, App
421	182.5	7.7	472	4	US-09-538-092-312	Sequence 312, Appli	494	167.5	7.1	1638	4	US-09-071-035-262	Sequence 262, App
422	181	7.7	234	4	US-09-895-674A-1	Sequence 8, Appli	495	167.5	7.1	1638	4	US-09-071-035-266	Sequence 266, App
423	180	7.6	730	4	US-09-961-403-8	Sequence 8, Appli	496	167.5	7.1	1747	4	US-09-134-000C-5999	Sequence 5999, Ap
424	180	7.6	731	2	US-08-911-364-1	Sequence 1, Appli	497	166.5	7.0	1088	3	US-09-130-242-2	Sequence 2, Appli
425	180	7.6	733	3	US-08-464-700-2	Sequence 2, Appli	498	166.5	7.0	1088	4	US-09-583-610D-2	Sequence 2, Appli
426	180	7.6	732	2	US-08-678-039A-40	Sequence 40, Appli	499	166.5	7.0	1088	4	US-09-949-016-6935	Sequence 6935, Ap
427	179.5	7.6	960	3	US-09-219-849-5	Sequence 5, Appli	500	166.5	7.0	2504	4	US-09-328-352-5821	Sequence 5821, Ap
428	179	7.6	345	4	US-09-270-767-45883	Sequence 45883, A	501	165.5	7.0	116	3	US-08-963-168C-13	Sequence 13, Appli
429	178.5	7.6	216	4	US-09-248-796A-14221	Sequence 14221, A	502	165.5	7.0	132	3	US-08-963-168C-9	Sequence 9, Appli
430	178	7.5	889	3	US-09-336-447A-15	Sequence 15, Appli	503	165.5	7.0	416	4	US-09-902-540-9752	Sequence 11959, A
431	178	7.5	889	4	US-09-352-267B-15	Sequence 15, Appli	504	165	7.0	715	4	US-09-902-540-9752	Sequence 9752, Ap
432	177.5	7.5	337	4	US-09-270-767-46550	Sequence 46550, A	505	165	7.0	823	4	US-09-538-092-439	Sequence 439, App
433	177	7.5	190	2	US-08-560-398-8	Sequence 8, Appli	506	164.5	7.0	112	3	US-08-963-168C-16	Sequence 16, Appli
434	177	7.5	731	4	US-09-340-736B-1	Sequence 1, Appli	507	164.5	7.0	356	4	US-09-252-991A-18206	Sequence 18206, A
435	177	7.5	731	4	US-09-964-662-1	Sequence 1, Appli	508	164.5	7.0	732	4	US-09-270-767-44652	Sequence 44652, A
436	177	7.5	2732	4	US-09-086-436-30	Sequence 30, Appli	509	163.5	6.9	331	4	US-09-949-016-7015	Sequence 7015, Ap
437	176.5	7.5	571	3	US-09-334-001C-3865	Sequence 3865, Ap	510	163.5	6.9	335	4	US-09-949-016-7995	Sequence 7995, Ap
438	174.5	7.4	385	1	US-08-891-254-3	Sequence 3, Appli	511	163.5	6.9	414	1	US-08-343-682-1	Sequence 1, Appli
439	174.5	7.4	385	2	US-08-819-539-3	Sequence 3, Appli	512	163.5	6.9	414	2	US-08-705-660-26	Sequence 26, Appli
440	174.5	7.4	385	5	PCT-US96-08819-3	Sequence 3, Appli	513	163.5	6.9	414	4	US-09-976-594-373	Sequence 373, App
441	174.5	7.4	403	2	US-08-200-724A-2	Sequence 2, Appli	514	163.5	6.9	414	4	US-09-315-355A-26	Sequence 26, Appli
442	174.5	7.4	403	2	US-09-030-270A-3	Sequence 3, Appli	515	163.5	6.9	414	4	US-09-949-016-11345	Sequence 11345, A
443	174.5	7.4	403	3	US-08-851-276A-2	Sequence 2, Appli	516	163.5	6.9	666	2	US-08-737-716-14	Sequence 14, Appli
444	174.5	7.4	403	3	US-08-984-207-3	Sequence 3, Appli	517	163	6.9	384	4	US-09-949-016-11034	Sequence 11034, A
445	174.5	7.4	403	3	US-09-013-587-3	Sequence 3, Appli	518	163	6.9	535	3	US-09-029-348-1	Sequence 1, Appli
446	174.5	7.4	403	4	US-09-086-118-23	Sequence 23, Appli	519	163	6.9	537	3	US-09-029-348-4	Sequence 4, Appli
447	174.5	7.4	403	4	US-09-431-614-3	Sequence 3, Appli	520	163	6.9	920	4	US-09-538-092-1197	Sequence 1197, Ap
448	174.5	7.4	1261	3	US-09-208-742-4	Sequence 4, Appli	521	163	6.9	1216	4	US-09-134-000C-5130	Sequence 5130, Ap
449	174.5	7.4	1261	3	US-09-332-295-2	Sequence 2, Appli	522	163	6.9	1709	4	US-09-949-016-11345	Sequence 11345, A
450	174.5	7.4	1261	4	US-10-147-268-2	Sequence 2, Appli	523	162.5	6.9	878	4	US-09-540-236-3401	Sequence 3401, Ap
451	174.5	7.4	1261	4	US-09-709-979-2	Sequence 2, Appli	524	162	6.9	683	4	US-09-620-412C-357	Sequence 357, App
452	174	7.4	521	4	US-09-270-767-46291	Sequence 46291, A	525	162	6.9	683	4	US-09-598-419-357	Sequence 357, App
453	173.5	7.3	432	4	US-09-403-089A-1	Sequence 1, Appli	526	162	6.9	717	4	US-09-252-991A-31195	Sequence 31195, A
454	173.5	7.3	432	4	US-09-809-517A-25	Sequence 25, Appli	527	161.5	6.8	319	4	US-09-248-796A-18138	Sequence 18138, A
455	173.5	7.3	434	4	US-09-809-517A-23	Sequence 23, Appli	528	161.5	6.8	424	3	US-09-120-817-2	Sequence 2, Appli
456	173.5	7.3	434	4	US-08-358-160-5	Sequence 26, Appli	529	161.5	6.8	424	4	US-09-431-614-14	Sequence 14, Appli
457	173.5	7.3	482	1	US-08-358-160-7	Sequence 7, Appli	530	161.5	6.8	534	3	US-09-029-348-5	Sequence 5, Appli
458	173.5	7.3	484	1	US-08-358-160-7	Sequence 7, Appli	531	161.5	6.8	557	3	US-09-320-095-10	Sequence 10, Appli
459	173	7.3	656	2	US-08-343-443B-2	Sequence 2, Appli	532	161.5	6.8	557	3	US-09-523-487-10	Sequence 52, Appli
460	173	7.3	656	3	US-09-214-564B-4	Sequence 4, Appli	533	161	6.8	503	3	US-08-845-258-52	Sequence 52, Appli
461	173	7.3	656	4	US-09-538-092-1250	Sequence 1250, Ap	534	161	6.8	503	3	US-08-990-571-52	Sequence 52, Appli
462	172.5	7.3	289	4	US-09-436-434-2	Sequence 2, Appli	535	161	6.8	503	4	US-09-528-784A-52	Sequence 52, Appli
463	172.5	7.3	385	5	PCT-US93-06243-2	Sequence 2, Appli	536	161	6.8	503	4	US-09-569-098A-52	Sequence 52, Appli
464	172	7.3	1268	4	US-09-270-767-45320	Sequence 45320, A	537	161	6.8	666	4	US-09-528-784A-85	Sequence 85, Appli
465	171.5	7.3	361	4	US-09-248-796A-20099	Sequence 20099, A	538	161	6.8	666	4	US-09-569-098A-85	Sequence 85, Appli

539	161	6.8	1091	4	US-09-949-016-8595	Sequence 8595, Ap	612	149	6.3	171	3	US-09-029-156-2	Sequence 2, Appli
540	161	6.8	1132	4	US-09-528-784A-87	Sequence 87, Appl	613	149	6.3	351	3	US-09-011-735-1	Sequence 1, Appli
541	161	6.8	1132	4	US-09-569-098A-87	Sequence 87, Appl	614	149	6.3	351	3	US-09-029-156-1	Sequence 1, Appli
542	161	6.8	1850	4	US-09-620-093A-5	Sequence 5, Appli	615	149	6.3	601	4	US-09-252-991A-27784	Sequence 27784, A
543	160.5	6.8	553	4	US-09-252-991A-17984	Sequence 2, Appli	616	148.5	6.3	266	4	US-09-495-880A-26	Sequence 26, Appl
544	160	6.8	300	3	US-08-765-856-2	Sequence 2, Appli	617	148.5	6.3	336	4	US-09-252-991A-17002	Sequence 17002, A
545	160	6.8	300	3	US-08-935-009A-2	Sequence 2, Appli	618	148.5	6.3	656	4	US-09-252-991A-30630	Sequence 30630, A
546	160	6.8	354	4	US-09-949-016-10178	Sequence 10178, A	619	148	6.3	247	4	US-09-248-796A-14517	Sequence 14517, A
547	160	6.8	336	4	US-09-640-211A-1055	Sequence 1055, Ap	620	148	6.3	447	3	US-09-120-927-2	Sequence 2, Appli
548	160	6.8	671	2	US-08-737-716-13	Sequence 13, Appl	621	148	6.3	447	3	US-09-431-614-6	Sequence 6, Appli
549	160	6.8	720	3	US-09-219-849-4	Sequence 4, Appli	622	147.5	6.2	1584	3	US-09-457-040B-27	Sequence 27, Appl
550	160	6.8	777	1	US-08-642-255-53	Sequence 53, Appl	623	147	6.2	97	1	US-08-175-155-15	Sequence 15, Appl
551	159	6.7	546	4	US-09-252-991A-18637	Sequence 18637, A	624	147	6.2	97	1	US-08-477-509B-50	Sequence 50, Appl
552	158	6.7	106	3	US-08-963-168C-14	Sequence 14, Appl	625	147	6.2	97	3	US-08-482-085B-50	Sequence 50, Appl
553	158	6.7	126	3	US-08-963-168C-7	Sequence 7, Appli	626	147	6.2	97	3	US-09-444-791A-50	Sequence 50, Appl
554	158	6.7	166	4	US-09-297-269-1	Sequence 41, Appl	627	147	6.2	98	2	US-08-707-237A-22	Sequence 22, Appl
555	158	6.7	435	4	US-09-270-767-43092	Sequence 43092, A	628	147	6.2	212	4	US-09-270-767-41907	Sequence 41907, A
556	157.5	6.7	430	2	US-08-945-848-8	Sequence 8, Appli	629	147	6.2	230	4	US-09-248-796A-28509	Sequence 28509, A
557	157.5	6.7	1032	4	US-09-270-767-44433	Sequence 44433, A	630	147	6.2	284	3	US-09-128-450-21	Sequence 21, Appl
558	157	6.6	272	4	US-09-949-016-9966	Sequence 9966, Ap	631	147	6.2	264	3	US-09-823-494-21	Sequence 21, Appl
559	157	6.6	272	4	US-09-949-016-9967	Sequence 9967, Ap	632	147	6.2	760	1	US-08-195-152-2	Sequence 2, Appli
560	157	6.6	461	2	US-08-463-587A-26	Sequence 26, Appl	633	147	6.2	760	1	US-08-754-311B-2	Sequence 2, Appli
561	157	6.6	461	2	US-08-463-587A-4	Sequence 4, Appli	634	147	6.2	908	4	US-08-714-741-44	Sequence 44, Appl
562	157	6.6	461	3	US-08-923-854-26	Sequence 26, Appl	635	146.5	6.2	365	4	US-09-270-767-46506	Sequence 46506, A
563	157	6.6	461	5	PCT-US91-09133-27	Sequence 27, Appl	636	146.5	6.2	368	4	US-09-248-796A-17306	Sequence 17306, A
564	156.5	6.6	471	2	US-08-399-889-24	Sequence 24, Appl	637	146.5	6.2	410	4	US-09-252-991A-25812	Sequence 25812, A
565	156.5	6.6	471	3	US-09-167-364-24	Sequence 24, Appl	638	146.5	6.2	717	3	US-08-910-925-1	Sequence 1, Appli
566	156.5	6.6	471	3	US-09-439-897-2	Sequence 2, Appli	639	146.5	6.2	918	3	US-09-041-886-11	Sequence 11, Appl
567	156	6.6	238	4	US-09-495-880A-42	Sequence 42, Appl	640	146	6.2	84	1	US-08-175-155-17	Sequence 17, Appl
568	156	6.6	694	4	US-09-949-016-7117	Sequence 7117, Ap	641	146	6.2	84	1	US-08-477-509B-52	Sequence 52, Appl
569	155.5	6.6	187	4	US-09-634-238-414	Sequence 414, App	642	146	6.2	84	2	US-08-707-237A-23	Sequence 23, Appl
570	155.5	6.6	746	3	US-09-134-001C-3214	Sequence 3214, Ap	643	146	6.2	84	3	US-08-482-085B-52	Sequence 52, Appl
571	155	6.6	618	4	US-09-252-991A-27666	Sequence 27666, A	644	146	6.2	219	4	US-09-380-015B-2	Sequence 2, Appli
572	154.5	6.5	136	4	US-09-252-991A-23071	Sequence 23071, A	645	146	6.2	415	4	US-09-328-352-6430	Sequence 6430, Ap
573	154.5	6.5	302	3	US-08-765-856-4	Sequence 4, Appli	646	146	6.2	467	4	US-09-949-016-7778	Sequence 7778, Ap
574	154.5	6.5	302	3	US-08-935-009A-4	Sequence 4, Appli	647	146	6.2	467	4	US-09-072-596-255	Sequence 255, App
575	154	6.5	1461	4	US-10-142-231-86	Sequence 86, Appl	648	145.5	6.2	99	4	US-09-072-596-260	Sequence 260, App
576	153	6.5	561	1	US-08-642-255-52	Sequence 52, Appl	649	145.5	6.2	99	4	US-09-072-596-260	Sequence 260, App
577	152.5	6.5	166	4	US-09-270-767-41190	Sequence 41190, A	650	145.5	6.2	93	3	US-08-910-925-3	Sequence 3, Appli
578	152.5	6.5	166	4	US-09-270-767-56406	Sequence 56406, A	651	145.5	6.2	743	4	US-09-949-016-6261	Sequence 6261, Ap
579	152.5	6.5	195	4	US-09-270-767-44458	Sequence 44458, A	652	145.5	6.2	970	4	US-09-270-767-42741	Sequence 42741, A
580	152.5	6.5	284	4	US-09-431-887-24	Sequence 24, Appl	653	145	6.1	264	4	US-09-431-887-27	Sequence 27, Appl
581	152.5	6.5	336	4	US-09-270-767-43241	Sequence 43241, A	654	145	6.1	328	1	US-08-229-287-4	Sequence 4, Appli
582	152.5	6.5	335	4	US-09-821-687-11	Sequence 11, Appl	655	145	6.1	553	3	US-09-083-351-2	Sequence 2, Appli
583	152.5	6.5	504	3	US-09-219-849-3	Sequence 3, Appli	656	145	6.1	553	3	US-09-083-352-2	Sequence 2, Appli
584	152.5	6.5	790	4	US-09-328-352-4283	Sequence 4283, Ap	657	145	6.1	553	3	US-09-612-809B-2	Sequence 2, Appli
585	152.5	6.5	1395	4	US-09-252-991A-30345	Sequence 30345, A	658	145	6.1	572	4	US-09-489-039A-11826	Sequence 11826, A
586	152	6.4	1010	4	US-09-248-796A-16379	Sequence 16379, A	659	145	6.1	633	4	US-09-976-594-282	Sequence 282, App
587	152	6.4	1417	3	US-08-900-230-3	Sequence 3, Appli	660	145	6.1	633	4	US-09-821-687-10	Sequence 10, Appl
588	151.5	6.4	461	1	US-08-186-222-2	Sequence 2, Appli	661	145	6.1	792	4	US-09-252-991A-25823	Sequence 25823, A
589	151	6.4	313	4	US-09-949-016-9265	Sequence 9265, Ap	662	145	6.1	919	4	US-09-538-092-895	Sequence 895, App
590	150.5	6.4	162	3	US-09-575-574-4	Sequence 4, Appli	663	145	6.1	923	4	US-09-497-822C-19	Sequence 19, Appl
591	150.5	6.4	251	1	US-08-209-747-8	Sequence 8, Appli	664	145	6.1	1186	2	US-08-861-464-8	Sequence 8, Appli
592	150.5	6.4	251	1	US-08-458-298-8	Sequence 8, Appli	665	145	6.1	1186	2	US-08-396-001-8	Sequence 8, Appli
593	150.5	6.4	447	4	US-09-916-109-5	Sequence 5, Appli	666	145	6.1	1186	3	US-09-323-433A-8	Sequence 8, Appli
594	150.5	6.4	447	4	US-10-211-412B-5	Sequence 5, Appli	667	145	6.1	1186	4	US-09-826-752-8	Sequence 8, Appli
595	150.5	6.4	483	4	US-09-916-109-4	Sequence 4, Appli	668	145	6.1	2314	3	US-09-268-347-49	Sequence 49, Appl
596	150.5	6.4	483	4	US-10-211-412B-4	Sequence 4, Appli	669	145	6.1	2763	3	US-08-496-944-2	Sequence 2, Appli
597	150.5	6.4	483	4	US-09-538-092-1162	Sequence 1162, Ap	670	144.5	6.1	258	4	US-09-248-796A-23723	Sequence 23723, A
598	150	6.3	72	4	US-09-513-999C-5563	Sequence 5563, Ap	671	144.5	6.1	302	4	US-09-657-013-49	Sequence 49, Appl
599	150	6.3	72	4	US-09-513-999C-5564	Sequence 5564, Ap	672	144.5	6.1	302	4	US-09-949-016-6893	Sequence 6893, Ap
600	150	6.3	207	4	US-10-029-180-70	Sequence 70, Appl	673	144.5	6.1	411	4	US-09-657-013-57	Sequence 57, Appl
601	150	6.3	423	1	US-08-383-744-2	Sequence 2, Appli	674	144.5	6.1	411	4	US-09-949-016-6439	Sequence 6439, Ap
602	150	6.3	423	2	US-08-999-336-2	Sequence 2, Appli	675	144.5	6.1	477	4	US-09-863-901-5	Sequence 5, Appli
603	150	6.3	423	5	PCT-US96-01427-2	Sequence 2, Appli	676	144.5	6.1	906	4	US-09-863-901-6	Sequence 6, Appli
604	149.5	6.3	121	4	US-09-072-596-253	Sequence 253, App	677	144	6.1	91	4	US-09-270-767-39789	Sequence 39789, A
605	149.5	6.3	121	4	US-09-072-596-258	Sequence 258, App	678	144	6.1	91	4	US-09-270-767-55006	Sequence 55006, A
606	149.5	6.3	445	4	US-09-252-991A-24354	Sequence 24354, A	679	144	6.1	123	1	US-07-609-716-103	Sequence 103, App
607	149.5	6.3	1060	3	US-08-911-393-2	Sequence 2, Appli	680	144	6.1	123	3	US-08-475-411A-103	Sequence 103, App
608	149.5	6.3	1060	4	US-09-955-909-2	Sequence 2, Appli	681	144	6.1	123	3	US-08-478-029A-103	Sequence 103, App
609	149	6.3	60	4	US-08-832-297A-12	Sequence 12, Appl	682	144	6.1	375	4	US-09-600-932-29	Sequence 29, Appl
610	149	6.3	124	4	US-09-340-236-3076	Sequence 3076, Ap	683	144	6.1	351	4	US-09-595-017B-2	Sequence 2, Appli
611	149	6.3	171	3	US-09-011-735-2	Sequence 2, Appli	684	144	6.1	402	4	US-09-252-991A-20683	Sequence 20683, A

685	144	6.1	1475	4	US-09-538-092-1160	Sequence 1160, Ap	758	140	5.9	101	3	US-09-247-806-5	Sequence 5, Appli
686	144	6.1	1712	4	US-09-949-016-9450	Sequence 9450, Ap	759	140	5.9	101	3	US-09-247-806-7	Sequence 7, Appli
687	144	6.1	1833	4	US-08-621-944A-4	Sequence 4, Appli	760	140	5.9	101	4	US-09-863-859-11	Sequence 11, Appl
688	144	6.1	1833	4	US-08-945-567D-4	Sequence 4, Appli	761	140	5.9	101	4	US-09-248-796A-26837	Sequence 26837, A
689	144	6.1	1992	4	US-08-621-944A-3	Sequence 3, Appli	762	140	5.9	234	1	US-08-642-255-51	Sequence 51, Appl
690	144	6.1	1992	4	US-08-945-567D-3	Sequence 3, Appli	763	140	5.9	705	4	US-09-252-991A-30792	Sequence 30792, A
691	144	6.1	2123	3	US-08-968-685A-10	Sequence 10, Appl	764	140	5.9	892	3	US-09-336-447A-5	Sequence 5, Appli
692	143.5	6.1	482	4	US-09-509-031-16	Sequence 16, Appl	765	140	5.9	892	4	US-09-952-267B-5	Sequence 5, Appli
693	143.5	6.1	563	4	US-09-949-016-10153	Sequence 10153, A	766	140	5.9	956	4	US-09-949-016-8159	Sequence 8159, Ap
694	143.5	6.1	2142	4	US-09-540-236-3459	Sequence 3459, Ap	767	139.5	5.9	219	4	US-09-809-517A-24	Sequence 24, Appl
695	143	6.1	165	4	US-09-270-767-59895	Sequence 59895, A	768	139.5	5.9	219	4	US-09-809-517A-27	Sequence 27, Appl
696	143	6.1	263	1	US-08-242-188-3	Sequence 3, Appli	769	139.5	5.9	253	4	US-09-252-991A-20659	Sequence 20659, A
697	143	6.1	263	1	US-08-509-261A-3	Sequence 3, Appli	770	139.5	5.9	449	2	US-08-927-394-2	Sequence 2, Appli
698	143	6.1	263	1	US-08-660-626-9	Sequence 9, Appli	771	139.5	5.9	449	4	US-09-538-092-1372	Sequence 1372, Ap
699	143	6.1	263	1	US-08-692-892-3	Sequence 3, Appli	772	139.5	5.9	449	4	US-09-949-016-6604	Sequence 6604, Ap
700	143	6.1	263	2	US-08-713-339A-3	Sequence 3, Appli	773	139.5	5.9	467	4	US-09-252-991A-31427	Sequence 31427, A
701	143	6.1	263	2	US-08-868-162A-23	Sequence 23, Appl	774	139.5	5.9	489	4	US-09-366-009-8	Sequence 8, Appli
702	143	6.1	263	2	US-09-031-168-9	Sequence 9, Appli	775	139.5	5.9	489	4	US-08-809-156B-8	Sequence 8, Appli
703	143	6.1	263	3	US-09-036-579-3	Sequence 3, Appli	776	139.5	5.9	537	4	US-09-252-991A-27024	Sequence 27024, A
704	143	6.1	263	3	US-09-550-374-3	Sequence 3, Appli	777	139.5	5.9	537	4	US-09-345-473B-50	Sequence 50, Appl
705	143	6.1	263	4	US-09-943-906-3	Sequence 3, Appli	778	139.5	5.9	743	4	US-09-252-991A-21854	Sequence 21854, A
706	143	6.1	263	4	US-09-669-516C-9	Sequence 9, Appli	779	139.5	5.9	2391	4	US-09-252-991A-21854	Sequence 21854, A
707	143	6.1	264	4	US-09-627-218B-11	Sequence 11, Appl	780	139	5.9	393	4	US-09-252-991A-30202	Sequence 30202, A
708	143	6.1	544	4	US-09-252-991A-27138	Sequence 27138, A	781	139	5.9	481	4	US-09-252-991A-16955	Sequence 16955, A
709	142.5	6.0	3969	4	US-09-538-092-1262	Sequence 1262, Ap	782	138.5	5.9	415	4	US-09-252-991A-16955	Sequence 16955, A
710	142	6.0	137	4	US-09-270-767-56792	Sequence 56792, A	783	138.5	5.9	421	4	US-09-252-991A-32326	Sequence 32326, A
711	142	6.0	269	4	US-09-538-092-412	Sequence 412, App	784	138.5	5.9	437	4	US-09-921-099A-17	Sequence 17, Appl
712	142	6.0	367	4	US-09-252-991A-16628	Sequence 16628, A	785	138.5	5.9	1261	4	US-09-473-716-2	Sequence 2, Appli
713	142	6.0	434	4	US-09-252-991A-22945	Sequence 22945, A	786	138.5	5.9	1261	4	US-10-175-158-2	Sequence 2, Appli
714	142	6.0	1135	4	US-09-294-298A-21	Sequence 21, Appl	787	138	5.8	1497	4	US-09-060-854B-2	Sequence 2, Appli
715	142	6.0	1325	4	US-09-294-298A-6	Sequence 6, Appli	788	138	5.8	1497	4	US-09-529-904-3	Sequence 3, Appli
716	142	6.0	1376	4	US-09-294-298A-4	Sequence 4, Appli	789	138	5.8	1815	4	US-09-270-767-42654	Sequence 42654, A
717	142	6.0	1423	4	US-09-294-298A-2	Sequence 2, Appli	790	138	5.8	2736	4	US-09-252-991A-30227	Sequence 30227, A
718	141.5	6.0	233	2	US-08-458-568A-4	Sequence 4, Appli	791	137.5	5.8	263	4	US-09-252-991A-31863	Sequence 31863, A
719	141.5	6.0	474	4	US-09-702-705-1812	Sequence 1812, Ap	792	137.5	5.8	371	4	US-09-252-991A-30926	Sequence 30926, A
720	141.5	6.0	474	4	US-09-736-457-1812	Sequence 1812, Ap	793	137.5	5.8	425	4	US-09-252-991A-31834	Sequence 31834, A
721	141.5	6.0	474	4	US-09-671-325-1812	Sequence 1812, Ap	794	137.5	5.8	518	4	US-09-252-991A-25203	Sequence 25203, A
722	141.5	6.0	474	4	US-09-538-092-1279	Sequence 1279, Ap	795	137.5	5.8	745	4	US-09-841-334A-38	Sequence 38, Appl
723	141.5	6.0	487	4	US-09-386-962C-14	Sequence 14, Appl	796	137.5	5.8	745	4	US-09-837-969A-38	Sequence 38, Appl
724	141.5	6.0	487	4	US-09-386-959-65	Sequence 65, Appl	797	137.5	5.8	1005	1	US-07-853-913-2	Sequence 2, Appli
725	141	6.0	211	1	US-08-276-852-34	Sequence 34, Appl	798	137	5.8	867	4	US-09-540-236-2676	Sequence 2676, Ap
726	141	6.0	211	1	US-08-133-011-16	Sequence 16, Appl	799	137	5.8	995	4	US-09-252-991A-22297	Sequence 22297, A
727	141	6.0	211	1	US-08-322-730A-16	Sequence 16, Appl	800	136.5	5.8	223	4	US-09-248-796A-27735	Sequence 27735, A
728	141	6.0	211	1	US-08-387-874-16	Sequence 16, Appl	801	136.5	5.8	464	2	US-08-836-854-19	Sequence 19, Appl
729	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	802	136.5	5.8	464	4	US-09-366-009-7	Sequence 7, Appli
730	141	6.0	211	1	US-08-899-575-34	Sequence 34, Appl	803	136.5	5.8	464	4	US-08-809-156B-7	Sequence 7, Appli
731	141	6.0	211	2	US-08-899-575-34	Sequence 34, Appl	804	136.5	5.8	703	3	US-08-910-925-4	Sequence 4, Appli
732	141	6.0	211	3	US-08-907-739-16	Sequence 16, Appl	805	136.5	5.8	850	4	US-09-129-603-2	Sequence 2, Appli
733	141	6.0	211	4	US-09-729-597-16	Sequence 16, Appl	806	136.5	5.8	1113	4	US-09-252-991A-24385	Sequence 24385, A
734	141	6.0	211	5	PCT-US93-08364-16	Sequence 16, Appl	807	136.5	5.8	1290	3	US-09-150-460B-6	Sequence 6, Appli
735	141	6.0	211	5	PCT-US94-05669A-6	Sequence 34, Appl	808	136.5	5.8	1376	4	US-09-252-991A-30344	Sequence 30344, A
736	141	6.0	211	5	PCT-US95-08743-34	Sequence 4, Appli	809	136.5	5.8	1388	4	US-09-463-048A-6	Sequence 6, Appli
737	141	6.0	233	3	US-08-438-745-4	Sequence 4, Appli	810	136	5.8	50	4	US-09-863-901-22	Sequence 22, Appl
738	141	6.0	233	3	US-08-438-745-6	Sequence 6, Appli	811	136	5.8	199	3	US-08-506-553C-8	Sequence 8, Appli
739	141	6.0	233	3	US-09-219-019-4	Sequence 4, Appli	812	136	5.8	247	4	US-09-252-991A-21412	Sequence 21412, A
740	141	6.0	233	3	US-09-219-019-6	Sequence 6, Appli	813	136	5.8	339	4	US-09-252-991A-32096	Sequence 32096, A
741	141	6.0	233	5	PCT-US94-05669A-4	Sequence 4, Appli	814	135.5	5.7	260	4	US-09-431-887-6	Sequence 6, Appli
742	141	6.0	378	4	US-09-395-017B-1	Sequence 1, Appli	815	135.5	5.7	400	3	US-09-086-010-2	Sequence 2, Appli
743	141	6.0	434	4	US-09-270-767-61286	Sequence 61286, A	816	135.5	5.7	590	4	US-09-252-991A-19127	Sequence 19127, A
744	141	6.0	684	4	US-09-823-240A-9	Sequence 9, Appli	817	135	5.7	139	4	US-09-050-739-68	Sequence 68, Appl
745	141	6.0	1059	4	US-09-270-767-45764	Sequence 45764, A	818	135	5.7	302	2	US-08-893-853-3	Sequence 3, Appli
746	141	6.0	234	4	US-09-252-991A-23547	Sequence 23547, A	819	135	5.7	302	3	US-09-113-921-3	Sequence 3, Appli
747	140.5	5.9	456	4	US-09-252-991A-19417	Sequence 19417, A	820	135	5.7	302	4	US-09-451-067-3	Sequence 3, Appli
748	140.5	5.9	482	4	US-09-248-796A-14808	Sequence 14808, A	821	135	5.7	310	3	US-08-845-258-19	Sequence 19, Appl
749	140.5	5.9	484	4	US-09-242-913B-17	Sequence 17, Appl	822	135	5.7	310	3	US-08-990-571-19	Sequence 19, Appl
750	140.5	5.9	506	4	US-09-949-016-11518	Sequence 11518, A	823	135	5.7	310	3	US-08-723-142A-19	Sequence 19, Appl
751	140.5	5.9	569	4	US-09-252-991A-24513	Sequence 24513, A	824	135	5.7	310	4	US-09-528-784A-19	Sequence 19, Appl
752	140.5	5.9	1776	4	US-09-556-877-179	Sequence 179, App	825	135	5.7	310	4	US-09-569-098A-19	Sequence 19, Appl
753	140.5	5.9	1776	4	US-09-620-412C-179	Sequence 179, App	826	135	5.7	545	4	US-09-252-991A-30910	Sequence 30910, A
754	140.5	5.9	1776	4	US-09-598-419-179	Sequence 179, App	827	135	5.7	558	3	US-09-199-637A-277	Sequence 277, App
755	140.5	5.9	3969	3	US-08-061-376-5	Sequence 5, Appli	828	135	5.7	2516	3	US-08-374-077C-2	Sequence 2, Appli
756	140	5.9	101	3	US-08-556-978B-22	Sequence 22, Appl	829	135	5.7	2516	4	US-08-895-590-2	Sequence 2, Appli
757	140	5.9	101	3	US-08-556-978B-62	Sequence 62, Appl	830	135	5.7	2516	4	US-09-539-879A-2	Sequence 2, Appli





977	127.5	5.4	406	4	US-09-949-016-8507	Sequence 8507, Ap	1050	125	5.3	254	3	US-09-823-494-26	Sequence 26, Appl
978	127.5	5.4	630	4	US-09-252-991A-19702	Sequence 19702, A	1051	125	5.3	349	3	US-08-469-318-151	Sequence 151, App
979	127.5	5.4	878	3	US-08-653-648A-15	Sequence 15, Appl	1052	125	5.3	349	3	US-08-468-609A-151	Sequence 151, App
980	127.5	5.4	878	4	US-09-564-418-8	Sequence 8, Appl	1053	125	5.3	349	3	US-08-446-872A-151	Sequence 151, App
981	127	5.4	253	1	US-08-242-188-2	Sequence 2, Appl	1054	125	5.3	349	4	US-08-762-227A-151	Sequence 151, App
982	127	5.4	253	1	US-08-509-261A-2	Sequence 2, Appl	1055	125	5.3	349	5	PCT-US95-01185-151	Sequence 151, App
983	127	5.4	253	1	US-08-660-626-8	Sequence 8, Appl	1056	125	5.3	349	4	US-09-248-796A-16450	Sequence 16450, A
984	127	5.4	253	1	US-08-692-892-2	Sequence 2, Appl	1057	125	5.3	349	4	US-09-248-796A-16474	Sequence 16474, A
985	127	5.4	253	2	US-08-713-939A-2	Sequence 2, Appl	1058	125	5.3	716	4	US-09-107-532A-5208	Sequence 5208, Ap
986	127	5.4	253	2	US-08-868-162A-22	Sequence 2, Appl	1059	124.5	5.3	60	3	US-08-469-318-195	Sequence 195, App
987	127	5.4	253	3	US-09-031-168-8	Sequence 8, Appl	1060	124.5	5.3	60	3	US-08-468-609A-195	Sequence 195, App
988	127	5.4	253	3	US-09-128-450-20	Sequence 20, Appl	1061	124.5	5.3	60	3	US-08-446-872A-195	Sequence 195, App
989	127	5.4	253	3	US-09-036-579-2	Sequence 2, Appl	1062	124.5	5.3	60	4	US-08-762-227A-195	Sequence 195, App
990	127	5.4	253	3	US-09-823-494-20	Sequence 20, Appl	1063	124.5	5.3	60	5	PCT-US95-01185-195	Sequence 195, App
991	127	5.4	253	3	US-09-550-374-2	Sequence 2, Appl	1064	124.5	5.3	184	4	US-09-270-767-59165	Sequence 59165, A
992	127	5.4	253	4	US-09-431-887-1	Sequence 1, Appl	1065	124.5	5.3	281	4	US-09-252-991A-21873	Sequence 21873, A
993	127	5.4	253	4	US-09-431-887-2	Sequence 2, Appl	1066	124.5	5.3	294	4	US-09-270-767-43772	Sequence 43772, A
994	127	5.4	253	4	US-09-431-887-3	Sequence 3, Appl	1067	124.5	5.3	349	3	US-08-469-318-139	Sequence 139, App
995	127	5.4	253	4	US-09-431-887-4	Sequence 4, Appl	1068	124.5	5.3	349	3	US-08-468-609A-139	Sequence 139, App
996	127	5.4	253	4	US-09-431-887-8	Sequence 8, Appl	1069	124.5	5.3	349	3	US-08-446-872A-139	Sequence 139, App
997	127	5.4	253	4	US-09-431-887-19	Sequence 19, Appl	1070	124.5	5.3	349	4	US-08-762-227A-139	Sequence 139, App
998	127	5.4	253	4	US-09-943-506-2	Sequence 2, Appl	1071	124.5	5.3	349	5	PCT-US95-01185-139	Sequence 139, App
999	127	5.4	253	4	US-09-669-516C-8	Sequence 8, Appl	1072	124.5	5.3	383	4	US-09-252-991A-24223	Sequence 24223, A
1000	127	5.4	253	4	US-09-904-987-3	Sequence 3, Appl	1073	124.5	5.3	425	4	US-09-252-991A-19054	Sequence 19054, A
1001	127	5.4	257	4	US-09-431-887-29	Sequence 29, Appl	1074	124.5	5.3	510	4	US-09-252-991A-33084	Sequence 33084, A
1002	127	5.4	298	3	US-08-122-458D-11	Sequence 11, Appl	1075	124.5	5.3	534	4	US-09-252-991A-20468	Sequence 20468, A
1003	127	5.4	331	4	US-09-270-767-45830	Sequence 45830, A	1076	124.5	5.3	757	4	US-09-252-991A-23569	Sequence 23569, A
1004	127	5.4	374	4	US-09-248-796A-17283	Sequence 17283, A	1077	124.5	5.3	1261	4	US-09-248-796A-16620	Sequence 16620, A
1005	127	5.4	886	4	US-09-252-991A-24378	Sequence 24378, A	1078	124.5	5.3	1665	4	US-09-858-664A-2	Sequence 2, Appl
1006	127	5.4	1004	3	US-09-268-347-30	Sequence 30, Appl	1079	124.5	5.3	1665	4	US-10-274-978-2	Sequence 2, Appl
1007	126.5	5.4	217	4	US-09-270-767-31877	Sequence 31877, A	1080	124.5	5.3	1665	4	US-10-697-263-2	Sequence 2, Appl
1008	126.5	5.4	217	4	US-09-270-767-47094	Sequence 47094, A	1081	124	5.2	76	1	US-08-089-862-10	Sequence 10, Appl
1009	126.5	5.4	219	4	US-09-248-796A-23661	Sequence 23661, A	1082	124	5.2	76	1	US-08-587-333-17	Sequence 17, Appl
1010	126.5	5.4	256	4	US-09-431-887-25	Sequence 25, Appl	1083	124	5.2	76	5	PCT-US94-07776-15	Sequence 15, Appl
1011	126.5	5.4	256	4	US-09-431-887-28	Sequence 28, Appl	1084	124	5.2	155	4	US-09-252-991A-27532	Sequence 27532, A
1012	126.5	5.4	351	4	US-09-252-991A-29678	Sequence 29678, A	1085	124	5.2	212	4	US-09-252-991A-24512	Sequence 24512, A
1013	126.5	5.4	405	4	US-09-166-265-1	Sequence 1, Appl	1086	124	5.2	212	4	US-09-252-991A-27887	Sequence 27887, A
1014	126.5	5.4	427	4	US-09-270-767-45426	Sequence 45426, A	1087	124	5.2	462	4	US-09-252-991A-26584	Sequence 26584, A
1015	126.5	5.4	439	4	US-09-252-991A-16736	Sequence 16736, A	1088	124	5.2	482	4	US-09-270-767-43292	Sequence 43292, A
1016	126.5	5.4	451	4	US-09-252-991A-25804	Sequence 25804, A	1089	124	5.2	586	4	US-09-252-991A-24514	Sequence 24514, A
1017	126.5	5.4	476	4	US-09-252-991A-17887	Sequence 17887, A	1090	123.5	5.2	229	4	US-09-248-796A-24831	Sequence 24831, A
1018	126.5	5.4	650	4	US-09-252-991A-23546	Sequence 23546, A	1091	123.5	5.2	325	4	US-09-902-540-13678	Sequence 13678, A
1019	126.5	5.4	834	4	US-09-252-991A-28145	Sequence 28145, A	1092	123.5	5.2	501	4	US-09-252-991A-19191	Sequence 19191, A
1020	126.5	5.4	1011	4	US-09-252-991A-32419	Sequence 32419, A	1093	123.5	5.2	704	4	US-09-270-767-46262	Sequence 46262, A
1021	126.5	5.4	2142	4	US-09-538-092-1142	Sequence 1142, Ap	1094	123.5	5.2	742	4	US-09-949-016-7729	Sequence 7729, Ap
1022	126.5	5.4	2442	3	US-09-514-247A-10	Sequence 10, Appl	1095	123.5	5.2	783	4	US-09-252-991A-18035	Sequence 18035, A
1023	126.5	5.4	2442	4	US-09-538-092-1370	Sequence 1370, Ap	1096	123.5	5.2	1403	2	US-08-387-942C-3	Sequence 3, Appl
1024	126	5.3	97	1	US-07-609-716-99	Sequence 99, Appl	1097	123	5.2	179	4	US-09-270-767-57837	Sequence 57837, A
1025	126	5.3	97	3	US-08-475-411A-99	Sequence 99, Appl	1098	123	5.2	208	4	US-09-252-991A-27661	Sequence 27661, A
1026	126	5.3	97	3	US-08-478-029A-99	Sequence 99, Appl	1099	123	5.2	252	4	US-09-431-887-17	Sequence 17, Appl
1027	126	5.3	208	3	US-09-128-450-18	Sequence 18, Appl	1100	123	5.2	321	3	US-08-485-511A-4	Sequence 4, Appl
1028	126	5.3	208	3	US-09-823-494-18	Sequence 18, Appl	1101	123	5.2	522	4	US-09-538-092-1096	Sequence 1096, Ap
1029	126	5.3	253	4	US-09-919-172-57	Sequence 57, Appl	1102	123	5.2	524	4	US-09-252-991A-23901	Sequence 23901, A
1030	126	5.3	253	4	US-09-976-594-72	Sequence 72, Appl	1103	123	5.2	588	4	US-09-252-991A-18578	Sequence 18578, A
1031	126	5.3	374	4	US-09-949-016-7191	Sequence 7191, Ap	1104	123	5.2	801	1	US-07-906-349A-6	Sequence 6, Appl
1032	126	5.3	383	4	US-09-252-991A-22283	Sequence 22283, A	1105	123	5.2	1620	1	US-08-542-363-2	Sequence 2, Appl
1033	126	5.3	584	4	US-09-252-991A-21071	Sequence 21071, A	1106	123	5.2	1620	3	US-09-100-089-2	Sequence 2, Appl
1034	126	5.3	819	4	US-09-252-991A-19569	Sequence 19569, A	1107	123	5.2	1620	4	US-09-670-827-2	Sequence 2, Appl
1035	126	5.3	891	4	US-09-949-016-7798	Sequence 7798, Ap	1108	123	5.2	1620	4	US-09-827-949-2	Sequence 2, Appl
1036	126	5.3	1394	4	US-09-902-540-16497	Sequence 16497, A	1109	122.5	5.2	155	1	US-08-209-747-15	Sequence 15, Appl
1037	126	5.3	1400	3	US-08-630-915A-37	Sequence 37, Appl	1110	122.5	5.2	155	1	US-08-458-298-15	Sequence 15, Appl
1038	126	5.3	1400	4	US-09-879-957-37	Sequence 37, Appl	1111	122.5	5.2	189	4	US-09-710-279-2692	Sequence 2692, Ap
1039	125.5	5.3	232	6	5171843-7	Patent No. 5171843	1112	122.5	5.2	203	4	US-09-270-767-35326	Sequence 35326, A
1040	125.5	5.3	232	6	5171843-7	Patent No. 5171843	1113	122.5	5.2	203	4	US-09-270-767-50543	Sequence 50543, A
1041	125.5	5.3	333	2	US-08-712-948-1	Sequence 1, Appl	1114	122.5	5.2	226	4	US-09-252-991A-23893	Sequence 23893, A
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1043	125.5	5.3	556	4	US-09-252-991A-27601	Sequence 27601, A	1116	122.5	5.2	601	4	US-09-252-991A-22594	Sequence 22594, A
1044	125.5	5.3	757	4	US-09-252-991A-25918	Sequence 25918, A	1117	122.5	5.2	606	4	US-09-248-796A-14276	Sequence 14276, A
1045	125.5	5.3	933	3	US-08-293-728-2	Sequence 2, Appl	1118	122.5	5.2	763	4	US-09-252-991A-30146	Sequence 30146, A
1046	125.5	5.3	933	3	US-08-421-868-2	Sequence 2, Appl	1119	122.5	5.2	930	4	US-09-198-452A-470	Sequence 470, App
1047	125.5	5.3	936	4	US-08-956-1718-5249	Sequence 5249, Ap	1120	122.5	5.2	938	4	US-09-438-185A-448	Sequence 448, App
1048	125.5	5.3	936	4	US-08-781-986A-5249	Sequence 5249, Ap	1121	122.5	5.2	1085	4	US-09-841-334A-39	Sequence 39, Appl
1049	125	5.3	254	3	US-09-128-450-26	Sequence 26, Appl	1122	122.5	5.2	1085	4	US-09-837-969A-39	Sequence 39, Appl

1123	122.5	5.2	1633	4	US-09-902-540-12892	Sequence 12892, A	1196	121	5.1	917	4	US-09-252-991A-25101	Sequence 25101, A
1124	122	5.2	253	4	US-09-431-887-7	Sequence 7, Appl	1197	121	5.1	2104	2	US-08-808-793-4	Sequence 4, Appl
1125	122	5.2	253	4	US-09-431-887-9	Sequence 9, Appl	1198	121	5.1	2104	3	US-08-772-512A-4	Sequence 4, Appl
1126	122	5.2	253	4	US-09-431-887-10	Sequence 10, Appl	1199	121	5.1	2104	4	US-09-428-371-4	Sequence 4, Appl
1127	122	5.2	253	4	US-09-431-887-11	Sequence 11, Appl	1200	120.5	5.1	83	1	US-07-609-716-101	Sequence 101, App
1128	122	5.2	253	4	US-09-431-887-12	Sequence 12, Appl	1201	120.5	5.1	83	3	US-08-475-411A-101	Sequence 101, App
1129	122	5.2	253	4	US-09-431-887-14	Sequence 14, Appl	1202	120.5	5.1	83	3	US-08-478-029A-101	Sequence 101, App
1130	122	5.2	256	4	US-09-431-887-26	Sequence 26, Appl	1203	120.5	5.1	88	4	US-09-248-796A-27988	Sequence 27988, A
1131	122	5.2	302	4	US-10-029-180-18	Sequence 18, Appl	1204	120.5	5.1	119	4	US-09-902-540-10158	Sequence 10158, A
1132	122	5.2	304	4	US-09-252-991A-23016	Sequence 23016, A	1205	120.5	5.1	133	4	US-09-270-767-39893	Sequence 39893, A
1133	122	5.2	311	4	US-09-949-016-8142	Sequence 8142, Ap	1206	120.5	5.1	133	4	US-09-270-767-55110	Sequence 55110, A
1134	122	5.2	380	4	US-09-270-767-43626	Sequence 43626, Ap	1207	120.5	5.1	133	4	US-09-252-991A-21852	Sequence 21852, A
1135	122	5.2	392	4	US-09-949-016-6078	Sequence 6078, Ap	1208	120.5	5.1	252	4	US-09-431-887-32	Sequence 32, Appl
1136	122	5.2	466	3	US-09-215-221-24	Sequence 24, Appl	1209	120.5	5.1	308	4	US-09-252-991A-27249	Sequence 27249, A
1137	122	5.2	471	4	US-09-538-092-837	Sequence 837, App	1210	120.5	5.1	374	4	US-09-252-991A-28527	Sequence 28527, A
1138	122	5.2	476	4	US-09-248-796A-18994	Sequence 18994, A	1211	120.5	5.1	394	4	US-09-252-991A-28148	Sequence 28148, A
1139	122	5.2	551	2	US-09-033-537A-1	Sequence 1, Appl	1212	120.5	5.1	408	4	US-09-543-681A-6442	Sequence 6442, Ap
1140	122	5.2	552	4	US-09-252-991A-25589	Sequence 25589, A	1213	120.5	5.1	443	4	US-09-252-991A-30036	Sequence 30036, A
1141	122	5.2	639	4	US-09-252-991A-28453	Sequence 28453, A	1214	120.5	5.1	474	4	US-09-252-991A-28084	Sequence 28084, A
1142	122	5.2	735	4	US-09-949-016-10120	Sequence 10120, A	1215	120.5	5.1	491	4	US-09-252-991A-22394	Sequence 22394, A
1143	122	5.2	989	3	US-08-213-419B-2	Sequence 2, Appl	1216	120.5	5.1	863	4	US-09-252-991A-26099	Sequence 26099, A
1144	122	5.2	989	3	US-08-213-419B-4	Sequence 4, Appl	1217	120.5	5.1	918	4	US-09-200-650B-1	Sequence 1, Appl
1145	122	5.2	1239	2	US-08-937-931-2	Sequence 2, Appl	1218	120.5	5.1	1591	4	US-09-270-767-45698	Sequence 45698, A
1146	122	5.2	1239	3	US-09-285-502-2	Sequence 2, Appl	1219	120.5	5.1	72	1	US-07-609-716-44	Sequence 44, Appl
1147	122	5.2	1239	3	US-09-709-126-2	Sequence 2, Appl	1220	120	5.1	72	3	US-08-475-411A-44	Sequence 44, Appl
1148	122	5.2	1239	3	US-09-871-385A-2	Sequence 2, Appl	1221	120	5.1	72	3	US-08-478-029A-44	Sequence 44, Appl
1149	121.5	5.1	75	1	US-07-609-716-39	Sequence 39, Appl	1222	120	5.1	171	4	US-09-489-039A-8235	Sequence 8235, Ap
1150	121.5	5.1	75	3	US-08-475-411A-39	Sequence 39, Appl	1223	120	5.1	262	4	US-09-949-016-7209	Sequence 7209, Ap
1151	121.5	5.1	75	3	US-08-478-029A-39	Sequence 39, Appl	1224	120	5.1	269	3	US-09-134-001C-3461	Sequence 3461, Ap
1152	121.5	5.1	86	1	US-07-609-716-102	Sequence 102, App	1225	120	5.1	271	4	US-09-252-991A-17292	Sequence 17292, A
1153	121.5	5.1	86	3	US-08-475-411A-102	Sequence 102, App	1226	120	5.1	337	3	US-08-469-318-148	Sequence 148, App
1154	121.5	5.1	86	3	US-08-478-029A-102	Sequence 102, App	1227	120	5.1	337	3	US-08-468-609A-148	Sequence 148, App
1155	121.5	5.1	180	4	US-10-029-180-38	Sequence 38, Appl	1228	120	5.1	337	3	US-08-446-872A-148	Sequence 148, App
1156	121.5	5.1	207	4	US-09-248-796A-21137	Sequence 21137, A	1229	120	5.1	337	4	US-08-762-227A-148	Sequence 148, App
1157	121.5	5.1	236	4	US-09-248-796A-21126	Sequence 21126, A	1230	120	5.1	337	5	PCT-US95-01185-148	Sequence 148, App
1158	121.5	5.1	236	4	US-09-252-991A-25670	Sequence 25670, A	1231	120	5.1	382	3	US-08-213-419B-19	Sequence 19, Appl
1159	121.5	5.1	286	2	US-08-712-948-2	Sequence 2, Appl	1232	120	5.1	468	4	US-09-863-901-4	Sequence 4, Appl
1160	121.5	5.1	330	4	US-09-949-016-6621	Sequence 6621, Ap	1233	120	5.1	477	4	US-09-252-991A-19831	Sequence 19831, A
1161	121.5	5.1	334	4	US-09-949-016-7988	Sequence 7988, Ap	1234	120	5.1	508	4	US-09-949-016-6316	Sequence 6316, Ap
1162	121.5	5.1	495	4	US-09-270-767-61287	Sequence 61287, A	1235	120	5.1	508	4	US-09-902-540-10562	Sequence 10562, A
1163	121.5	5.1	495	3	US-08-928-741B-4	Sequence 4, Appl	1236	120	5.1	518	4	US-09-949-016-11589	Sequence 11589, A
1164	121.5	5.1	495	3	US-09-160-567-4	Sequence 4, Appl	1237	120	5.1	518	2	US-08-818-024-4	Sequence 4, Appl
1165	121.5	5.1	495	4	US-09-710-299-4	Sequence 4, Appl	1238	120	5.1	539	3	US-09-334-775A-4	Sequence 4, Appl
1166	121.5	5.1	495	4	US-09-509-031-4	Sequence 4, Appl	1239	120	5.1	539	3	US-08-789-275-6	Sequence 6, Appl
1167	121.5	5.1	514	3	US-08-796-899-25	Sequence 25, Appl	1240	119.5	5.1	213	4	US-09-489-039A-11130	Sequence 11130, A
1168	121.5	5.1	635	4	US-09-252-991A-17122	Sequence 17122, A	1241	119.5	5.1	354	4	US-09-949-016-11550	Sequence 11550, A
1169	121.5	5.1	633	4	US-09-949-016-11117	Sequence 11117, A	1242	119.5	5.1	420	2	US-08-845-998-8	Sequence 8, Appl
1170	121.5	5.1	718	4	US-09-902-540-14365	Sequence 14365, A	1243	119.5	5.1	420	3	US-09-206-537-8	Sequence 8, Appl
1171	121	5.1	191	4	US-09-252-991A-18626	Sequence 18626, A	1244	119.5	5.1	464	4	US-09-430-854-8	Sequence 8, Appl
1172	121	5.1	194	4	US-09-431-887-13	Sequence 13, Appl	1245	119.5	5.1	531	4	US-09-949-016-9828	Sequence 9828, Ap
1173	121	5.1	252	4	US-09-252-991A-33118	Sequence 33118, A	1246	119.5	5.1	531	4	US-09-252-991A-31109	Sequence 31109, A
1174	121	5.1	283	1	US-09-270-767-46301	Sequence 46301, A	1247	119.5	5.1	650	4	US-09-248-796A-19169	Sequence 19169, A
1175	121	5.1	330	1	US-08-642-255-32	Sequence 32, Appl	1248	119.5	5.1	1427	4	US-09-252-991A-22577	Sequence 22577, A
1176	121	5.1	335	3	US-08-469-318-143	Sequence 143, App	1249	119.5	5.1	1548	4	US-09-252-991A-22301	Sequence 22301, A
1177	121	5.1	335	3	US-08-468-609A-143	Sequence 143, App	1250	119	5.0	163	4	US-09-270-767-39871	Sequence 39871, A
1178	121	5.1	335	3	US-08-446-872A-143	Sequence 143, App	1251	119	5.0	163	4	US-09-270-767-55088	Sequence 55088, A
1179	121	5.1	335	4	US-08-762-227A-143	Sequence 143, App	1252	119	5.0	213	4	US-09-252-991A-16621	Sequence 16621, A
1180	121	5.1	335	5	PCT-US95-01185-143	Sequence 143, App	1253	119	5.0	255	1	US-08-242-188-4	Sequence 4, Appl
1181	121	5.1	337	4	US-09-270-767-45762	Sequence 45762, A	1254	119	5.0	255	1	US-08-509-261A-4	Sequence 4, Appl
1182	121	5.1	367	3	US-08-213-419B-15	Sequence 15, Appl	1255	119	5.0	255	1	US-08-660-626-10	Sequence 10, Appl
1183	121	5.1	408	1	US-07-609-716-65	Sequence 65, Appl	1256	119	5.0	255	1	US-08-692-892-4	Sequence 4, Appl
1184	121	5.1	408	3	US-08-475-411A-65	Sequence 65, Appl	1257	119	5.0	255	2	US-08-713-939A-4	Sequence 4, Appl
1185	121	5.1	408	3	US-08-478-029A-65	Sequence 65, Appl	1258	119	5.0	255	2	US-08-868-162A-24	Sequence 24, Appl
1186	121	5.1	412	4	US-09-252-991A-26284	Sequence 26284, A	1259	119	5.0	255	3	US-09-031-168-10	Sequence 10, Appl
1187	121	5.1	444	4	US-09-252-991A-22448	Sequence 22448, A	1260	119	5.0	255	3	US-09-036-579-4	Sequence 4, Appl
1188	121	5.1	461	4	US-09-902-540-10506	Sequence 10506, A	1261	119	5.0	255	3	US-09-550-374-4	Sequence 4, Appl
1189	121	5.1	509	4	US-09-252-991A-32576	Sequence 32576, A	1262	119	5.0	255	4	US-09-943-906-4	Sequence 4, Appl
1190	121	5.1	546	2	US-09-067-351-1	Sequence 1, Appl	1263	119	5.0	255	4	US-09-669-516C-10	Sequence 10, Appl
1191	121	5.1	546	3	US-09-360-490-1	Sequence 1, Appl	1264	119	5.0	259	4	US-09-252-991A-21547	Sequence 21547, A
1192	121	5.1	642	4	US-09-252-991A-21889	Sequence 21889, A	1265	119	5.0	322	1	US-08-014-943A-2	Sequence 2, Appl
1193	121	5.1	686	4	US-09-252-991A-20509	Sequence 20509, A	1266	119	5.0	322	1	US-08-486-421-3	Sequence 3, Appl
1194	121	5.1	859	4	US-08-395-580-2	Sequence 2, Appl	1267	119	5.0	322	1	US-08-470-911-3	Sequence 3, Appl
1195	121	5.1	859	5	PCT-US95-02792-2	Sequence 2, Appl	1268	119	5.0	322	2	US-08-486-809-3	Sequence 3, Appl







APPLICANT: Dorman, Mary A.  
TITLE OF INVENTION: Methods for Preparing Synthetic  
TITLE OF INVENTION: Repetitive DNA  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/175,155  
FILING DATE: 29-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: A-55186-5/BIR  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1177 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-175-155-29

Query Match 17.0%; Score 402.5; DB 1; Length 1177;

Best Local Similarity 30.4%; Pred. No. 3e-20;

Matches 126; Conservative 36; Mismatches 224; Indels 27; Gaps 10;

Qy 17 GSCEAGPLOSGETSTGNIIEALCHGLDLSBQVKGKAIKEAGGAGSKVSEALGQCTR 76  
Db 771 GAGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 830  
Qy 77 EAVGTGVQR-VPGFGAALGNRVGEAAHALGNTGHEIGRQAEVDVIRHGADAVRGSQGV 135  
Db 831 AGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 890  
Qy 136 PGHSGAWETSGGHI-FGSQGGGLG-CGQGNPGLGTPWVHGYPGNSAGSGFGMNPQAPW 193  
Db 891 GSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 943  
Qy 194 GQG-GNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGSGS-----SNSGGG 247  
Db 944 GSGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003  
Qy 248 SGSQSGS---SGSGSNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS 304  
Db 1004 SGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 1063  
Qy 305 GSSESSWSSSTGSSGNHG---GSGGNGHKGPKCEKPNKNEARGSGE-SGIQGFQGGVSSN 360  
Db 1064 GAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGS 1123  
Qy 361 MREISKEGNELLLGSGDNYEGSSWSSGSGDAGVGVTNSETSPGMFNFDTFW 415  
Db 1124 AGAGSGAG---AGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 1174

RESULT 5

US-08-477-509B-64

; Sequence 64, Application US/08477509B

; Patent No. 5770697

GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W  
APPLICANT: Dorman, Mary A  
TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1177 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-477-509B-64

Query Match 17.0%; Score 402.5; DB 1; Length 1177;

Best Local Similarity 30.4%; Pred. No. 3e-20;

Matches 126; Conservative 38; Mismatches 224; Indels 27; Gaps 10;

Qy 17 GSCEAGPLOSGETSTGNIIEALCHGLDLSBQVKGKAIKEAGGAGSKVSEALGQCTR 76  
Db 771 GAGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 830  
Qy 77 EAVGTGVQR-VPGFGAALGNRVGEAAHALGNTGHEIGRQAEVDVIRHGADAVRGSQGV 135  
Db 831 AGSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 890  
Qy 136 PGHSGAWETSGGHI-FGSQGGGLG-CGQGNPGLGTPWVHGYPGNSAGSGFGMNPQAPW 193  
Db 891 GSGAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGA 943  
Qy 194 GQG-GNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGSGS-----SNSGGG 247  
Db 944 GSGAGAGSAGAGSAGAGYAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAG 1003  
Qy 248 SGSQSGS---SGSGSNDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS 304











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; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-10/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; US-08-707-237A-54

Query Match 16.9%; Score 399; DB 2; Length 1059;
Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSGEAGPLQSGERSTGNTIGELGHLGDLSEGVGKAIGKEAGGAGSKVSEALGQOTR 76
Db 666 GSG-AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 724
QY 77 EAVGTGVRQVPGFGAALGNRVGEAAHALGNTGHEIGRQAEVIRHGADAVRGSGVGP 136
Db 725 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 784
QY 137 GHSAMETSGCHGIFGSGGLG-GQGQGNPGLGTPWVHGYPGNAGSFCMNPQGAPWGQ 195
Db 785 AGSGAGAGSGAGA--GSGAGAGSGAGAGSGAGS-----GAGAGSGAGAGSGAGS 835
QY 196 GNGGPPNFTGTQGAQVAPGYSVRASNQNEGTNPPPSGGSGS-SNSGGSGSGSGS 254
Db 836 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 895
QY 255 -SGSGGNDNNNGSSG-GSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGS 312
Db 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 955
QY 313 STGSSGNHGGSGGNHKGPKCEKPGNEARSGE-SGIQGRQGVSSNNREISKEGNRL 371
Db 956 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 1015
QY 372 LGSGDNYRGQSGSGSGGDAVGVNTVNSSETSPGMFNFDTFW 415
Db 1016 GAGAGS---GAGAGSGAGAGSGAGAMPDGRYQLSAGRYHQLVM 1056

RESULT 13
US-08-806-029-10
; Sequence 10, Application US/08806029
; Patent No. 6380154
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Stedronsky, Erwin R.
; TITLE OF INVENTION: Synthetic Proteins for in vivo Drug
; TITLE OF INVENTION: Delivery and Tissue Augmentation
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fleher, Hobbach, Teet, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,029
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US 08/212,237
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-58847-2/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-806-029-10

Query Match 16.9%; Score 399; DB 3; Length 1059;
Best Local Similarity 30.4%; Pred. No. 4.7e-20;
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSGEAGPLQSGERSTGNTIGELGHLGDLSEGVGKAIGKEAGGAGSKVSEALGQOTR 76
Db 666 GSG-AGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 724
QY 77 EAVGTGVRQVPGFGAALGNRVGEAAHALGNTGHEIGRQAEVIRHGADAVRGSGVGP 136
Db 725 AGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAG 784
QY 137 GHSAMETSGCHGIFGSGGLG-GQGQGNPGLGTPWVHGYPGNAGSFCMNPQGAPWGQ 195
Db 785 AGSGAGAGSGAGA--GSGAGAGSGAGAGSGAGS-----GAGAGSGAGAGSGAGS 835
QY 196 GNGGPPNFTGTQGAQVAPGYSVRASNQNEGTNPPPSGGSGS-SNSGGSGSGSGS 254
Db 836 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 895
QY 255 -SGSGGNDNNNGSSG-GSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGS 312
Db 896 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 955
QY 313 STGSSGNHGGSGGNHKGPKCEKPGNEARSGE-SGIQGRQGVSSNNREISKEGNRL 371
Db 956 GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS 1015
QY 372 LGSGDNYRGQSGSGSGGDAVGVNTVNSSETSPGMFNFDTFW 415
Db 1016 GAGAGS---GAGAGSGAGAGSGAGAMPDGRYQLSAGRYHQLVM 1056

RESULT 14
US-08-477-509B-83
; Sequence 83, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W
; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/477,509B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-7/RPT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 83:  
LENGTH: 1101 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-509B-83

Query Match 16.9%; Score 399; DB 1; Length 1101;  
Best Local Similarity 30.4%; Pred. No. 4.9e-20;  
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSSEAGPLQSGESTGTNIGALHGLDLSGVGKAIGKEAGGAAGSKVSEALGQCTR 76  
DB 708 GSG-AGAGSGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 766  
QY 77 EAVGTGVRQVPGFGAALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWGVP 136  
DB 767 AGSGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 826  
QY 137 GHSAGMETSGHGIFGSGGLG-QGQGNPGLGTPTWVHGYPGNAGSFGMNPQAPWGQ 195  
DB 827 AGSGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 877  
QY 196 GNGGPPNFTNTQGAQVAPQYGSVRASNQNCGTNPPTPSGGGS-SNSGGSGSGSGS 254  
DB 878 GAGAGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 937  
QY 255 -SGSGGNDNNSSG-SGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSS 312  
DB 938 GAGAGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 997  
QY 313 STGSSGNGHGGGNGHFKPCCKPQNEARSGSE-SGIOGFRGQGVSSNNREISKEGNRL 371  
DB 998 GAGAGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1057  
QY 372 LGSGDNYRCGSSGSGGDDAVGGVNTVNSGTPGMFNFTTW 415

Db 1058 GAGAGS---GAGAGSGAGAGGAGAMPGRYQLSAGRYHYQLVW 1098

RESULT 15

US-08-482-085B-83  
Sequence 83, Application US/08482085B  
Patent No. 6018030  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Richardson, Charles  
APPLICANT: Chambers, James  
APPLICANT: Causey, Stuart  
APPLICANT: Pollock, Thomas J.  
APPLICANT: Cappello, Joseph  
APPLICANT: Crissman, John W.  
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive  
UNITS OF AMINO ACIDS AND DNA SEQUENCES ENCODING THE SAME  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RPT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1101 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-482-085B-83

Query Match 16.9%; Score 399; DB 3; Length 1101;  
Best Local Similarity 30.4%; Pred. No. 4.9e-20;  
Matches 123; Conservative 43; Mismatches 220; Indels 18; Gaps 9;

QY 17 GSSEAGPLQSGESTGTNIGALHGLDLSGVGKAIGKEAGGAAGSKVSEALGQCTR 76  
DB 708 GSG-AGAGSGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 766  
QY 77 EAVGTGVRQVPGFGAALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWGVP 136  
DB 767 AGSGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 826

Qy	137	GHSGAWETSGHGTFGSGGLG-CQGGNPGGLGTPWVHGYPGNSAGSGFQMNPOGAPWQ	195
Db	827	AGSGAGAGSGAGA--GSGAGAGSGAGAGAGS-----GAGAGAGAGSGAGAGS	877
Qy	196	GGNGGPPNFGTNTQGAVAQFCYGSVRASNQNEGCTNPPPSGGGGS-SNSGGGSGSQSGS	254
Db	878	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	937
Qy	255	-SGSGSGNDNNNGSSG-GSSSGSSSGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSGS	312
Db	938	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	997
Qy	313	STGSSSGNHGSGGGNGHKPCCKPGNEARGSG-SGIQGFRCQGVSSNMREISKEGNRL	371
Db	998	GAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGSGAGAGS	1057
Qy	372	LGGSGDNYRQGGSGGSDAVGGVNTVNSETSPGMFNFTFW	415
Db	1058	GAGAGS---GAGAGSGAGAGSGAGAGMDPGRYQLSAGRYHYQLVW	1098

Search completed: May 15, 2005, 06:04:30  
Job time : 73 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2005, 06:02:23 ; Search time 92 Seconds  
(without alignments)  
1597.639 Million cell updates/sec

Perfect score: 2363

Sequence: 1 MKFGPLACLLALCLSGE.....KLGFINWDAINKDQSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
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- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
146	2363	100.0	440	14	US-10-066-269-106
516	2363	100.0	440	14	US-10-223-085-150
522	2363	100.0	440	14	US-10-219-065-156
565	2363	100.0	440	14	US-10-223-084-150
566	2363	100.0	440	14	US-10-223-088-150
567	2363	100.0	440	14	US-10-223-090-150
573	2363	100.0	440	14	US-10-223-087-150
586	2363	100.0	440	14	US-10-223-089-150
592	2363	100.0	440	14	US-10-223-089-150
618	2363	100.0	440	14	US-10-174-587-202
688	2363	100.0	440	14	US-10-063-742-52
764	2363	100.0	440	14	US-10-013-909A-52
769	2363	100.0	440	14	US-10-223-081-150
807	2363	100.0	440	14	US-10-223-082-150

839	2363	100.0	440	15	US-10-305-654-150	Sequence 150, App
848	2363	100.0	440	15	US-10-081-056-150	Sequence 150, App
859	2363	100.0	440	17	US-10-972-317-52	Sequence 52, Appl
860	2030	85.9	386	14	US-10-050-704-100	Sequence 100, App
861	2030	85.9	386	16	US-10-798-512-100	Sequence 100, App
862	450.5	19.1	1079	10	US-09-820-843A-20	Sequence 20, Appl
863	439.5	18.6	1306	15	US-10-282-122A-64405	Sequence 64405, A
864	415.5	17.6	1381	15	US-10-282-122A-64895	Sequence 64895, A
865	412.5	17.5	484	10	US-09-820-843A-19	Sequence 19, Appl
866	412.5	17.5	484	15	US-10-282-122A-64867	Sequence 64867, A
867	406.5	17.2	357	9	US-09-864-761-35807	Sequence 35807, A
868	404.5	17.1	532	15	US-10-282-122A-64658	Sequence 64658, A
869	402.5	17.0	1136	8	US-08-806-029-9	Sequence 9, Appl
870	402.5	17.0	1177	14	US-10-096-986-64	Sequence 64, Appl
871	399	16.9	1059	8	US-08-806-029-10	Sequence 10, Appl
872	399	16.9	1101	14	US-10-096-986-83	Sequence 83, Appl
873	392.5	16.6	923	15	US-10-282-122A-64474	Sequence 64474, A
874	386	16.3	778	15	US-10-282-122A-64751	Sequence 64751, A
875	383	16.2	641	14	US-10-138-098-52	Sequence 52, Appl
876	383	16.2	641	14	US-10-294-804-4	Sequence 4, Appl
877	383	16.2	641	15	US-10-225-838B-22	Sequence 22, Appl
878	383	16.2	641	16	US-10-732-694-11	Sequence 11, Appl
879	383	16.2	641	17	US-10-476-615-52	Sequence 52, Appl
880	380.5	16.1	837	15	US-10-282-122A-64362	Sequence 64362, A
881	378	16.0	588	15	US-10-282-122A-64869	Sequence 64869, A
882	378	16.0	588	17	US-10-481-563A-4	Sequence 4, Appl
883	378	16.0	646	16	US-10-406-832-27	Sequence 27, Appl
884	378	16.0	646	17	US-10-893-588-27	Sequence 27, Appl
885	375	15.9	914	15	US-10-282-122A-64605	Sequence 64605, A
886	373.5	15.8	584	15	US-10-282-122A-64903	Sequence 64903, A
887	373.5	15.8	667	15	US-10-282-122A-64494	Sequence 64494, A
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889	371	15.7	615	15	US-10-282-122A-64786	Sequence 64786, A
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891	371	15.7	651	14	US-10-414-760-1	Sequence 1, Appl
892	371	15.7	651	17	US-10-887-100-1	Sequence 1, Appl
893	370.5	15.7	491	15	US-10-282-122A-64558	Sequence 64558, A
894	368	15.6	420	16	US-10-437-963-201378	Sequence 201378, A
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896	366	15.5	691	17	US-10-488-056-48	Sequence 48, Appl
897	366	15.5	766	14	US-10-096-986-88	Sequence 88, Appl
898	366	15.5	979	14	US-10-096-986-89	Sequence 89, Appl
899	365	15.4	576	15	US-10-282-122A-64547	Sequence 64547, A
900	365	15.4	591	15	US-10-282-122A-64363	Sequence 64363, A
901	364.5	15.4	2018	14	US-10-096-986-80	Sequence 80, Appl
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903	363	15.4	639	15	US-10-282-122A-64609	Sequence 64609, A
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905	359.5	15.2	1011	15	US-10-282-122A-64589	Sequence 64589, A
906	359	15.2	525	17	US-10-488-056-54	Sequence 54, Appl
907	359	15.2	854	17	US-10-488-056-47	Sequence 47, Appl
908	358.5	15.2	486	16	US-10-437-963-117435	Sequence 117435, A
909	358.5	15.2	2055	14	US-10-096-986-81	Sequence 81, Appl
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914	358	15.2	606	17	US-10-887-100-6	Sequence 6, Appl
915	358	15.2	606	17	US-10-887-100-8	Sequence 8, Appl
916	358	15.2	819	14	US-10-414-760-13	Sequence 13, Appl
917	358	15.2	818	14	US-10-414-760-22	Sequence 22, Appl
918	358	15.2	1617	14	US-10-414-760-14	Sequence 14, Appl
919	358	15.2	1626	14	US-10-414-760-24	Sequence 24, Appl
920	353	14.9	505	15	US-10-282-122A-62341	Sequence 62341, A
921	352	14.9	603	15	US-10-282-122A-64537	Sequence 64537, A
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925	350.5	14.8	2257	14	US-10-096-986-82	Sequence 82, Appl
926	349	14.8	618	15	US-10-282-122A-64608	Sequence 64608, A
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932	342.5	14.5	629	17	US-10-893-588-29	Sequence 29, Appl	1029	301.5	12.8	285	16	US-10-437-963-187773	Sequence 187773
933	342	14.5	535	15	US-10-282-122A-64613	Sequence 64613, A	1030	300.5	12.7	768	8	US-08-806-029-35	Sequence 35, Appl
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935	337	14.3	1002	17	US-10-488-056-46	Sequence 46, Appl	1032	299	12.7	373	17	US-10-488-056-40	Sequence 40, Appl
936	336	14.2	1169	8	US-08-806-029-33	Sequence 33, Appl	1033	297.5	12.6	270	16	US-10-437-963-122263	Sequence 122263
937	334	14.1	498	15	US-10-225-838B-21	Sequence 21, Appl	1034	296.5	12.5	1024	8	US-08-806-029-31	Sequence 31, Appl
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940	329	13.9	780	17	US-10-441-963-19	Sequence 19, Appl	1037	294	12.4	529	17	US-10-887-100-2	Sequence 2, Appl
941	329	13.9	780	16	US-10-800-179-19	Sequence 19, Appl	1038	294	12.4	821	15	US-10-292-798-1370	Sequence 1370, Ap
942	327.5	13.9	334	14	US-10-259-678-728	Sequence 728, App	1039	293.5	12.4	611	14	US-10-086-510-4	Sequence 4, Appl
943	326	13.8	422	16	US-10-437-963-121579	Sequence 121579, A	1040	293	12.4	256	10	US-09-820-843A-18	Sequence 18, Appl
944	325.5	13.8	439	15	US-10-282-122A-64905	Sequence 64905, A	1041	292	12.4	912	17	US-10-488-056-50	Sequence 50, Appl
945	324	13.7	1038	16	US-10-800-179-30	Sequence 30, Appl	1042	290.5	12.3	406	14	US-10-156-761-14828	Sequence 14828, A
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948	320	13.5	594	15	US-10-282-122A-64397	Sequence 64397, A	1045	289	12.2	627	16	US-10-406-832-28	Sequence 28, Appl
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950	319.5	13.5	318	14	US-10-259-678-727	Sequence 727, App	1047	288.5	12.2	953	8	US-08-806-029-14	Sequence 14, Appl
951	318	13.4	884	16	US-10-800-179-25	Sequence 25, Appl	1048	286	12.1	454	16	US-10-767-701-45105	Sequence 45105, A
952	317.5	13.4	988	8	US-08-806-029-28	Sequence 28, Appl	1049	286	12.1	563	17	US-10-488-056-43	Sequence 43, Appl
953	315.5	13.4	965	16	US-10-800-179-31	Sequence 31, Appl	1050	285.5	12.1	234	16	US-10-767-701-45603	Sequence 45603, A
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973	309.5	13.1	200	10	US-09-990-940-21	Sequence 21, Appl	1058	280	11.8	1466	14	US-10-177-293-68	Sequence 68, Appl
974	309.5	13.1	200	10	US-09-989-981A-13	Sequence 13, Appl	1059	280	11.8	1466	14	US-10-301-822-33	Sequence 33, Appl
975	309.5	13.1	200	10	US-09-850-948-29	Sequence 29, Appl	1060	280	11.8	1466	15	US-10-257-021-72	Sequence 72, Appl
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977	309.5	13.1	200	14	US-10-026-331B-21	Sequence 21, Appl	1062	280	11.8	1466	16	US-10-358-024-3	Sequence 3, Appl
978	309.5	13.1	200	14	US-10-026-021-8	Sequence 8, Appl	1063	280	11.8	1466	16	US-10-734-564-103	Sequence 103, App
979	309.5	13.1	200	14	US-10-160-663-3	Sequence 3, Appl	1064	277.5	11.7	1036	17	US-10-741-849-7179	Sequence 7179, Ap
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981	309.5	13.1	200	14	US-10-071-838-15	Sequence 15, Appl	1066	277.5	11.7	332	15	US-10-437-963-137540	Sequence 137540,
982	309.5	13.1	200	14	US-10-094-417-25	Sequence 25, Appl	1067	277	11.7	232	15	US-10-282-122A-68044	Sequence 68044, A
983	309.5	13.1	200	14	US-10-188-403-13	Sequence 13, Appl	1068	276	11.7	1040	15	US-10-104-889-30	Sequence 30, Appl
984	309.5	13.1	200	14	US-10-273-575-29	Sequence 29, Appl	1069	276	11.7	1040	15	US-10-104-889-32	Sequence 32, Appl
985	309.5	13.1	200	14	US-10-233-098-5	Sequence 5, Appl	1070	276	11.7	1078	14	US-10-058-124-21	Sequence 21, Appl
986	309.5	13.1	200	14	US-10-245-850-3	Sequence 3, Appl	1071	276	11.7	1366	10	US-09-918-715-214	Sequence 214, App
987	309.5	13.1	200	14	US-10-293-582-27	Sequence 27, Appl	1072	276	11.7	1366	10	US-09-918-715-234	Sequence 234, App
988	309.5	13.1	200	14	US-10-100-818-14	Sequence 14, Appl	1073	276	11.7	1366	14	US-09-918-715-265	Sequence 265, App
989	309.5	13.1	200	14	US-10-237-467-18	Sequence 18, Appl	1074	276	11.7	1366	14	US-10-171-311-38	Sequence 38, Appl
990	309.5	13.1	200	14	US-10-321-204-54	Sequence 54, Appl	1075	276	11.7	1366	14	US-10-301-822-31	Sequence 31, Appl
991	309.5	13.1	200	14	US-10-179-766-12	Sequence 12, Appl	1076	276	11.7	1366	16	US-10-734-564-95	Sequence 95, Appl
992	309.5	13.1	200	14	US-10-123-568-4	Sequence 4, Appl	1077	275	11.6	208	14	US-10-029-386-33055	Sequence 33055, A
993	309.5	13.1	200	14	US-10-123-731-10	Sequence 10, Appl	1078	275	11.6	525	15	US-10-755-889-650	Sequence 650, App
994	309.5	13.1	200	15	US-10-308-393-53	Sequence 53, Appl	1079	274	11.6	593	15	US-10-435-696-50	Sequence 50, Appl
995	309.5	13.1	200	15	US-10-352-724-5	Sequence 5, Appl	1080	272.5	11.5	696	15	US-10-441-965-21	Sequence 21, Appl
996	309.5	13.1	200	15	US-10-328-916-57	Sequence 57, Appl	1081	272	11.5	696	8	US-08-806-029-36	Sequence 36, Appl
997	309.5	13.1	200	15	US-10-452-015-3	Sequence 3, Appl	1082	272	11.5	696	15	US-10-441-965-23	Sequence 23, Appl
998	309.5	13.1	200	15	US-10-364-861-94	Sequence 94, Appl	1083	272	11.5	750	8	US-08-806-029-25	Sequence 25, Appl
999	309.5	13.1	200	15	US-10-231-956A-521	Sequence 521, App	1084	271.5	11.5	370	15	US-10-282-122A-64566	Sequence 64566, A
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1001	309.5	13.1	200	15	US-10-459-190-24	Sequence 24, Appl	1086	270.5	11.4	1268	16	US-10-437-963-108730	Sequence 108730
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1004	309.5	13.1	200	16	US-10-620-052A-78	Sequence 78, Appl	1089	270.5	11.4	1366	16	US-10-788-792-153	Sequence 153, App
1005	309.5	13.1	200	17	US-10-616-403-7	Sequence 7, Appl	1090	270	11.4	920	15	US-10-292-798-1514	Sequence 1514, Ap
1006	309	13.1	201	9	US-09-818-094-40	Sequence 40, Appl	1091	270	11.4	1466	15	US-10-402-089-12	Sequence 12, Appl
1007	309	13.1	201	9	US-09-848-990-22	Sequence 22, Appl	1092	270	11.4	1466	15	US-10-402-072A-12	Sequence 12, Appl
1008	309	13.1	201	9	US-09-760-364-14	Sequence 14, Appl	1093	269.5	11.4	360	17	US-10-425-114-54522	Sequence 54522, A
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1011	307.5	13.0	1670	14	US-10-123-155-325	Sequence 325, App	1096	268.5	11.4	1027	15	US-10-360-101-221	Sequence 221, App
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1024	304.5	12.9	889	8	US-08-806-029-19	Sequence 19, Appl	1098	267.5	11.3	1366	15	US-10-257-021-76	Sequence 76, Appl
1025	302	12.8	592	15	US-10-369-493-17534	Sequence 17534, A	1099	266	11.3	1088	16	US-10-437-963-158455	Sequence 158455,



1100	265.5	11.2	265	16	US-10-437-963-154907	Sequence 154907,	1185	244.5	10.3	1464	16	US-10-788-792-150	Sequence 150, App
1101	265.5	11.2	568	14	US-10-086-510-5	Sequence 5, Appl	1186	244	10.3	266	14	US-10-148-306-20	Sequence 20, Appl
1102	265.5	11.2	1366	15	US-10-402-089-10	Sequence 10, Appl	1187	244	10.3	266	14	US-10-639-286-12	Sequence 12, Appl
1103	265.5	11.2	1366	15	US-10-402-072A-10	Sequence 10, Appl	1188	244	10.3	591	14	US-10-233-553-23	Sequence 23, Appl
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PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 8
ID ABL95635 standard; cDNA; 1734 BP.
DE Human angiogenesis related cDNA PRO1411 SEQ ID NO: 149.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERR ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 9
ID ACA89475 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 10  
ID ACA73485 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US20030361146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 11  
ID ACA05800 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 12  
ID ACA66634 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO protein #101.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 13  
ID ACA91189 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 14  
ID ACD81566 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO411.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 15  
ID ACF20209 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 16  
ID ACF19595 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 17  
ID ACD1883 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 18  
ID ACF13048 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036160-A1.

PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 19  
ID ACD25151 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 20  
ID ACF00200 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 21  
ID ACA60388 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 22  
ID ACA7257 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 23  
ID ACD04781 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 24  
ID ACD18242 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 25  
ID ACD08249 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 26  
ID ACA88683 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 27  
ID ACA04997 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

```
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACA70125 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036134-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACD12347 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ACC74262 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027275-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ACD15890 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003027334-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 32
ID ACD25458 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 33
ID ACD17935 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036123-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 34
ID ACC98222 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036148-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 35
ID ACD21576 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040060-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 36
ID ACD18643 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044916-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 37
ID ACAS5835 standard; cDNA; 1734 BP.
DE cDNA encoding human secreted polypeptide PRO1411.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 38
ID ABX98253 standard; cDNA; 1734 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 201.
PN US2003036156-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 39
ID ACD14004 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032117-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 40
ID ACD09784 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036128-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 41
ID ACC88529 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027266-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 42
ID ACD21269 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 43
ID ABX75641 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1411.
PN US2003022298-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 44
ID ACAS4011 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #26.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 45	Query Match:	100.00%	Indels:	0
ID ABX97844 standard; cDNA; 1734 BP.	RESULT 54			
DE Human PRO polynucleotide #101.	ID ACA91275 standard; cDNA; 1734 BP.			
PN US2003032102-A1.	DE cDNA encoding human PRO polypeptide #26.			
PD 13-FEB-2003.	PN US2003018168-A1.			
Percent Similarity: 100.00%	PD 23-JAN-2003.			
Best Local Similarity: 100.00%	PA (GETH ) GENENTECH INC.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 46	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACA97320 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Novel human secreted and transmembrane protein PRO1411 cDNA.	RESULT 55			
PN US2003036117-A1.	ID ACC89143 standard; cDNA; 1734 BP.			
PD 20-FEB-2003.	DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.			
Percent Similarity: 100.00%	PN US2003027269-A1.			
Best Local Similarity: 100.00%	PD 06-FEB-2003.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 47	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACA57783 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Human PRO1411 cDNA.	RESULT 56			
PN US2003036143-A1.	ID ACC86499 standard; cDNA; 1734 BP.			
PD 20-FEB-2003.	DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.			
Percent Similarity: 100.00%	PN US2003027268-A1.			
Best Local Similarity: 100.00%	PD 06-FEB-2003.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 48	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACD14311 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Human PRO polynucleotide #101.	RESULT 57			
PN US2003032130-A1.	ID ACC89757 standard; cDNA; 1734 BP.			
PD 13-FEB-2003.	DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.			
Percent Similarity: 100.00%	PN US2003027274-A1.			
Best Local Similarity: 100.00%	PD 06-FEB-2003.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 49	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACC91094 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.	RESULT 58			
PN US2003032138-A1.	ID ACC92936 standard; cDNA; 1734 BP.			
PD 13-FEB-2003.	DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.			
PA (GETH ) GENENTECH INC.	PN US2003032135-A1.			
Percent Similarity: 100.00%	PD 13-FEB-2003.			
Best Local Similarity: 100.00%	PA (GETH ) GENENTECH INC.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 50	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACC88836 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.	RESULT 59			
PN US2003036132-A1.	ID ACA72564 standard; cDNA; 1734 BP.			
PD 20-FEB-2003.	DE Human PRO polynucleotide #101.			
Percent Similarity: 100.00%	PN US2003022295-A1.			
Best Local Similarity: 100.00%	PD 30-JAN-2003.			
Query Match: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
RESULT 51	Best Local Similarity: 100.00%	Mismatches: 0		
ID ACD07033 standard; cDNA; 1734 BP.	Query Match: 100.00%	Indels: 0		
DE Human PRO polynucleotide #101.	RESULT 60			
PN US2003008353-A1.	ID ACA89082 standard; cDNA; 1734 BP.			
PD 09-JAN-2003.	DE Human secreted/transmembrane protein (PRO) cDNA #101.			
PA (GETH ) GENENTECH INC.	PN US2003022297-A1.			
Percent Similarity: 100.00%	PD 30-JAN-2003.			
Best Local Similarity: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
Query Match: 100.00%	Best Local Similarity: 100.00%	Mismatches: 0		
RESULT 52	Query Match: 100.00%	Indels: 0		
ID ACA67484 standard; cDNA; 1734 BP.	RESULT 61			
DE Human PRO polynucleotide #101.	ID ACA69818 standard; cDNA; 1734 BP.			
PN US2003017542-A1.	DE Human secreted/transmembrane protein (PRO) cDNA #101.			
PD 23-JAN-2003.	PN US2003032105-A1.			
Percent Similarity: 100.00%	PD 13-FEB-2003.			
Best Local Similarity: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
Query Match: 100.00%	Best Local Similarity: 100.00%	Mismatches: 0		
RESULT 53	Query Match: 100.00%	Indels: 0		
ID ACC81539 standard; cDNA; 1734 BP.	RESULT 62			
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.	ID ACA96961 standard; cDNA; 1734 BP.			
PN US2003032137-A1.	DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
PD 13-FEB-2003.	PN US2003032123-A1.			
Percent Similarity: 100.00%	PD 13-FEB-2003.			
Best Local Similarity: 100.00%	Percent Similarity: 100.00%	Conservative: 0		
Query Match: 100.00%	Best Local Similarity: 100.00%	Mismatches: 0		
	Query Match: 100.00%	Indels: 0		
	Percent Similarity: 100.00%	Conservative: 0		

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 63
ID ACA90957 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 64
ID ACA70739 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032111-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ACA95249 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 66
ID ACC86192 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US200307283-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 67
ID ACD45174 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane polypeptide PRO411 cDNA.
PN US200309012-A1.
PD 09-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ACC90064 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ACD12672 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US20030316125-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ACF19902 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ABX76846 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ACA60527 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ACA73178 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ACA68721 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ACA74565 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ACA04517 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003032062-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ACA70432 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ACD14618 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003040066-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ACA93722 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003045684-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ACA68290 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
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PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 81
ID ABX98755 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 82
ID ACA67296 standard; cDNA; 1734 BP.
DE cDNA encoding human secreted polypeptide PRO1411.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 83
ID ACA9556 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 84
ID ACA9556 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 85
ID ACD04474 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 86
ID ACA68574 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 87
ID ACC87915 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 88
ID ACF12577 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040058-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 89
ID ACB66269 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 90
ID ACA96292 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003017540-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 91
ID ACA65066 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032106-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 92
ID ACA73792 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032129-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 93
ID ACA74204 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 94
ID ACA96599 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032103-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 95
ID ACD10705 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003032107-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 96
ID ACC91401 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032139-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 97
ID ACD02736 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003022301-A1.
PD 30-JAN-2003.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
RESULT 98
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ID ACC97301 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ACC85885 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027262-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ACA55373 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032110-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 101
ID ACA94190 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036142-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 102
ID ACA97934 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003036145-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 103
ID ACA91436 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 104
ID ACA90650 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 105
ID ACD16197 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044931-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 106
ID ACD17358 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036150-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 107
ID ACC92015 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040069-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 108
ID ACD02323 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 109
ID ACA74872 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003022293-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 110
ID ACA91743 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032128-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 111
ID ACA89314 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 112
ID ACA71387 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032116-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 113
ID ACC90787 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032122-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 114
ID ACA65797 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO protein #101.
PN US2003036139-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 115
ID ACA68951 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
RESULT 116
ID ACA94942 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003017541-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 117
ID ACD16504 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003017543-A1.
PD 23-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 118
ID ACD15583 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036152-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 119
ID ACA98473 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 120
ID ABX16686 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein #101.
PN US2002127594-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 121
ID ACA63398 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #26.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 122
ID ACA97627 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003032115-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ACA65658 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ACA99076 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ACC91708 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ACD11119 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ACD14969 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044922-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 128
ID ACD11733 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032118-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ACC95862 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036135-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ACF16425 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ACF02543 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ACF02850 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ACF02543 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ACF02543 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 133
ID ACF21437 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ACF10121 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ACF78014 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ACD46719 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ACD49482 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ACF28249 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ACD88939 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ACD84334 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ACD99108 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADA77953 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ACF48850 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ACD09170 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 145
ID ACF11963 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 146
ID ACF41197 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 147
ID ACF15811 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 148
ID ACF16118 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 149
ID ABT44303 standard; cDNA; 1734 BP.
DE Human PRO1411 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 150  
ID ADB17108 standard; cDNA; 1734 BP.  
DE Human cDNA clone (seqid 51) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 151  
ID ACD31945 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 152  
ID ACF18753 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 153  
ID ACF09200 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 154  
ID ACF78321 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 155  
ID ACF51920 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 156  
ID ACF26407 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 157  
ID ACF24200 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0

Query Match: 100.00%      Indels: 0  
RESULT 158  
ID ACF63511 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 159  
ID ACF50385 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 160  
ID ACH07856 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 161  
ID ACF13662 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 162  
ID ACD41588 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 163  
ID ACF32001 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 164  
ID ACF23279 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0  
RESULT 165  
ID ACF3969 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%      Conservative: 0  
Best Local Similarity: 100.00%      Mismatches: 0  
Query Match: 100.00%      Indels: 0

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RESULT 166
ID ACD45491 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ACF53148 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168
ID ACF77093 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ACF45166 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ACF29784 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ACD89860 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ACD84641 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ACD98801 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ACD98801 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ACF76786 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ACF49771 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ACF50078 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ACD09477 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ACD08556 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ACH03601 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ACF12270 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036330-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ACC94778 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 183
ID ACD22497 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054470-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 184
ID ACF15197 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044917-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ACC97292 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044929-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ACC92322 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059880-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ACF13969 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064465-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ACF14276 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054478-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ACF09507 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068718-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ACD68275 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003073130-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ACD45798 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064454-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ACD47947 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003064461-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ACD67678 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003068724-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ACF25486 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068727-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ACF29170 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068772-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ACD84948 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068714-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ACD84027 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003068758-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ACD88018 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068776-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ACF30705 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
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PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 200
ID ACF32308 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 201
ID ACH11968 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049788-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 202
ID ACH12275 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 203
ID ADA19913 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 204
ID ACD40667 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 205
ID ADB17296 standard; cDNA; 1734 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 206
ID ACF18139 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 207
ID ACF08586 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 208
ID ACF31387 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 209
ID ACF52227 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 210
ID ACD50096 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 211
ID ACF38799 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 212
ID ACF6714 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 213
ID ACF24814 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 214
ID ACF46394 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 215
ID ACF27942 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ACD89246 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ACF63818 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ACF60458 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ACH12582 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ACH10005 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ACD03860 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ACD10398 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ACD12040 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ACF42425 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049751-A1.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ACP18446 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ACF02236 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ACP21744 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ACF10428 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ACF33880 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ACF44842 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ACD90474 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ACD91087 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049751-A1.
```



PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 233  
ID ACF30398 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 234  
ID ACD87097 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 235  
ID ACF60151 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 236  
ID ACF46701 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 237  
ID ACF75558 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 238  
ID ADA79745 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 239  
ID ACF17218 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 240  
ID ACF22972 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 241  
ID ACF07972 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 242  
ID ACF08279 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 243  
ID ACF40583 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 244  
ID ACP53762 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 245  
ID ACD47026 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 246  
ID ACF47929 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 247  
ID ACF47315 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 248  
ID ADA47277 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 249  
ID ADA47277 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

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ID ACF46087 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ACD86176 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 251
ID ACF52534 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID ACF52841 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 253
ID ACF64834 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 254
ID ACF76479 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 255
ID ACF61379 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 256
ID ACF61686 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 257
ID ACD30717 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032125-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 258
ID ACD31638 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 259
ID ACD32559 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 260
ID ADA20085 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 261
ID ACD82115 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 262
ID ACF17525 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 263
ID ACF07358 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 264
ID ACF20516 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 265
ID ACF21130 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 266
ID ACF20823 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073172-A1.
PD 17-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 267
ID ACD47640 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 268
ID ACF47622 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 269
ID ACF53455 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 270
ID ACD86790 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 271
ID ACH05038 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 272
ID ACF44535 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 273
ID ADA81472 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 274
ID ACF50692 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032121-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
```

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Query Match: 100.00% Indels: 0
RESULT 275
ID ACD24537 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044920-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 276
ID ACD39740 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003027265-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 277
ID ACD40047 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 278
ID ACF13355 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 279
ID ACF03157 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 280
ID ACF78628 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 281
ID ACF11349 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073171-A1.
PD 17-APR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 282
ID ACF50692 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032121-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 283  
ID ACF34187 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 284  
ID ACD46412 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 285  
ID ACD48254 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 286  
ID ACF27635 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 287  
ID ACF24507 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 288  
ID ACD8562 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 289  
ID ACD90167 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 290  
ID ACD83720 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
RESULT 291  
ID ACF49157 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 292  
ID ACH07242 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 293  
ID ACH07549 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 294  
ID ACH08163 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 295  
ID ACH11354 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 296  
ID ACH11661 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 297  
ID ACH10312 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 298  
ID ACF01315 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 299  
ID ACF40890 standard; cDNA; 1734 BP.



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RESULT 316
ID ADA83270 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 317
ID ACC92629 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 318
ID ACC93243 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 319
ID ACF19288 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 320
ID ACD12979 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 321
ID ACF06437 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 322
ID ACC94471 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 323
ID ACC97899 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 324
ID ACC94164 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003022720-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 325
ID ABT44586 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 326
ID ACF42118 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 327
ID ACD31024 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 328
ID ACD43053 standard; cDNA; 1734 BP.
DE CDNA encoding human PRO polypeptide #101.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 329
ID ACD43360 standard; cDNA; 1734 BP.
DE CDNA encoding human PRO polypeptide #101.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 330
ID ACF14890 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 331
ID ACF01622 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 332
ID ACF31694 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 333
ID ACD67371 standard; cDNA; 1734 BP.
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DE cDNA encoding human PRO polypeptide #101.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 334
ID ACD48561 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 335
ID ACD48868 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 336
ID ACF51306 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 337
ID ACF54069 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 338
ID ACF25793 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 339
ID ACF39106 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 340
ID ACF28863 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 341
ID ACD90780 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 342
ID ACD86483 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 343
ID ACH05345 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 344
ID ACF65141 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 345
ID ADB20313 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 346
ID ACF43614 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 347
ID ACH09084 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 348
ID ACH09391 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 349
ID ADA78565 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003073181-A1.
PD 17-APR-2003.
```

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 350  
ID ACD8253 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 351  
ID ACF09814 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 352  
ID ADA00382 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 411 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 353  
ID ACF50999 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 354  
ID ACF23893 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 355  
ID ACD88325 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 356  
ID ACH09698 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 357  
ID ACH10619 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 358  
ID ACD11426 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 359  
ID ACC96476 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 360  
ID ACH04377 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 361  
ID ACC98506 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 362  
ID ACF41811 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 363  
ID ACF16732 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 364  
ID ACD3252 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 365  
ID ACD30410 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 366  
ID ACD41281 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064467-A1.



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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 367
ID ACF07665 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 368
ID ACF31080 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 369
ID ACF77400 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 370
ID ACF11042 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 371
ID ACF32922 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 372
ID ACF26100 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 373
ID ACD83413 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 374
ID ACF23586 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 375
ID ACF43000 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 376
ID ACF43307 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 377
ID ACH05959 standard; cDNA; 1734 BP.
DE CDNA encoding human PRO polypeptide #101.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 378
ID ACH08777 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 379
ID ACC90371 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 380
ID ACF10735 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 381
ID ACC93550 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 382
ID ACC96169 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 383
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ID ACD24844 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044921-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 384
ID ACF01929 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 385
ID ACF22051 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 386
ID ACF22665 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 387
ID ACF08893 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 388
ID ACF33229 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 389
ID ACF54683 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 390
ID ACF48543 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 391
ID ACD47333 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036151-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
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PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 392
ID ACD49175 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 393
ID ACF37878 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 394
ID ACF30091 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 395
ID ACD87404 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 396
ID ACF61993 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104538-A1.
PD 05-JUN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 397
ID ACH10926 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 398
ID ACD10091 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036158-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 399
ID ACD16816 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003036151-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 400
ID ACC99113 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040067-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 401
ID ACF00507 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054456-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 402
ID ACD40974 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054482-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 403
ID ACF14593 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054457-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 404
ID ACF22358 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003059883-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 405
ID ACF78935 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003049764-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 406
ID ACD67921 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003073129-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 407
ID ACF11656 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073177-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 408
ID ACF44228 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104556-A1.
ID ACF51613 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064442-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 409
ID ACF33536 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064450-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 410
ID ACD49789 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068731-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 411
ID ACF37571 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068683-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 412
ID ACF28556 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068754-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 413
ID ACD88632 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068691-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 414
ID ACF75251 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003096351-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 415
ID ACF61072 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003096358-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 416
ID ACF44228 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104556-A1.
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PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 417  
ID ACH08470 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 418  
ID ACC93857 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 419  
ID ACD20962 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 420  
ID ACF06744 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 421  
ID ACD20655 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040077-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 422  
ID ACD22804 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 423  
ID ACD30274 standard; cDNA; 1734 BP.  
DE Human cDNA encoding Pro1411.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 424  
ID ACF41504 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 425

ID ABT43959 standard; cDNA; 1734 BP.  
DE Human membrane bound receptor/protein PRO1411 cDNA sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 426  
ID ACF07051 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 427  
ID ACF77707 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 428  
ID ACD46105 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 429  
ID ACF47008 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 430  
ID ACF54376 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 431  
ID ACF45780 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 432  
ID ACF45473 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
RESULT 433  
ID ACF38492 standard; cDNA; 1734 BP.

DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 434  
ID ACD89553 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 435  
ID ACD85255 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 436  
ID ACD85869 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 437  
ID ACF75865 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 438  
ID ACF60765 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 439  
ID ACD85652 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 440  
ID ADA82636 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 441  
ID ADB85624 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 442  
ID ADB83645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 443  
ID ADB80751 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 444  
ID ADB73292 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 445  
ID ACF55911 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 446  
ID ADB78374 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 447  
ID ACF55297 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 448  
ID ADB85022 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 449  
ID ADB78128 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092886-A1.  
PD 15-MAY-2003.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 450
ID ADB85944 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 451
ID ACF56218 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 452
ID ACF56525 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 453
ID ADB87194 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #78.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 454
ID ADB84776 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #78.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 455
ID ADB68303 standard; cDNA; 1734 BP.
DE Human PRO1411 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 456
ID ADB68110 standard; cDNA; 1734 BP.
DE Human PRO1411 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 457
ID ACF55604 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 458
ID ACF54990 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 459
ID ADB83891 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 460
ID ADB73046 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 461
ID ADB90927 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 462
ID ADC07007 standard; cDNA; 1734 BP.
DE Human PRO1411 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 463
ID ADC17920 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #15.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 464
ID ADC17186 standard; cDNA; 1734 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 51).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 465
ID ADC14884 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Conservative: 0
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Query Match:	100.00%	Indels:	0
RESULT 474			
ID ADC78102 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003096972-A1.			
PD 22-MAY-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 475			
ID ADD06337 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003073816-A1.			
PD 17-APR-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 476			
ID ADD05674 standard; cDNA; 1734 BP.			
DE Human secreted/transmembrane protein (PRO) cDNA #101.			
FN US2003087376-A1.			
PD 08-MAY-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 477			
ID ADD10438 standard; cDNA; 1734 BP.			
DE Human secreted/transmembrane PRO polypeptide cDNA #75.			
FN US2003105011-A1.			
PD 05-JUN-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 478			
ID ADC77856 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003088066-A1.			
PD 08-MAY-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 479			
ID ADD1398 standard; cDNA; 1734 BP.			
DE Human secreted/transmembrane PRO polypeptide cDNA #75.			
FN US2003105013-A1.			
PD 05-JUN-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 480			
ID ADD50819 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003105291-A1.			
PD 05-JUN-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 481			
ID ADD51065 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003105290-A1.			
PD 05-JUN-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 482			
ID ADD51065 standard; cDNA; 1734 BP.			
DE Novel human secreted and transmembrane protein PRO1411 cDNA.			
FN US2003105290-A1.			
PD 05-JUN-2003			
PA (GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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RESULT 482
ID ADD70566 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 483
ID ADD39643 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 484
ID ADD70089 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 485
ID ADD37191 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #75.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 486
ID ADD36055 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003105238-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 487
ID ADD38210 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 488
ID ADD39166 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 489
ID ADD50546 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #78.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 490
ID ADD70566 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 491
ID ADD38689 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 492
ID ADD40120 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 493
ID ADD51311 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 494
ID ADE50341 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 495
ID ADE19953 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 496
ID ADE49864 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 497
ID ADE21422 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 498
ID ADF29847 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 499
ID ADE21422 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 500
ID ADF29847 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 499  
ID ADF55740 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 500  
ID ADG01056 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 501  
ID ADG08609 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 502  
ID ADG02669 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 503  
ID ADG01376 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 504  
ID ADF95551 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 505  
ID ADF95230 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 506  
ID ADG12366 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 507  
ID ADH24083 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 508  
ID ADH34109 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 509  
ID ADH2942 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 510  
ID ADH23913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 511  
ID ADH09026 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 512  
ID ADG85317 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 513  
ID ADH24593 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 514  
ID ADH37449 standard; cDNA; 1734 BP.  
DE Human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181846-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 515
ID ADH20338 standard; cDNA; 1734 BP.
DE Human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 516
ID ADH37619 standard; cDNA; 1734 BP.
DE Human secreted and transmembrane protein PRO411 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 517
ID ADH37619 standard; cDNA; 1734 BP.
DE Human secreted and transmembrane protein PRO411 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 518
ID ADH24253 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 519
ID ADH38547 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 520
ID ADG63786 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 521
ID ADG83668 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 522
ID ADH29476 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 523
ID ADH27592 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 524
ID ADH37789 standard; cDNA; 1734 BP.
DE Human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 525
ID ADH37966 standard; cDNA; 1734 BP.
DE Human secreted and transmembrane protein PRO411 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 526
ID ADH57386 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 527
ID ADH33528 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 528
ID ADH53698 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 529
ID ADH52034 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 530
ID ADH49889 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
```



```
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003032112-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 548
ID ACC97608 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027278-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 549
ID ACC96994 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036159-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 550
ID ACD04167 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040070-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 551
ID ACA9498 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003032113-A1.
PD 13-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 552
ID ACA90343 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 553
ID ACC89450 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003027264-A1.
PD 06-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 554
ID ACA98241 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 555
ID ACA93883 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036149-A1.
PD 20-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 556
ID ACA66918 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #78.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 557
ID ACD15276 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003044923-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 558
ID ACD0863 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040062-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 559
ID ACC96783 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040056-A1.
PD 27-FEB-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 560
ID ACF15504 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044526-A1.
PD 06-MAR-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 561
ID ACD4388 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO141 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 562
ID ACD68670 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 563
ID ACA72871 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 564
ID ACD03043 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 565  
ID AC001858 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 566  
ID ACA92050 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 567  
ID ADI05071 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 568  
ID ADI03421 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 569  
ID ADI04816 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 570  
ID ADH78270 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 571  
ID ADI19614 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 572  
ID ADH90362 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 573  
ID ADI03081 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 574  
ID ADH77930 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 575  
ID ADH97913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 576  
ID ADI01298 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 577  
ID ADI01993 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 578  
ID ADI03251 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 579  
ID ADI11438 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 580  
ID ADI02340 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 581  
ID ADI11778 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181685-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 582  
ID ADI05415 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 583  
ID ADH79487 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 584  
ID ADI19444 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 585  
ID ADI05245 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 586  
ID ADH79657 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 587  
ID ADI01483 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 588  
ID ADI01653 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 589  
ID ADI01823 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 590  
ID ADH79827 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 591  
ID ADI04645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 592  
ID ADI02781 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 593  
ID ADH78100 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 594  
ID ADI25739 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 595  
ID ADI25909 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 596  
ID ADK65421 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 597  
ID ADH98763 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 598  
ID ADH80004 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 599  
ID ADJ32807 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 600  
ID ADM30341 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 601  
ID ADJ93735 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 602  
ID ADC48858 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 603  
ID ADC52189 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 604  
ID ADE21029 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 605  
ID ADE05873 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 606  
ID ADD75102 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 607  
ID ADD75848 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 608  
ID ADD85080 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 609  
ID ADD86906 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 610  
ID ADE20783 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 611  
ID ADE39080 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 612  
ID ADE05627 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 613  
ID ADD73612 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

Query Match: 100.00% Indels: 0  
RESULT 614  
ID ADD78452 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 615  
ID ADE41399 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #75.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 616  
ID ADE74338 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 617  
ID ADE21275 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 618  
ID ADD77390 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 619  
ID ADE20537 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 620  
ID ADD75602 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 621  
ID ADD74118 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 622

ID ADD74364 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 623  
ID ADD76094 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 624  
ID ADD8586 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 625  
ID ADE05135 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 626  
ID ADD75348 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 627  
ID ADD76892 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 628  
ID ADD86660 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 629  
ID ADE41200 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 630  
ID ADD78128 standard; cDNA; 1734 BP.



DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 631  
ID ADE74950 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 632  
ID ADD77636 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 633  
ID ADD77882 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 634  
ID ADD85340 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 635  
ID ADD73872 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 636  
ID ADD74610 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 637  
ID ADD77138 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 638  
ID ADD85832 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100720-A1.

PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 639  
ID ADE05381 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 640  
ID ADD74856 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 641  
ID ADE96424 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 642  
ID ADF25735 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 643  
ID ADF24634 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 644  
ID ADF29370 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 645  
ID ADE96901 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 646  
ID ADG05668 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096959-A1.  
PD 22-MAY-2003.



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Query Match: 100.00% Indels: 0
RESULT 663
ID ADH02378 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 664
ID ADH07985 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 665
ID ADG6382 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 666
ID ADH39203 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 667
ID ADH03893 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 668
ID ADH03416 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 669
ID ADH26131 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 670
ID ADG83943 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 671
ID ADH39061 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 672
ID ADG85487 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US200316848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 673
ID ADG63635 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 674
ID ADH06281 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 675
ID ADH30111 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 676
ID ADH24423 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 677
ID ADH33100 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 678
ID ADG69552 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 679
ID ADG69552 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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ID ADH07815 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 680

ID ADG85827 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 681

ID ADH39373 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 682

ID ADH33565 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 683

ID ADH33905 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 684

ID ADH01115 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 685

ID ADG69722 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 686

ID ADH02208 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 687

ID ADG69212 standard; cDNA; 1734 BP.

DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 688

ID ADG85997 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 689

ID ADH24933 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 690

ID ADH39550 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 691

ID ADH02548 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 692

ID ADG69042 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 693

ID ADH07645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 694

ID ADG86167 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 695

ID ADH24763 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.



PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 712  
ID ADJ54839 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
RESULT 713  
ID ADJ98577 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 714  
ID ADJ98747 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 715  
ID ADH78906 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 716  
ID ADJ99140 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 717  
ID ADJ99310 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 718  
ID ADJ98928 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 719  
ID ADH79076 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 720  
ID ADK00936 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 721  
ID ADK14457 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 722  
ID ADM27273 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 723  
ID ADK82927 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #75.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 724  
ID ADJ64610 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 725  
ID ADK66631 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 726  
ID ADM31506 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 727  
ID ADM36553 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Indels: 0  
Conservative: 0

Best Local Similarity: 100.00%	Mismatches: 0	Query Match: 83.11%	Indels: 30
Query Match: 100.00%	Indels: 0	RESULT 736	
ID - ADM40358 standard; cDNA; 1734 BP.		ID AAZ43802 standard; cDNA; 1493 BP.	
DE Novel human secreted and transmembrane protein PRO1411 cDNA.		DE Human adult skin cDNA clone vd3_1.	
PN US2004048335-A1.		PN WO9955721-A1.	
PD 11-MAR-2004.		PD 04-NOV-1999.	
PA (GETH ) GENENTECH INC.		PA (ALPH-) ALPHAGENE INC.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 83.41%	Conservative: 1
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 83.18%	Mismatches: 2
Query Match: 100.00%	Indels: 0	Query Match: 80.34%	Indels: 72
RESULT 729		RESULT 737	
ID ADM80906 standard; cDNA; 1734 BP.		ID AAZ42019 standard; cDNA; 914 BP.	
DE Human PRO polynucleotide #26.		DE Human endometrium tumour cDNA derived EST 39.	
PN US2004058411-A1.		PN DE19817948-A1.	
PD 25-MAR-2004.		PD 21-OCT-1999.	
PA (GETH ) GENENTECH INC.		PA (META-) METAGEN GES GENOMFORSCHUNG MBH.	
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 2
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 98.39%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 28.31%	Indels: 0
RESULT 730		RESULT 738	
ID ADL94570 standard; cDNA; 1734 BP.		Percent Similarity: 39.34%	Conservative: 40
DE Human cDNA encoding secreted/transmembrane protein PRO1411.		Best Local Similarity: 30.55%	Mismatches: 181
PN US2004073015-A1.		Query Match: 19.06%	Indels: 95
PD 15-APR-2004.		RESULT 739	
PA (GETH ) GENENTECH INC.		Percent Similarity: 39.34%	Conservative: 40
Percent Similarity: 100.00%	Conservative: 0	Best Local Similarity: 30.55%	Mismatches: 181
Best Local Similarity: 100.00%	Mismatches: 0	Query Match: 19.06%	Indels: 95
Query Match: 100.00%	Indels: 0	RESULT 740	
RESULT 731		Percent Similarity: 41.69%	Conservative: 40
ID ADN37966 standard; cDNA; 1734 BP.		Best Local Similarity: 32.82%	Mismatches: 176
DE Novel human secreted and transmembrane protein PRO1411 cDNA.		Query Match: 18.71%	Indels: 87
PN US2004091959-A1.		RESULT 741	
PD 13-MAY-2004.		Percent Similarity: 40.04%	Conservative: 36
PA (GETH ) GENENTECH INC.		Best Local Similarity: 32.17%	Mismatches: 181
Percent Similarity: 100.00%	Conservative: 0	Query Match: 18.66%	Indels: 93
Best Local Similarity: 100.00%	Mismatches: 0	RESULT 742	
Query Match: 100.00%	Indels: 0	ID ACA40351 standard; DNA; 3921 BP.	
RESULT 732		DE Prokaryotic essential gene #22008.	
ID AAC69515 standard; DNA; 1441 BP.		PN WO200277183-A2.	
DE Human secreted protein gene 4 clone HKAKJ47.		PD 03-OCT-2002.	
PN WO200061623-A1.		PA (ELIT-) ELITRA PHARM INC.	
PD 19-OCT-2000.		Percent Similarity: 37.91%	Conservative: 34
PA (HUMA-) HUMAN GENOME SCI INC.		Best Local Similarity: 30.94%	Mismatches: 194
Percent Similarity: 87.73%	Conservative: 1	Query Match: 18.60%	Indels: 109
Best Local Similarity: 87.50%	Mismatches: 0	RESULT 743	
Query Match: 85.91%	Indels: 54	Percent Similarity: 37.91%	Conservative: 34
RESULT 733		Best Local Similarity: 30.94%	Mismatches: 194
ID ABL88146 standard; cDNA; 1320 BP.		Query Match: 18.60%	Indels: 109
DE Human PRO1411 cDNA sequence SEQ ID NO:149.		RESULT 744	
PN WO200200690-A2.		Percent Similarity: 37.91%	Conservative: 34
PD 03-JAN-2002.		Best Local Similarity: 30.94%	Mismatches: 194
PA (GETH ) GENENTECH INC.		Query Match: 18.60%	Indels: 109
Percent Similarity: 100.00%	Conservative: 0	RESULT 745	
Best Local Similarity: 100.00%	Mismatches: 0	ID AALS1694 standard; cDNA; 1199 BP.	
Query Match: 85.82%	Indels: 0	DE Kukulcania hibernalis spider silk protein coding sequence #2.	
RESULT 734		PN WO200299082-A2.	
ID AAZ43803 standard; cDNA; 1897 BP.		PD 12-DEC-2002.	
DE Human adult skin cDNA clone vd4_1.		PA (UYWV-) UNIV WYOMING.	
PN WO9955721-A1.		Percent Similarity: 40.54%	Conservative: 29
PD 04-NOV-1999.		Best Local Similarity: 33.42%	Mismatches: 194
PA (ALPH-) ALPHAGENE INC.		Query Match: 18.37%	Indels: 48
Percent Similarity: 88.02%	Conservative: 2	RESULT 746	
Best Local Similarity: 87.56%	Mismatches: 1	ID ACH87528 standard; DNA; 1083 BP.	
Query Match: 85.08%	Indels: 51	DE Human genome derived single exon probe #20723.	
RESULT 735		PN US2003194704-A1.	
ID ADH52204 standard; cDNA; 1629 BP.		PD 16-OCT-2003.	
DE Novel human secreted and transmembrane protein PRO1411 cDNA.		PA (PENN/) PENN S G.	
PN US2003180921-A1.		PA (RANK/) RANK D R.	
PD 25-SEP-2003.		PA (HANZ/) HANZEL D K.	
PA (GETH ) GENENTECH INC.		Percent Similarity: 39.49%	Conservative: 13
Percent Similarity: 93.17%	Mismatches: 0	Best Local Similarity: 35.80%	Mismatches: 168
Best Local Similarity: 93.17%	Mismatches: 10	Query Match: 18.22%	Indels: 45
		RESULT 747	





Query Match:	17.29%	Indels:	77
RESULT 764			
ID ABA44805 standard; DNA; 1973 BP.			
DE Human breast cell single exon nucleic acid probe #3500.			
PN WO200157271-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 765			
ID ABA25005 standard; DNA; 1973 BP.			
DE Probe #3471 for gene expression analysis in human heart cell sample.			
PN WO200157274-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 766			
ID AAK28970 standard; DNA; 1973 BP.			
DE Human bone marrow expressed single exon probe SEQ ID NO: 3527.			
PN WO200157276-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 767			
ID AAK03514 standard; DNA; 1973 BP.			
DE Human brain expressed single exon probe SEQ ID NO: 3505.			
PN WO200157275-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 768			
ID ABS28585 standard; DNA; 1973 BP.			
DE Human liver single exon probe, SEQ ID NO 3575.			
PN WO200157273-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 769			
ID AAI03446 standard; DNA; 1973 BP.			
DE Probe #3437 used to measure gene expression in human breast sample.			
PN WO200157270-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 770			
ID ABS03504 standard; DNA; 1973 BP.			
DE Human genome-derived single exon probe from lung SEQ ID NO 3495.			
PN WO200186003-A2.			
PD 15-NOV-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	35.97%	Conservative:	24
Best Local Similarity:	30.22%	Mismatches:	190
Query Match:	17.29%	Indels:	77
RESULT 771			
ID ACH87341 standard; DNA; 2543 BP.			
DE Human genome derived single exon probe #20536.			
PN US2003194704-A1.			
PD 16-OCT-2003.			
PA (PENN/) PENN S G.			
PA (RANK/) RANK D R.			
PA (HANZ/) HANZEL D K.			
Percent Similarity:	37.78%	Conservative:	17
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.29%	Indels:	75
RESULT 772			
ID AAI21781 standard; DNA; 1075 BP.			
DE Probe #11714 for gene expression analysis in human cervical cell sample.			
PN WO200157278-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 773			
ID ABA66852 standard; DNA; 1075 BP.			
DE Human foetal liver single exon nucleic acid probe #15157.			
PN WO200157277-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 774			
ID AAI47064 standard; DNA; 1075 BP.			
DE Probe #15750 used to measure gene expression in human placenta sample.			
PN WO200157272-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 775			
ID ABA48937 standard; DNA; 1075 BP.			
DE Human breast cell single exon nucleic acid probe #7632.			
PN WO200157271-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 776			
ID ABA33921 standard; DNA; 1075 BP.			
DE Probe #12387 for gene expression analysis in human heart cell sample.			
PN WO200157274-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 777			
ID AAK41011 standard; DNA; 1075 BP.			
DE Human bone marrow expressed single exon probe SEQ ID NO: 15568.			
PN WO200157276-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 778			
ID AAK15288 standard; DNA; 1075 BP.			
DE Human brain expressed single exon probe SEQ ID NO: 15279.			
PN WO200157275-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75
RESULT 779			
ID ABS40603 standard; DNA; 1075 BP.			
DE Human liver single exon probe, SEQ ID NO 15593.			
PN WO200157273-A2.			
PD 09-AUG-2001.			
PA (MOLE-) MOLECULAR DYNAMICS INC.			
Percent Similarity:	36.84%	Conservative:	21
Best Local Similarity:	31.58%	Mismatches:	177
Query Match:	17.20%	Indels:	75

Query Match: 17.20% Indels: 75  
 RESULT 780  
 ID AAI07466 standard; DNA; 1075 BP.  
 DE Probe #7457 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.84%  
 Best Local Similarity: 31.58%  
 Best Local Similarity: 17.20%  
 Query Match:  
 RESULT 781  
 ID ABS14983 standard; DNA; 1075 BP.  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 14974.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.84%  
 Best Local Similarity: 31.58%  
 Best Local Similarity: 17.20%  
 Query Match:  
 RESULT 782  
 ID AAI12593 standard; DNA; 1403 BP.  
 DE Probe #2526 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 783  
 ID ABA54290 standard; DNA; 1403 BP.  
 DE Human foetal liver single exon nucleic acid probe #2595.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 784  
 ID AAI33941 standard; DNA; 1403 BP.  
 DE Probe #2627 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 785  
 ID ABA43834 standard; DNA; 1403 BP.  
 DE Human breast cell single exon nucleic acid probe #2529.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 786  
 ID ABA24047 standard; DNA; 1403 BP.  
 DE Probe #2513 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 787  
 ID AAK28010 standard; DNA; 1403 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 2567.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 788  
 ID AAK02574 standard; DNA; 1403 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 2565.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 789  
 ID ABS27605 standard; DNA; 1403 BP.  
 DE Human liver single exon probe, SEQ ID No 2595.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 790  
 ID AAI02498 standard; DNA; 1403 BP.  
 DE Probe #2489 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 791  
 ID ABS02482 standard; DNA; 1403 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 2473.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 792  
 ID ACA40604 standard; DNA; 1599 BP.  
 DE Prokaryotic essential gene #22261.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) ELITRA PHARM INC.  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 793  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 794  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 795  
 Percent Similarity: 37.53%  
 Best Local Similarity: 31.24%  
 Best Local Similarity: 16.91%  
 Query Match:  
 RESULT 796  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 797  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 798  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 799  
 ID ACA40420 standard; DNA; 2772 BP.  
 DE Prokaryotic essential gene #22077.  
 PN WO200277183-A2.

RESULT 788  
 ID AAK02574 standard; DNA; 1403 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 2565.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 789  
 ID ABS27605 standard; DNA; 1403 BP.  
 DE Human liver single exon probe, SEQ ID No 2595.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 790  
 ID AAI02498 standard; DNA; 1403 BP.  
 DE Probe #2489 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 791  
 ID ABS02482 standard; DNA; 1403 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 2473.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 36.87%  
 Best Local Similarity: 31.82%  
 Best Local Similarity: 17.16%  
 Query Match:  
 RESULT 792  
 ID ACA40604 standard; DNA; 1599 BP.  
 DE Prokaryotic essential gene #22261.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (BLIT-) ELITRA PHARM INC.  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 793  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 794  
 Percent Similarity: 40.89%  
 Best Local Similarity: 32.48%  
 Best Local Similarity: 17.12%  
 Query Match:  
 RESULT 795  
 Percent Similarity: 37.53%  
 Best Local Similarity: 31.24%  
 Best Local Similarity: 16.91%  
 Query Match:  
 RESULT 796  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 797  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 798  
 Percent Similarity: 37.53%  
 Best Local Similarity: 30.02%  
 Best Local Similarity: 16.72%  
 Query Match:  
 RESULT 799  
 ID ACA40420 standard; DNA; 2772 BP.  
 DE Prokaryotic essential gene #22077.  
 PN WO200277183-A2.

PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.99%  
 Best Local Similarity: 27.74%  
 Query Match: 16.61%  
 RESULT 800  
 Percent Similarity: 34.99%  
 Best Local Similarity: 27.74%  
 Query Match: 16.61%  
 RESULT 801  
 Percent Similarity: 34.99%  
 Best Local Similarity: 27.74%  
 Query Match: 16.61%  
 RESULT 802  
 Percent Similarity: 34.99%  
 Best Local Similarity: 27.74%  
 Query Match: 16.61%  
 ID ADM98959 standard; DNA; 69350 BP.  
 DE Diterpene synthase DNA #19.  
 PN US2004072323-A1.  
 PD 15-APR-2004.  
 PA (MATS/) MATSUDA S P T.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 32.18%  
 Query Match: 16.59%  
 RESULT 803  
 Percent Similarity: 35.83%  
 Best Local Similarity: 28.54%  
 Query Match: 16.59%  
 RESULT 804  
 Percent Similarity: 39.31%  
 Best Local Similarity: 32.18%  
 Query Match: 16.59%  
 RESULT 805  
 Percent Similarity: 39.31%  
 Best Local Similarity: 32.18%  
 Query Match: 16.59%  
 RESULT 806  
 Percent Similarity: 35.83%  
 Best Local Similarity: 28.54%  
 Query Match: 16.59%  
 RESULT 807  
 Percent Similarity: 39.08%  
 Best Local Similarity: 32.18%  
 Query Match: 16.59%  
 RESULT 808  
 Percent Similarity: 35.07%  
 Best Local Similarity: 30.06%  
 Query Match: 16.53%  
 RESULT 809  
 ID ADQ97928 standard; DNA; 138808 BP.  
 DE Human cancer associated sequence HD11-024, SEQ ID 905.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 36.76%  
 Best Local Similarity: 30.59%  
 Query Match: 16.40%  
 RESULT 810  
 ID ACA0697 standard; DNA; 2337 BP.  
 DE Prokaryotic essential gene #22354.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.05%  
 Best Local Similarity: 31.25%  
 Query Match: 16.34%  
 RESULT 811  
 Percent Similarity: 37.05%  
 Best Local Similarity: 31.25%  
 Query Match: 16.34%  
 RESULT 812  
 ID ADQ52666 standard; DNA; 513 BP.  
 DE Novel canine microarray-related DNA sequence SeqID3968.  
 PN WO2004063324-A2.

PD 29-JUL-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 63.40%  
 Best Local Similarity: 54.90%  
 Query Match: 16.23%  
 RESULT 813  
 ID AAA50254 standard; DNA; 1926 BP.  
 DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.  
 PN WO200047778-A1.  
 PD 17-AUG-2000.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 814  
 ID AAF82902 standard; DNA; 1926 BP.  
 DE EBV tethering protein EBNA1 encoding DNA.  
 PN WO200125484-A2.  
 PD 12-APR-2001.  
 PA (UNMI) UNIV MICHIGAN.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 815  
 ID AAA75454 standard; DNA; 2580 BP.  
 DE Nucleotide sequence of the Epstein Barr nuclear antigen.  
 PN US6114111-A.  
 PD 05-SEP-2000.  
 PA (RIGE-) RIGEL PHARM INC.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 816  
 ID AAI64275 standard; DNA; 2580 BP.  
 DE Epstein-Barr virus nuclear antigen coding sequence.  
 PN US6316223-B1.  
 PD 13-NOV-2001.  
 PA (RIGE-) RIGEL PHARM INC.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 817  
 ID AAX90923 standard; DNA; 5452 BP.  
 DE Anti-sense strand of pCMVEBNA plasmid.  
 PN WO9947647-A1.  
 PD 23-SEP-1999.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 818  
 ID AAZ23778 standard; DNA; 8705 BP.  
 DE Vector pShuttle DNA.  
 PN WO9950457-A1.  
 PD 07-OCT-1999.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 819  
 ID ADM10659 standard; DNA; 8705 BP.  
 DE Expression vector pShuttle.  
 PN US2004077082-A1.  
 PD 22-APR-2004.  
 PA (KOEH/) KOEHN R K.  
 PA (RUFF/) RUFFNER D E.  
 PA (PRAK/) PRAKASH R K.  
 Percent Similarity: 40.10%  
 Best Local Similarity: 30.99%  
 Query Match: 16.21%  
 RESULT 820  
 ID ADP64415 standard; DNA; 9482 BP.

DE Vector pCEPpu nucleotide sequence SEQ ID NO:1.  
PN WO2004053137-A2.  
PD 24-JUN-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 821  
ID AAV21683 standard; DNA; 9600 BP.  
DE Vector plasmid pCMVkmTR-EPI.  
PN WO9806437-A2.  
PD 19-FEB-1998.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 822  
ID ABS71027 standard; DNA; 10285 BP.  
DE pCEP-Xa-Fc construct DNA sequence.  
PN WO200256905-A2.  
PD 25-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 823  
ID ABS66453 standard; DNA; 10285 BP.  
DE Plasmid pCEP-Xa-Fc<sup>+</sup> expressing human IgG/protease cleavage site.  
PN WO200256907-A2.  
PD 25-JUL-2002.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
PA (NOVS ) NOVARTIS PHARMA AG.  
PA (MAUR/) MAURER P.  
PA (LECH/) LECHNER F.  
PA (ORTM/) ORTMANN R.  
PA (LUEO/) LUEOEND R.  
PA (STAU/) STAUFENBIEL M.  
PA (FREY/) FREY P.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 824  
ID ADL67154 standard; DNA; 10330 BP.  
DE Plasmid pCEP-mb7-H6 (ECD) -comp-FL-C nucleotide sequence SEQ ID NO:24.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 825  
ID AAZ22248 standard; DNA; 10380 BP.  
DE Nucleotide sequence of pCEP4 vector.  
PN WO9947921-A1.  
PD 23-SEP-1999.  
PA (PHAR-) PHARMACOPRIA INC.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 826  
ID ADL67152 standard; DNA; 10477 BP.  
DE Plasmid pCEP-mb7-H5 (ECD) -comp-FL-C nucleotide sequence SEQ ID NO:22.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 827  
ID ADL67150 standard; DNA; 10516 BP.  
DE Plasmid pCEP-hsB7-H5 (ECD) -comp-FL-C nucleotide sequence SEQ ID NO:20.  
PN WO2004022594-A2.  
PD 18-MAR-2004.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 828  
ID ADL67148 standard; DNA; 10561 BP.  
DE Plasmid pCEP-hsB7-H4 (ECD) -comp-FL-C nucleotide sequence SEQ ID NO:18.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 829  
ID AAQ51731 standard; DNA; 10596 BP.  
DE Plasmid pCisEBON for subcloning huHGF variants.  
PN WO9323541-A1.  
PD 25-NOV-1993.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 830  
ID AAX15650 standard; DNA; 10596 BP.  
DE Nucleotide sequence of plasmid pCis.EBON.  
PN US5879910-A.  
PD 09-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 831  
ID AAT40348 standard; DNA; 10596 BP.  
DE Plasmid pCisEBON for expression of hepatocyte growth factor.  
PN US5547856-A.  
PD 20-AUG-1996.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 832  
ID ADL67175 standard; DNA; 10615 BP.  
DE Plasmid pCEP-hsB7-H6-COMP-FLAG nucleotide sequence SEQ ID NO:45.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 833  
ID ADL67153 standard; DNA; 10774 BP.  
DE Plasmid pCEP-mb7-H6 (ECD) -Fc nucleotide sequence SEQ ID NO:23.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 834  
ID ADL67151 standard; DNA; 10921 BP.  
DE Plasmid pCEP-mb7-H5 (ECD) -Fc nucleotide sequence SEQ ID NO:21.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Percent Similarity: 40.10%  
Best Local Similarity: 30.99%  
Query Match: 16.21%  
Conservative: 35  
Mismatch: 186  
Indels: 44  
RESULT 835  
ID ADL67149 standard; DNA; 10961 BP.  
DE Plasmid pCEP-hsB7-H5 (ECD) -Fc nucleotide sequence SEQ ID NO:19.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 836  
 ID ADL67147 standard; DNA; 11006 BP.  
 DE Plasmid pCEP-hbB7-H4 (ECD) -Fc nucleotide sequence SEQ ID NO:17.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 837  
 ID ADL67176 standard; DNA; 11059 BP.  
 DE Plasmid pCEP-hbB7-H6-XaI-Fc\* nucleotide sequence SEQ ID NO:46.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 838  
 ID ADL12379 standard; DNA; 11693 BP.  
 DE Vector pCMR2.  
 PN WO2004065561-A2.  
 PD 05-AUG-2004.  
 PA (PTCT-) PTC THERAPEUTICS INC.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 839  
 ID ADO07395 standard; DNA; 11924 BP.  
 DE Modified human hepsin plasmid pCEP4W/hep36.  
 PN WO2004033630-A2.  
 PD 22-APR-2004.  
 PA (SCHD) SCHERING AG.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 840  
 ID ADO07394 standard; DNA; 12242 BP.  
 DE Modified human hepsin plasmid pCEP4W/hepEK.  
 PN WO2004033630-A2.  
 PD 22-APR-2004.  
 PA (SCHD) SCHERING AG.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 841  
 ID AAA59553 standard; DNA; 16080 BP.  
 DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.  
 PN WO2004047618-A2.  
 PD 17-AUG-2000.  
 PA (ELAN-) ELAN PHARM INC.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 842  
 ID ADL1910 standard; cDNA; 17753 BP.  
 DE Expression vector pCytB-OPE.  
 PN WO2004018506-A2.  
 PD 04-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 843  
 ID ADN12161 standard; DNA; 172281 BP.  
 DE Epstein-Barr virus genome B95-8.  
 PN WO2004027036-A2.  
 PD 01-APR-2004.  
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 Percent Similarity: 40.10% Conservative: 35

Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.21% Indels: 44  
 RESULT 844  
 ID ADK65580 standard; DNA; 1926 BP.  
 DE Human herpesvirus 4 nuclear antigen-1 coding sequence.  
 PN DE10207135-A1.  
 PD 11-SEP-2003.  
 PA (EURO-) EUROIMMUN GMBH.  
 Percent Similarity: 40.10% Conservative: 35  
 Best Local Similarity: 30.99% Mismatches: 186  
 Query Match: 16.12% Indels: 44  
 RESULT 845  
 ID ACA40308 standard; DNA; 2514 BP.  
 DE Prokaryotic essential gene #21965.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.32% Conservative: 37  
 Best Local Similarity: 30.53% Mismatches: 164  
 Query Match: 16.10% Indels: 129  
 RESULT 846  
 Percent Similarity: 38.32% Conservative: 37  
 Best Local Similarity: 30.53% Mismatches: 164  
 Query Match: 16.10% Indels: 129  
 RESULT 847  
 Percent Similarity: 37.58% Conservative: 34  
 Best Local Similarity: 30.24% Mismatches: 210  
 Query Match: 16.10% Indels: 79  
 RESULT 848  
 ID AAT85356 standard; DNA; 2004 BP.  
 DE Nephila clavipes spider silk protein 2 Kb DNA sequence.  
 PN WO9708315-A1.  
 PD 06-MAR-1997.  
 PA (BASE/) BASEL R M.  
 Percent Similarity: 37.18% Conservative: 50  
 Best Local Similarity: 27.24% Mismatches: 211  
 Query Match: 16.06% Indels: 106  
 RESULT 849  
 ID ACA40815 standard; DNA; 1767 BP.  
 DE Prokaryotic essential gene #22472.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.78% Conservative: 43  
 Best Local Similarity: 30.11% Mismatches: 176  
 Query Match: 16.00% Indels: 92  
 RESULT 850  
 ID ADM40789 standard; DNA; 1767 BP.  
 DE Mycobacterial disease detection method related gene Rv3367.  
 PN WO2003073101-A2.  
 PD 04-SEP-2003.  
 PA (UNYNY) UNIV NEW YORK STATE.  
 Percent Similarity: 39.78% Conservative: 43  
 Best Local Similarity: 30.11% Mismatches: 176  
 Query Match: 16.00% Indels: 92  
 RESULT 851  
 ID ABS58306 standard; cDNA; 1852 BP.  
 DE Spider dragline cDNA repetitive nucleotide sequence.  
 PN US2002137211-A1.  
 PD 26-SEP-2002.  
 PA (UYSI-) UNIV SICHUAN TIANYOU BIOLOGIC ENG CO LTD.  
 Percent Similarity: 40.33% Conservative: 37  
 Best Local Similarity: 31.50% Mismatches: 188  
 Query Match: 16.00% Indels: 62  
 RESULT 852  
 ID ACA40493 standard; DNA; 1731 BP.  
 DE Prokaryotic essential gene #22150.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.23% Conservative: 40  
 Best Local Similarity: 27.55% Mismatches: 207

Query Match:	15.95%	Indels:	87
RESULT 853		Conservative:	40
Percent Similarity:	36.23%	Mismatches:	207
Best Local Similarity:	27.55%	Indels:	87
Query Match:	15.95%		
RESULT 854		Conservative:	33
Percent Similarity:	37.28%	Mismatches:	210
Best Local Similarity:	30.17%	Indels:	81
Query Match:	15.93%		
RESULT 855			
ID ACA040552 standard; DNA; 2745 BP.			
DE Prokaryotic essential gene #22209.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	39.95%	Conservative:	30
Best Local Similarity:	33.18%	Mismatches:	165
Query Match:	15.87%	Indels:	102
RESULT 856			
Percent Similarity:	39.95%	Conservative:	30
Best Local Similarity:	33.18%	Mismatches:	165
Query Match:	15.87%	Indels:	102
RESULT 857			
Percent Similarity:	39.95%	Conservative:	30
Best Local Similarity:	33.18%	Mismatches:	165
Query Match:	15.87%	Indels:	102
RESULT 858			
ID AAS36979 standard; cDNA; 410 BP.			
DE Novel human diagnostic and therapeutic gene #37.			
PN WO200166753-A2.			
PD 13-SEP-2001.			
PA (CHIR ) CHIRON CORP.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	72.81%	Conservative:	4
Best Local Similarity:	69.30%	Mismatches:	14
Query Match:	15.85%	Indels:	18
RESULT 859			
ID ABL61038 standard; DNA; 3783 BP.			
DE N. clavipes spidroin synthetic homologue S01S01.			
PN DE10113781-A1.			
PD 13-DEC-2001.			
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.			
Percent Similarity:	40.77%	Conservative:	43
Best Local Similarity:	30.46%	Mismatches:	191
Query Match:	15.83%	Indels:	56
RESULT 860			
ID ABL61040 standard; DNA; 5658 BP.			
DE N. clavipes spidroin synthetic homologue S01SM12.			
PN DE10113781-A1.			
PD 13-DEC-2001.			
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.			
Percent Similarity:	40.77%	Conservative:	43
Best Local Similarity:	30.46%	Mismatches:	191
Query Match:	15.83%	Indels:	56
RESULT 861			
ID AAL51696 standard; cDNA; 1682 BP.			
DE Argiope trifasciata spider silk protein coding sequence #1.			
PN WO200299082-A2.			
PD 12-DEC-2002.			
PA (UYWT-) UNIV WYOMING.			
Percent Similarity:	41.55%	Conservative:	48
Best Local Similarity:	29.95%	Mismatches:	185
Query Match:	15.81%	Indels:	57
RESULT 862			
ID ACA0849 standard; DNA; 1755 BP.			
DE Prokaryotic essential gene #22506.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	40.58%	Conservative:	37
Best Local Similarity:	32.29%	Mismatches:	175
Query Match:	15.81%	Indels:	91
RESULT 863			
ID ACA0440 standard; DNA; 2004 BP.			
DE Prokaryotic essential gene #22097.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	35.93%	Conservative:	37
Best Local Similarity:	28.54%	Mismatches:	178
Query Match:	15.81%	Indels:	143
RESULT 864			
Percent Similarity:	35.93%	Conservative:	37
Best Local Similarity:	28.54%	Mismatches:	178
Query Match:	15.81%	Indels:	143
RESULT 865			
Percent Similarity:	40.58%	Conservative:	37
Best Local Similarity:	32.29%	Mismatches:	175
Query Match:	15.81%	Indels:	91
RESULT 866			
Percent Similarity:	40.58%	Conservative:	37
Best Local Similarity:	32.29%	Mismatches:	175
Query Match:	15.81%	Indels:	91
RESULT 867			
ID AAZ80280 standard; cDNA; 686 BP.			
DE Human colon cancer cell line SW480 cDNA clone SEQ ID NO:364.			
PN WO9964576-A2.			
PD 16-DEC-1999.			
PA (FARB ) BAYER CORP.			
Percent Similarity:	59.68%	Conservative:	1
Best Local Similarity:	58.87%	Mismatches:	0
Query Match:	15.79%	Indels:	50
RESULT 868			
ID AAH23810 standard; cDNA; 700 BP.			
DE Human transferase HTFS-10 cDNA, SEQ ID NO:52.			
PN WO200132888-A2.			
PD 10-MAY-2001.			
PA (INCY-) INCYTE GENOMICS INC.			
Percent Similarity:	59.68%	Conservative:	1
Best Local Similarity:	58.87%	Mismatches:	0
Query Match:	15.79%	Indels:	50
RESULT 869			
ID ADE28278 standard; DNA; 703 BP.			
DE Human WDDT DNA - SEQ ID 128.			
PN WO2003046152-A2.			
PD 05-JUN-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Percent Similarity:	59.68%	Conservative:	1
Best Local Similarity:	58.87%	Mismatches:	0
Query Match:	15.79%	Indels:	50
RESULT 870			
ID ADM02457 standard; cDNA; 1579 BP.			
DE Human cDNA of the invention SEQ ID NO:1142.			
PN EP1347046-A1.			
PD 24-SEP-2003.			
PA (REAS-) RES ASSOC BIOTECHNOLOGY.			
Percent Similarity:	59.68%	Conservative:	1
Best Local Similarity:	58.87%	Mismatches:	0
Query Match:	15.79%	Indels:	50
RESULT 871			
ID ADQ24565 standard; DNA; 1608 BP.			
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7385.			
PN WO2004048938-A2.			
PD 10-JUN-2004.			
PA (PROT-) PROTEIN DESIGN LABS INC.			
Percent Similarity:	59.68%	Conservative:	1
Best Local Similarity:	58.87%	Mismatches:	0
Query Match:	15.79%	Indels:	50
RESULT 872			
ID AAQ14183 standard; cDNA; 2338 BP.			
DE N.clavipes dragline silk protein coding sequence.			
PN EP452925-A.			
PD 23-OCT-1991.			
PA (UYWY-) UNIV OF WYOMING.			
Percent Similarity:	38.85%	Conservative:	46
Best Local Similarity:	29.09%	Mismatches:	200

Query Match:	15.79%	Indels:	89
RESULT 873			
ID AAV23249 standard; cDNA; 2338 BP.			
DE Nephila clavipes spider silk protein encoding cDNA.			
PN US5728810-A.			
PD 17-MAR-1998.			
PA (UYWY-) UNIV WYOMING.			
Percent Similarity:	38.85%	Conservative:	46
Best Local Similarity:	29.09%	Mismatches:	200
Query Match:	15.79%	Indels:	89
RESULT 874			
ID AAZ38195 standard; cDNA; 2338 BP.			
DE N. clavipes spider silk protein 1 encoding cDNA.			
PN US5989894-A.			
PD 23-NOV-1999.			
PA (UYWY-) UNIV WYOMING.			
Percent Similarity:	38.85%	Conservative:	46
Best Local Similarity:	29.09%	Mismatches:	200
Query Match:	15.79%	Indels:	89
RESULT 875			
ID AAZ38195 standard; cDNA; 2338 BP.			
DE N. clavipes spider silk protein 1 encoding cDNA.			
PN US5989894-A.			
PD 23-NOV-1999.			
PA (UYWY-) UNIV WYOMING.			
Percent Similarity:	38.85%	Conservative:	46
Best Local Similarity:	29.09%	Mismatches:	200
Query Match:	15.79%	Indels:	89
RESULT 876			
ID ACA40672 standard; DNA; 2085 BP.			
DE Prokaryotic essential gene #22329.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	38.83%	Conservative:	41
Best Local Similarity:	30.27%	Mismatches:	187
Query Match:	15.74%	Indels:	106
RESULT 877			
ID ABL61039 standard; DNA; 2985 BP.			
DE N. clavipes spider protein synthetic homologue SOISM12.			
PN DE10113781-A1.			
PD 13-DEC-2001.			
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.			
Percent Similarity:	38.41%	Conservative:	46
Best Local Similarity:	28.54%	Mismatches:	208
Query Match:	15.72%	Indels:	80
RESULT 878			
ID ACA40732 standard; DNA; 1848 BP.			
DE Prokaryotic essential gene #22389.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	36.88%	Conservative:	30
Best Local Similarity:	30.37%	Mismatches:	191
Query Match:	15.70%	Indels:	100
RESULT 879			
ID ACA40504 standard; DNA; 1476 BP.			
DE Prokaryotic essential gene #22161.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	36.88%	Conservative:	30
Best Local Similarity:	30.37%	Mismatches:	191
Query Match:	15.70%	Indels:	100
RESULT 880			
ID ACA40504 standard; DNA; 1476 BP.			
DE Prokaryotic essential gene #22161.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	39.65%	Conservative:	52
Best Local Similarity:	28.32%	Mismatches:	184
Query Match:	15.68%	Indels:	93
RESULT 881			
ID AAX30924 standard; DNA; 1925 BP.			
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.			
PN WO9947647-A1.			
PD 23-SEP-1999.			
PA (PHAR-) PHARMACOEPIA INC.			
Percent Similarity:	40.10%	Conservative:	35
Best Local Similarity:	30.99%	Mismatches:	186
Query Match:	15.59%	Indels:	45
RESULT 882			
Percent Similarity:	37.40%	Conservative:	39
Best Local Similarity:	29.60%	Mismatches:	188
Query Match:	15.53%	Indels:	125
RESULT 883			
ID ABL22159 standard; DNA; 1833 BP.			
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17950.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE ) PE CORP NY.			
Percent Similarity:	37.83%	Conservative:	22
Best Local Similarity:	32.53%	Mismatches:	164
Query Match:	15.49%	Indels:	94
RESULT 884			
ID AAD55732 standard; DNA; 2078 BP.			
DE Dolomedes tenebrosus fibroin 2 DNA.			
PN WO2003020916-A2.			
PD 13-MAR-2003.			
PA (UYWY-) UNIV WYOMING.			
Percent Similarity:	37.37%	Conservative:	49
Best Local Similarity:	26.96%	Mismatches:	221
Query Match:	15.49%	Indels:	74
RESULT 885			
ID ABL61043 standard; DNA; 1908 BP.			
DE N. clavipes spider protein synthetic homologue SO1.			
PN DE10113781-A1.			
PD 13-DEC-2001.			
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.			
Percent Similarity:	39.86%	Conservative:	43
Best Local Similarity:	29.59%	Mismatches:	189
Query Match:	15.47%	Indels:	63
RESULT 887			
ID ACA40309 standard; DNA; 1776 BP.			
DE Prokaryotic essential gene #21966.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	38.82%	Conservative:	40
Best Local Similarity:	29.41%	Mismatches:	150
Query Match:	15.45%	Indels:	110
RESULT 889			
ID ACA40410 standard; DNA; 1821 BP.			
DE Prokaryotic essential gene #22067.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	39.27%	Conservative:	44
Best Local Similarity:	29.83%	Mismatches:	167
Query Match:	15.40%	Indels:	116
RESULT 891			
ID ACA40555 standard; DNA; 1920 BP.			
DE Prokaryotic essential gene #22212.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	39.27%	Conservative:	44
Best Local Similarity:	29.83%	Mismatches:	167
Query Match:	15.40%	Indels:	116
RESULT 892			
ID ACA40555 standard; DNA; 1920 BP.			
DE Prokaryotic essential gene #22212.			
PN WO200277183-A2.			
PD 03-OCT-2002.			
PA (ELIT-) ELITRA PHARM INC.			
Percent Similarity:	39.27%	Conservative:	44
Best Local Similarity:	29.83%	Mismatches:	167
Query Match:	15.40%	Indels:	116

PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 894  
ID AAO51557 standard; DNA; 6530 BP.  
DE Loricrin gene.  
PN WO322431-A1.  
PD 11-NOV-1993.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 895  
ID AAZ22072 standard; DNA; 6530 BP.  
DE Nucleotide sequence of the loricrin gene.  
PN US958764-A.  
PD 28-SEP-1999.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 896  
ID AAC68948 standard; DNA; 6530 BP.  
DE Mouse loricrin gene.  
PN US6143727-A.  
PD 07-NOV-2000.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 897  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 898  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 899  
ID AAS37277 standard; cDNA; 404 BP.  
DE Novel human diagnostic and therapeutic gene #335.  
PN WO200166753-A2.  
PD 13-SEP-2001.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 51.43%  
Best Local Similarity: 49.14%  
Query Match: 15.34%  
RESULT 900  
Percent Similarity: 38.29%  
Best Local Similarity: 28.67%  
Query Match: 15.34%  
RESULT 901  
ID ACA40900 standard; DNA; 1797 BP.  
DE Prokaryotic essential gene #22557.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 41.38%  
Best Local Similarity: 32.51%  
Query Match: 15.28%  
RESULT 902  
ID AAV44448 standard; DNA; 2367 BP.  
DE Mycobacterium tuberculosis antigen RDIF7 DNA.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.76%  
Best Local Similarity: 29.32%  
Query Match: 15.28%  
RESULT 903  
ID AAV64557 standard; DNA; 2367 BP.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 894  
ID AAO51557 standard; DNA; 6530 BP.  
DE Loricrin gene.  
PN WO322431-A1.  
PD 11-NOV-1993.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 895  
ID AAZ22072 standard; DNA; 6530 BP.  
DE Nucleotide sequence of the loricrin gene.  
PN US958764-A.  
PD 28-SEP-1999.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 896  
ID AAC68948 standard; DNA; 6530 BP.  
DE Mouse loricrin gene.  
PN US6143727-A.  
PD 07-NOV-2000.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Percent Similarity: 38.18%  
Best Local Similarity: 31.82%  
Query Match: 15.36%  
RESULT 897  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 898  
Percent Similarity: 40.39%  
Best Local Similarity: 30.54%  
Query Match: 15.36%  
RESULT 899  
ID AAS37277 standard; cDNA; 404 BP.  
DE Novel human diagnostic and therapeutic gene #335.  
PN WO200166753-A2.  
PD 13-SEP-2001.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 51.43%  
Best Local Similarity: 49.14%  
Query Match: 15.34%  
RESULT 900  
Percent Similarity: 38.29%  
Best Local Similarity: 28.67%  
Query Match: 15.34%  
RESULT 901  
ID ACA40900 standard; DNA; 1797 BP.  
DE Prokaryotic essential gene #22557.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 41.38%  
Best Local Similarity: 32.51%  
Query Match: 15.28%  
RESULT 902  
ID AAV44448 standard; DNA; 2367 BP.  
DE Mycobacterium tuberculosis antigen RDIF7 DNA.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.76%  
Best Local Similarity: 29.32%  
Query Match: 15.28%  
RESULT 903  
ID AAV64557 standard; DNA; 2367 BP.  
DE Mycobacterium tuberculosis antigen RDIF7 DNA.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.76%  
Best Local Similarity: 29.32%  
Query Match: 15.28%  
RESULT 904  
ID AAZ19146 standard; DNA; 2367 BP.  
DE M. tuberculosis recombinant antigen DNA encoding RDIF7.  
PN WO9942118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.76%  
Best Local Similarity: 29.32%  
Query Match: 15.28%  
RESULT 905  
ID AAZ19358 standard; DNA; 2367 BP.  
DE M. tuberculosis antigen RDIF7 DNA sequence.  
PN WO9942076-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.76%  
Best Local Similarity: 29.32%  
Query Match: 15.28%  
RESULT 906  
ID ADQ97654 standard; DNA; 30191 BP.  
DE Mouse cancer associated sequence MD10-022, SEQ ID 631.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 39.90%  
Best Local Similarity: 30.97%  
Query Match: 15.28%  
RESULT 907  
Percent Similarity: 41.38%  
Best Local Similarity: 32.51%  
Query Match: 15.28%  
RESULT 908  
ID ACA40460 standard; DNA; 1689 BP.  
DE Prokaryotic essential gene #22117.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 37.14%  
Best Local Similarity: 28.86%  
Query Match: 15.23%  
RESULT 909  
ID ABN85850 standard; DNA; 2062 BP.  
DE Nucleotide sequence related to Bombyx mori silk fibroin.  
PN WO200240528-A1.  
PD 23-MAY-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Percent Similarity: 36.57%  
Best Local Similarity: 28.67%  
Query Match: 15.23%  
RESULT 910  
ID ABX09141 standard; DNA; 75216 BP.  
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv230.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP ) INST PASTEUR.  
Percent Similarity: 37.14%  
Best Local Similarity: 28.86%  
Query Match: 15.23%  
RESULT 911  
Percent Similarity: 37.14%  
Best Local Similarity: 28.86%  
Query Match: 15.23%  
RESULT 912  
Percent Similarity: 37.14%  
Best Local Similarity: 28.86%  
Query Match: 15.23%



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RESULT 913
ID ACA40535 standard; DNA; 3036 BP.
DE Prokaryotic essential gene #22192.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 39.76%
Best Local Similarity: 31.19%
Query Match: 15.21%
Conservative: 36
Mismatch: 188
Indels: 65
RESULT 914
Percent Similarity: 39.76%
Best Local Similarity: 31.19%
Query Match: 15.21%
Conservative: 36
Mismatch: 188
Indels: 65
RESULT 915
Percent Similarity: 37.72%
Best Local Similarity: 29.74%
Query Match: 15.21%
Conservative: 40
Mismatch: 186
Indels: 126
RESULT 916
ID AAL51691 standard; cDNA; 1711 BP.
DE Phidippus audax fibronin 1 coding sequence.
PN WO20029082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Percent Similarity: 40.36%
Best Local Similarity: 28.93%
Query Match: 15.19%
Conservative: 45
Mismatch: 207
Indels: 28
RESULT 917
ID AAD55738 standard; DNA; 1711 BP.
DE Phidippus audax fibroin 1 DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Percent Similarity: 40.36%
Best Local Similarity: 28.93%
Query Match: 15.19%
Conservative: 45
Mismatch: 207
Indels: 28
RESULT 918
ID AAD55731 standard; DNA; 2565 BP.
DE Dolomedes tenebrosus fibroin 1 DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Percent Similarity: 37.30%
Best Local Similarity: 27.34%
Query Match: 15.19%
Conservative: 51
Mismatch: 199
Indels: 124
RESULT 919
Percent Similarity: 33.76%
Best Local Similarity: 27.52%
Query Match: 15.17%
Conservative: 34
Mismatch: 177
Indels: 184
RESULT 920
ID AAS18230 standard; cDNA; 2457 BP.
DE Dragline protein 1 analogue DP-1B/his tag 8mer cDNA.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Percent Similarity: 42.42%
Best Local Similarity: 30.30%
Query Match: 15.15%
Conservative: 52
Mismatch: 163
Indels: 84
RESULT 921
ID AAS18231 standard; cDNA; 4861 BP.
DE Dragline protein 1 analogue DP-1B/his tag 16mer cDNA.
PN WO200190389-A2.
PD 29-NOV-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Percent Similarity: 42.42%
Best Local Similarity: 30.30%
Query Match: 15.15%
Conservative: 52
Mismatch: 163
Indels: 84
RESULT 922
ID AAL51693 standard; cDNA; 2282 BP.
DE Kukulcania hibernalis spider silk protein coding sequence #1.
PN WO20029082-A2.
PD 12-DEC-2002.
PA (UYWY-) UNIV WYOMING.
Percent Similarity: 38.22%
Conservative: 42

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Best Local Similarity: 28.12%
Query Match: 15.11%
Mismatch: 197
Indels: 60
RESULT 923
Percent Similarity: 39.76%
Best Local Similarity: 29.88%
Query Match: 15.09%
Conservative: 42
Mismatch: 175
Indels: 81
RESULT 924
ID ADC87240 standard; DNA; 1231 BP.
DE Human GPCR gene SEQ ID NO:1693.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Percent Similarity: 39.34%
Best Local Similarity: 31.69%
Query Match: 15.04%
Conservative: 28
Mismatch: 149
Indels: 74
RESULT 925
ID ACH91938 standard; DNA; 1493 BP.
DE Human genome derived single exon probe #25133.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Percent Similarity: 35.48%
Best Local Similarity: 29.82%
Query Match: 15.04%
Conservative: 22
Mismatch: 202
Indels: 49
RESULT 926
ID AAQ55750 standard; DNA; 1505 BP.
DE Genomic clone G11F, includes a Brassica root specific promoter.
PN WO9402619-A1.
PD 03-FEB-1994.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 32.82%
Best Local Similarity: 28.21%
Query Match: 15.02%
Conservative: 18
Mismatch: 148
Indels: 114
RESULT 927
ID ACA40307 standard; DNA; 2874 BP.
DE Prokaryotic essential gene #21964.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 39.80%
Best Local Similarity: 31.84%
Query Match: 14.98%
Conservative: 32
Mismatch: 164
Indels: 79
RESULT 928
Percent Similarity: 37.00%
Best Local Similarity: 30.62%
Query Match: 14.98%
Conservative: 29
Mismatch: 201
Indels: 85
RESULT 929
ID ACA38287 standard; DNA; 1515 BP.
DE Prokaryotic essential gene #19944.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 42.44%
Best Local Similarity: 32.36%
Query Match: 14.94%
Conservative: 38
Mismatch: 139
Indels: 78
RESULT 930
ID ACA25563 standard; DNA; 1062 BP.
DE Prokaryotic essential gene #7220.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.28%
Best Local Similarity: 33.61%
Query Match: 14.90%
Conservative: 24
Mismatch: 146
Indels: 69
RESULT 931
ID ACA40483 standard; DNA; 1812 BP.
DE Prokaryotic essential gene #22140.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

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Percent Similarity: 38.19% Conservative: 37  
 Best Local Similarity: 30.02% Mismatches: 195  
 Query Match: 14.90% Indels: 86  
 RESULT 932  
 Percent Similarity: 38.19% Conservative: 37  
 Best Local Similarity: 30.02% Mismatches: 195  
 Query Match: 14.90% Indels: 86  
 RESULT 933  
 ID ACA40696 standard; DNA; 1386 BP.  
 DE Prokaryotic essential gene #22353.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 43.49% Conservative: 49  
 Best Local Similarity: 31.45% Mismatches: 154  
 Query Match: 14.83% Indels: 77  
 RESULT 934  
 ID ADQ19956 standard; DNA; 1218 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2776.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 39.74% Conservative: 14  
 Best Local Similarity: 35.26% Mismatches: 94  
 Query Match: 14.81% Indels: 94  
 RESULT 935  
 ID ADO24041 standard; DNA; 1280 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6861.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 39.74% Conservative: 14  
 Best Local Similarity: 35.26% Mismatches: 94  
 Query Match: 14.81% Indels: 94  
 RESULT 936  
 ID ADJ39845 standard; cDNA; 1287 BP.  
 DE Plant cDNA #845.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GORF/) GORF S A.  
 PA (KAT/) KATAGIRI P.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICKS D.  
 PA (ZHUT/) ZHU T.  
 Percent Similarity: 37.82% Conservative: 29  
 Best Local Similarity: 30.46% Mismatches: 168  
 Query Match: 14.79% Indels: 79  
 RESULT 937  
 ID ADR96677 standard; DNA; 1854 BP.  
 DE M. tuberculosis antigen Rv1768 DNA SEQ ID NO:103.  
 PN WO2004083448-A2.  
 PD 30-SEP-2004.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PA (STAT-) STATENS SERUM INST.  
 Percent Similarity: 39.08% Conservative: 40  
 Best Local Similarity: 29.89% Mismatches: 179  
 Query Match: 14.77% Indels: 86  
 RESULT 938  
 ID ACA40554 standard; DNA; 1857 BP.  
 DE Prokaryotic essential gene #22311.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.08% Conservative: 40  
 Best Local Similarity: 29.89% Mismatches: 179  
 Query Match: 14.77% Indels: 86  
 RESULT 939

Percent Similarity: 39.08% Conservative: 40  
 Best Local Similarity: 29.89% Mismatches: 179  
 Query Match: 14.77% Indels: 86  
 RESULT 940  
 Percent Similarity: 39.08% Conservative: 40  
 Best Local Similarity: 29.89% Mismatches: 179  
 Query Match: 14.77% Indels: 86  
 RESULT 941  
 ID AAQ98470 standard; cDNA; 2744 BP.  
 DE MiSP1-containing plasmid pMISS1.  
 PN WO9525165-A1.  
 PD 21-SEP-1995.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 39.10% Conservative: 48  
 Best Local Similarity: 28.31% Mismatches: 203  
 Query Match: 14.75% Indels: 69  
 RESULT 942  
 ID AAT93610 standard; DNA; 3946 BP.  
 DE Mycobacterium tuberculosis genomic DNA fragment (I).  
 PN WO9741252-A2.  
 PD 06-NOV-1997.  
 PA (GBEB) GBF GES BIOTECH FORSCHUNG GMBH.  
 Percent Similarity: 40.20% Conservative: 33  
 Best Local Similarity: 32.01% Mismatches: 161  
 Query Match: 14.73% Indels: 81  
 RESULT 943  
 ID AAH26304 standard; DNA; 1588 BP.  
 DE Spider silk protein gene PETNCD5.  
 PN WO200153333-A1.  
 PD 26-JUL-2001.  
 PA (MELL/) MELLO C M.  
 PA (ARCI/) ARCIDIACONO S.  
 PA (BUTL/) BUTLER M M.  
 PA (USSA) US SEC OF ARMY.  
 Percent Similarity: 36.88% Conservative: 35  
 Best Local Similarity: 28.96% Mismatches: 196  
 Query Match: 14.71% Indels: 83  
 RESULT 944  
 Percent Similarity: 38.95% Conservative: 35  
 Best Local Similarity: 30.98% Mismatches: 211  
 Query Match: 14.68% Indels: 58  
 RESULT 945  
 ID ACA40559 standard; DNA; 1548 BP.  
 DE Prokaryotic essential gene #22216.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.89% Conservative: 41  
 Best Local Similarity: 29.26% Mismatches: 190  
 Query Match: 14.64% Indels: 105  
 RESULT 946  
 ID AAD55714 standard; DNA; 1947 BP.  
 DE Argiope trifasciata major ampullate spidroin 1 (MaSp1) DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 37.53% Conservative: 49  
 Best Local Similarity: 27.25% Mismatches: 186  
 Query Match: 14.64% Indels: 112  
 RESULT 947  
 ID AAC01489 standard; cDNA; 530 BP.  
 DE Human secreted protein 5' EST, SEQ ID NO: 1487.  
 PN EP1033401-A2.  
 PD 06-SEP-2000.  
 PA (GEST) GENSET.  
 Percent Similarity: 58.87% Conservative: 1  
 Best Local Similarity: 58.06% Mismatches: 1  
 Query Match: 14.60% Indels: 51  
 RESULT 948  
 ID AAQ03665 standard; DNA; 2465 BP.  
 DE Sequence homologous to Drosophila Per gene.  
 PN FR2635116-A.  
 PD 09-FEB-1990.

PA (GEOR/) GEORGS M.  
Percent Similarity: 36.36%  
Best Local Similarity: 27.72%  
Query Match: 14.60%  
Indels: 84  
Conservative: 39  
Mismatches: 203  
Indels: 84

RESULT 949  
ID ACA0709 standard; DNA; 1578 BP.  
DE Prokaryotic essential gene #22366.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 37.91%  
Best Local Similarity: 30.93%  
Query Match: 14.56%  
Indels: 91  
Conservative: 30  
Mismatches: 177  
Indels: 91

RESULT 950  
ID AAD5729 standard; DNA; 1958 BP.  
DE Argiope trifasciata flagelliform silk protein (Flag) encoding DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWI-) UNIV WYOMING.  
Percent Similarity: 32.80%  
Best Local Similarity: 27.20%  
Query Match: 14.56%  
Indels: 136  
Conservative: 28  
Mismatches: 201  
Indels: 136

RESULT 951  
Percent Similarity: 37.91%  
Best Local Similarity: 30.93%  
Query Match: 14.56%  
Indels: 91  
Conservative: 30  
Mismatches: 177  
Indels: 91

RESULT 952  
Percent Similarity: 39.57%  
Best Local Similarity: 31.75%  
Query Match: 14.56%  
Indels: 69  
Conservative: 33  
Mismatches: 187  
Indels: 69

RESULT 953  
ID AAH26302 standard; DNA; 2046 BP.  
DE Spider silk protein gene pQR((SP1)4/(SP2)1)4.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIADACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Percent Similarity: 39.40%  
Best Local Similarity: 28.27%  
Query Match: 14.52%  
Indels: 86  
Conservative: 52  
Mismatches: 197  
Indels: 86

RESULT 954  
ID AAH26303 standard; DNA; 2076 BP.  
DE Spider silk protein gene pET((SP1)4/(SP2)1)4.  
PN WO200153333-A1.  
PD 26-JUL-2001.  
PA (MELL/) MELLO C M.  
PA (ARCI/) ARCIADACONO S.  
PA (BUTL/) BUTLER M M.  
PA (USSA) US SEC OF ARMY.  
Percent Similarity: 39.40%  
Best Local Similarity: 28.27%  
Query Match: 14.52%  
Indels: 86  
Conservative: 52  
Mismatches: 197  
Indels: 86

RESULT 955  
ID ABL61053 standard; DNA; 2322 BP.  
DE N. clavipes spideroin homologue SM12-70xELP DNA for plant expression.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 39.95%  
Best Local Similarity: 29.43%  
Query Match: 14.49%  
Indels: 53  
Conservative: 44  
Mismatches: 198  
Indels: 53

RESULT 956  
ID ABL61054 standard; DNA; 2334 BP.  
DE N. clavipes spideroin homologue SM12-70xELP DNA for E. coli expression.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPRP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 39.95%  
Best Local Similarity: 29.43%  
Query Match: 14.49%  
Indels: 53  
Conservative: 44  
Mismatches: 198  
Indels: 53

RESULT 957  
ID AAV55831 standard; DNA; 799 BP.  
DE Nucleotide sequence of the stabilising sequence-encoding insert.

Percent Similarity: 38.81%  
Best Local Similarity: 30.59%  
Query Match: 14.49%  
Indels: 92  
Conservative: 36  
Mismatches: 176  
Indels: 92

RESULT 958  
ID ACA0293 standard; DNA; 1464 BP.  
DE Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.24%  
Best Local Similarity: 29.88%  
Query Match: 14.37%  
Indels: 67  
Conservative: 43  
Mismatches: 181  
Indels: 67

RESULT 959  
ID AAS92828 standard; cDNA; 1200 BP.  
DE DNA encoding novel human diagnostic protein #28632.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 39.39%  
Best Local Similarity: 36.74%  
Query Match: 14.30%  
Indels: 46  
Conservative: 7  
Mismatches: 115  
Indels: 46

RESULT 960  
ID ABK98631 standard; DNA; 12733 BP.  
DE Vector pPEPF14 containing L. lactis derived promoter sequence.  
PN WO200251982-A2.  
PD 04-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.21%  
Best Local Similarity: 33.21%  
Query Match: 14.30%  
Indels: 16  
Conservative: 0  
Mismatches: 161  
Indels: 16

RESULT 961  
ID ACD13882 standard; DNA; 12733 BP.  
DE L. lactis promoter containing plasmid pPEPF14.  
PN US2003027286-A1.  
PD 06-FEB-2003.  
PA (HASE/) HASELBECK R.  
PA (WALL/) WALL D.  
PA (GROS/) GROSS M.  
Percent Similarity: 33.21%  
Best Local Similarity: 33.21%  
Query Match: 14.30%  
Indels: 16  
Conservative: 0  
Mismatches: 161  
Indels: 16

RESULT 962  
ID ABK98592 standard; DNA; 12739 BP.  
DE Vector pPEPF1 containing XylR/XylO/CP25 sequences.  
PN WO200251982-A2.  
PD 04-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.21%  
Best Local Similarity: 33.21%  
Query Match: 14.30%  
Indels: 16  
Conservative: 0  
Mismatches: 161  
Indels: 16

RESULT 963  
ID ACD13843 standard; DNA; 12739 BP.  
DE Plasmid pPEPF1 containing a Xyl5-CP25 fusion promoter.  
PN US2003027286-A1.  
PD 06-FEB-2003.  
PA (HASE/) HASELBECK R.  
PA (WALL/) WALL D.  
PA (GROS/) GROSS M.  
Percent Similarity: 33.21%  
Best Local Similarity: 33.21%  
Query Match: 14.30%  
Indels: 16  
Conservative: 0  
Mismatches: 161  
Indels: 16

RESULT 964  
ID AAD55730 standard; DNA; 3008 BP.  
DE Argiope trifasciata flag protein encoding DNA fragment.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWI-) UNIV WYOMING.  
Percent Similarity: 36.70%  
Best Local Similarity: 29.45%  
Query Match: 14.26%  
Indels: 70  
Conservative: 33  
Mismatches: 218  
Indels: 70

RESULT 965  
ID AAV55831 standard; DNA; 799 BP.  
DE Nucleotide sequence of the stabilising sequence-encoding insert.

PN WO9822577-A1.  
 PD 28-MAY-1998.  
 PA (MASU/) MASUCCI M G.  
 Percent Similarity: 39.51%  
 Best Local Similarity: 28.34%  
 Query Match: 14.24%  
 Indels: 105  
 Conservative: 41  
 Mismatches: 117  
 Indels: 105

RESULT 966  
 ID ABV96116 standard; cDNA; 437 BP.  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 1524.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 56.90%  
 Best Local Similarity: 56.03%  
 Query Match: 14.22%  
 Indels: 50  
 Conservative: 1  
 Mismatches: 0  
 Indels: 50

RESULT 967  
 Percent Similarity: 35.68%  
 Best Local Similarity: 30.05%  
 Query Match: 14.18%  
 Indels: 112  
 Conservative: 24  
 Mismatches: 162  
 Indels: 112

RESULT 968  
 ID ABZ13007 standard; DNA; 768 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 812.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI ) SCRIPPS RES INST.  
 Percent Similarity: 37.04%  
 Best Local Similarity: 30.25%  
 Query Match: 14.13%  
 Indels: 88  
 Conservative: 22  
 Mismatches: 116  
 Indels: 88

RESULT 969  
 ID ACA0556 standard; DNA; 1497 BP.  
 DE Prokaryotic essential gene #2213.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.18%  
 Best Local Similarity: 29.32%  
 Query Match: 14.13%  
 Indels: 96  
 Conservative: 39  
 Mismatches: 176  
 Indels: 96

RESULT 970  
 ID AAD55713 standard; DNA; 1344 BP.  
 DE Argiope aurantia major ampullate spidroin 1 (Maspl) DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 39.11%  
 Best Local Similarity: 31.38%  
 Query Match: 14.11%  
 Indels: 76  
 Conservative: 33  
 Mismatches: 184  
 Indels: 76

RESULT 971  
 ID ABL61044 standard; DNA; 1110 BP.  
 DE N. clavipes spidroin synthetic homologue SM12.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPXP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Percent Similarity: 37.94%  
 Best Local Similarity: 27.87%  
 Query Match: 14.09%  
 Indels: 83  
 Conservative: 43  
 Mismatches: 183  
 Indels: 83

RESULT 972  
 ID ABL24269 standard; DNA; 1181 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24280.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE ) PE CORP NY.  
 Percent Similarity: 35.15%  
 Best Local Similarity: 29.45%  
 Query Match: 14.07%  
 Indels: 113  
 Conservative: 24  
 Mismatches: 160  
 Indels: 113

RESULT 973  
 ID ABL24268 standard; DNA; 4905 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24277.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE ) PE CORP NY.  
 Percent Similarity: 35.15%  
 Best Local Similarity: 29.45%  
 Query Match: 14.07%  
 Indels: 113  
 Conservative: 24  
 Mismatches: 160  
 Indels: 113

Query Match: 14.07%  
 Indels: 113  
 Conservative: 26  
 Mismatches: 157  
 Indels: 117

RESULT 974  
 Percent Similarity: 35.98%  
 Best Local Similarity: 29.91%  
 Query Match: 14.07%  
 Indels: 117  
 Conservative: 26  
 Mismatches: 157  
 Indels: 117

RESULT 975  
 ID ADC86984 standard; DNA; 1390 BP.  
 DE Human GPCR gene SEQ ID NO:1437.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 Percent Similarity: 40.14%  
 Best Local Similarity: 30.99%  
 Query Match: 14.05%  
 Indels: 86  
 Conservative: 42  
 Mismatches: 185  
 Indels: 103

RESULT 976  
 Percent Similarity: 37.53%  
 Best Local Similarity: 28.42%  
 Query Match: 14.03%  
 Indels: 103  
 Conservative: 42  
 Mismatches: 185  
 Indels: 103

RESULT 977  
 ID ABQ62495 standard; DNA; 1280 BP.  
 DE Mycobacterium bovis polynucleotide sequence SEQ ID NO:4.  
 PN WO9954487-A2.  
 PD 28-OCT-1999.  
 PA (INSP ) INST PASTEUR.  
 Percent Similarity: 39.85%  
 Best Local Similarity: 31.78%  
 Query Match: 14.01%  
 Indels: 86  
 Conservative: 33  
 Mismatches: 160  
 Indels: 86

RESULT 978  
 ID ACH90933 standard; DNA; 1935 BP.  
 DE Human genome derived single exon probe #24128.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 Percent Similarity: 38.01%  
 Best Local Similarity: 29.81%  
 Query Match: 13.97%  
 Indels: 118  
 Conservative: 38  
 Mismatches: 169  
 Indels: 118

RESULT 979  
 ID AAS87782 standard; cDNA; 2730 BP.  
 DE DNA encoding novel human diagnostic protein #23586.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 38.26%  
 Best Local Similarity: 30.28%  
 Query Match: 13.86%  
 Indels: 62  
 Conservative: 34  
 Mismatches: 202  
 Indels: 62

RESULT 980  
 ID ACA40851 standard; DNA; 1320 BP.  
 DE Prokaryotic essential gene #22508.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.12%  
 Best Local Similarity: 28.95%  
 Query Match: 13.77%  
 Indels: 109  
 Conservative: 30  
 Mismatches: 158  
 Indels: 109

RESULT 981  
 ID ACA40343 standard; DNA; 1785 BP.  
 DE Prokaryotic essential gene #22000.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.48%  
 Best Local Similarity: 30.88%  
 Query Match: 13.73%  
 Indels: 93  
 Conservative: 33  
 Mismatches: 175  
 Indels: 93

RESULT 982  
 Percent Similarity: 38.48%  
 Best Local Similarity: 30.88%  
 Query Match: 13.73%  
 Indels: 93  
 Conservative: 33  
 Mismatches: 175  
 Indels: 93

RESULT 983  
 ID ABL28035 standard; DNA; 1863 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35578.

PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 33.22%  
 Best Local Similarity: 43  
 Mismatches: 193  
 Indels: 206  
 Query Match: 13.54%  
 RESULT 984  
 ID AAD55726 standard; DNA; 5858 BP.  
 DE Nephila madagascariensis major ampullate spidroin 2 (MasP2)-like DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 34.95%  
 Best Local Similarity: 26.95%  
 Mismatches: 213  
 Indels: 96  
 Query Match: 13.54%  
 RESULT 985  
 ID ABT19761 standard; DNA; 5379 BP.  
 DE Aspergillus fumigatus essential gene #2119.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 42.00%  
 Best Local Similarity: 27.68%  
 Mismatches: 200  
 Indels: 44  
 Query Match: 13.48%  
 RESULT 986  
 ID AAS91437 standard; cDNA; 3297 BP.  
 DE DNA encoding novel human diagnostic protein #27241.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 35.91%  
 Best Local Similarity: 29.68%  
 Mismatches: 190  
 Indels: 68  
 Query Match: 13.44%  
 RESULT 987  
 ID AAD23835 standard; cDNA; 1172 BP.  
 DE Sugarcane proline rich protein 1 (SPRP1) cDNA clone insert.  
 PN WO200177318-A1.  
 PD 18-OCT-2001.  
 PA (TEXA ) UNIV TEXAS A & M.  
 Percent Similarity: 41.21%  
 Best Local Similarity: 34.91%  
 Mismatches: 158  
 Indels: 66  
 Query Match: 13.42%  
 RESULT 988  
 ID ADO59400 standard; cDNA; 9921 BP.  
 DE Antherea yamamai fibroin cDNA.  
 PN KR2002094304-A.  
 PD 18-DEC-2002.  
 PA (RURA-) RURAL DEV ADMINISTRATION.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 27.65%  
 Mismatches: 200  
 Indels: 80  
 Query Match: 13.42%  
 RESULT 989  
 ID AAZ52247 standard; DNA; 3416 BP.  
 DE Maize glycine-rich protein 3 partial genomic clone zmGRP3.  
 PN WO200015662-A1.  
 PD 23-MAR-2000.  
 PA (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.  
 Percent Similarity: 37.38%  
 Best Local Similarity: 27.18%  
 Mismatches: 129  
 Indels: 130  
 Query Match: 13.37%  
 RESULT 990  
 ID AAT86623 standard; DNA; 4992 BP.  
 DE C. thermocellum O1pB gene.  
 PN FR2748479-A1.  
 PD 14-NOV-1997.  
 PA (INSP ) INST PASTEUR.  
 Percent Similarity: 41.33%  
 Best Local Similarity: 30.00%  
 Mismatches: 189  
 Indels: 75  
 Query Match: 13.35%  
 RESULT 991  
 ID AAV55830 standard; DNA; 795 BP.  
 DE FLGA insert stabilising polypeptide encoding DNA.  
 PN WO9822577-A1.

PD 28-MAY-1998.  
 PA (MASU/) MASUCCI M G.  
 Percent Similarity: 38.15%  
 Best Local Similarity: 27.52%  
 Mismatches: 122  
 Indels: 106  
 Query Match: 13.31%  
 RESULT 992  
 ID ABX09142 standard; DNA; 80557 BP.  
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV2234.  
 PN WO200274903-A2.  
 PD 26-SEP-2002.  
 PA (INSP ) INST PASTEUR.  
 Percent Similarity: 37.85%  
 Best Local Similarity: 30.14%  
 Mismatches: 173  
 Indels: 93  
 Query Match: 13.31%  
 RESULT 993  
 Percent Similarity: 37.85%  
 Best Local Similarity: 30.14%  
 Mismatches: 173  
 Indels: 93  
 Query Match: 13.31%  
 RESULT 994  
 Percent Similarity: 37.85%  
 Best Local Similarity: 30.14%  
 Mismatches: 173  
 Indels: 93  
 Query Match: 13.31%  
 RESULT 995  
 ID AAL00189 standard; cDNA; 349 BP.  
 DE Human reproductive system related antigen cDNA SEQ ID NO: 190.  
 PN WO20015320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 98.25%  
 Mismatches: 0  
 Indels: 0  
 Query Match: 13.29%  
 RESULT 996  
 ID ABL09834 standard; cDNA; 5751 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23984.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 35.23%  
 Best Local Similarity: 26.22%  
 Mismatches: 237  
 Indels: 95  
 Query Match: 13.29%  
 RESULT 997  
 ID ACN54594 standard; cDNA; 629 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D2, SEQ:9375.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FENG/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Percent Similarity: 35.94%  
 Best Local Similarity: 33.20%  
 Mismatches: 103  
 Indels: 61  
 Query Match: 13.27%  
 RESULT 998  
 ID ADC87619 standard; DNA; 34981 BP.  
 DE Human GPCR related polynucleotide SEQ ID NO:2072.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Percent Similarity: 40.80%  
 Best Local Similarity: 33.11%  
 Mismatches: 137  
 Indels: 40  
 Query Match: 13.12%  
 RESULT 999  
 ID ABL09835 standard; cDNA; 3222 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23987.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKS ) PE CORP NY.  
 Percent Similarity: 35.74%  
 Best Local Similarity: 26.51%  
 Mismatches: 239  
 Indels: 82  
 Query Match: 13.08%  
 RESULT 1000  
 Percent Similarity: 37.01%  
 Conservative: 33

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Best Local Similarity: 28.92% Mismatches: 175
Query Match: 13.08% Indels: 82
RESULT 1001
ID ADJ44468 standard; cDNA; 705 BP.
DE Plant cDNA #5468.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 40.89% Conservative: 11
Best Local Similarity: 36.44% Mismatches: 108
Query Match: 12.82% Indels: 38
RESULT 1008
ID AAQ63879 standard; DNA; 4018 BP.
DE Polyhydroxyalkanoate decomposing activity polypeptide.
PN JP0608681-A.
PD 29-MAR-1994.
PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
PA (UYKA-) GH KANAGAWA DAIGAKU.
PA (ELED-) DENKI KAGAKU KOGYO KK.
Percent Similarity: 38.19% Conservative: 32
Best Local Similarity: 29.40% Mismatches: 140
Query Match: 12.82% Indels: 85
RESULT 1009
ID ADT42783 standard; cDNA; 1779 BP.
DE Bacterial polynucleotide #17534.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 32.28% Conservative: 19
Best Local Similarity: 27.67% Mismatches: 107
Query Match: 12.78% Indels: 172
RESULT 1010
ID AAQ76213 standard; DNA; 12001 BP.
DE HSV L/ST region.
PN W09428156-A1.
PD 08-DEC-1994.
PA (DAND) DANA FARBER CANCER INST INC.
Percent Similarity: 37.50% Conservative: 25
Best Local Similarity: 31.60% Mismatches: 157
Query Match: 12.78% Indels: 110
RESULT 1011
ID ADJ39659 standard; cDNA; 669 BP.
DE Plant cDNA #659.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 40.00% Conservative: 19
Best Local Similarity: 32.83% Mismatches: 82
Query Match: 12.76% Indels: 77
RESULT 1012
ID AAV22682 standard; DNA; 2214 BP.
DE New DNA sequence isolated from Pinctada fucata.
PN JP10080285-A.
PD 31-MAR-1998.
PA (MIKI-) MIKIMOTO SEIYAKU KK.
Percent Similarity: 32.75% Conservative: 43

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Best Local Similarity: 28.92% Mismatches: 175
Query Match: 13.08% Indels: 82
RESULT 1001
ID ADJ44468 standard; cDNA; 705 BP.
DE Plant cDNA #5468.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Percent Similarity: 39.61% Conservative: 12
Best Local Similarity: 34.90% Mismatches: 86
Query Match: 12.99% Indels: 68
RESULT 1002
ID ADK67003 standard; DNA; 15750 BP.
DE Gene #93 for inhibitory RNA to manipulate stem cell phenotype.
PN WO2003068961-A2.
PD 21-AUG-2003.
PA (AXOR-) AXORDIA LTD.
Percent Similarity: 37.83% Conservative: 46
Best Local Similarity: 28.57% Mismatches: 136
Query Match: 12.97% Indels: 114
RESULT 1003
ID ADQ85335 standard; cDNA; 15789 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2149.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 37.83% Conservative: 46
Best Local Similarity: 28.57% Mismatches: 136
Query Match: 12.97% Indels: 114
RESULT 1004
ID ACN39422 standard; cDNA; 15789 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325641, SEQ ID NO:3554.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.83% Conservative: 46
Best Local Similarity: 28.57% Mismatches: 136
Query Match: 12.97% Indels: 114
RESULT 1005
ID ADQ36956 standard; DNA; 1251 BP.
DE Cell proliferation-related nucleic acid sequence #58.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 40.36% Conservative: 25
Best Local Similarity: 33.85% Mismatches: 169
Query Match: 12.87% Indels: 60
RESULT 1006
ID ADQ15626 standard; DNA; 1251 BP.
DE Rice stress-related protein coding sequence #18.
PN WO2004061080-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 40.36% Conservative: 25
Best Local Similarity: 33.85% Mismatches: 169
Query Match: 12.87% Indels: 60
RESULT 1007
ID ADJ39682 standard; cDNA; 692 BP.
DE Plant cDNA #682.
PN US2004016025-A1.
PD 22-JAN-2004.

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Best Local Similarity: 24.37% Mismatches: 191  
 Query Match: 12.70% Indels: 154  
 RESULT 1013  
 ID AAV22683 standard; cDNA to mRNA; 3331 BP.  
 DE New DNA sequence isolated from Pinctada fucata.  
 PN JP10080285-A.  
 PD. 31-MAR-1998.  
 PA (MIKI-) MIKIMOTO SEIVAKU KK.  
 Percent Similarity: 32.75%  
 Best Local Similarity: 24.37%  
 Mismatches: 191  
 Indels: 154  
 Query Match: 12.70%  
 RESULT 1014  
 ID AAZ32021 standard; DNA; 3331 BP.  
 DE Human METH1 related EST D86074.  
 PN WO9937660-A1.  
 PD 29-JUL-1999.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 Percent Similarity: 32.75%  
 Best Local Similarity: 24.37%  
 Mismatches: 191  
 Indels: 154  
 Query Match: 12.70%  
 RESULT 1015  
 ID AAC90078 standard; DNA; 3331 BP.  
 DE D86074 cDNA clone.  
 PN WO200071577-A1.  
 PD 30-NOV-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK-) SMITHKLINE BEECHAM CORP.  
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 PA (JONA-) JONAK Z L.  
 PA (TRUL/) TRULLI S H.  
 PA (FORN/) FORNWARD J A.  
 PA (TERR/) TERRETT J A.  
 Percent Similarity: 32.75%  
 Best Local Similarity: 24.37%  
 Mismatches: 191  
 Indels: 154  
 Query Match: 12.70%  
 RESULT 1016  
 ID AAL04299 standard; DNA; 22595 BP.  
 DE Human reproductive system related antigen DNA SEQ ID NO: 6987.  
 PN WO200155320-A2.  
 PD. 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 37.04%  
 Best Local Similarity: 25.54%  
 Mismatches: 186  
 Indels: 139  
 Query Match: 12.70%  
 RESULT 1017  
 ID AAD55724 standard; DNA; 1118 BP.  
 DE Latrodectus Geometricus major ampullate spideroin 2 (MaSp2) DNA #1.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 37.23%  
 Best Local Similarity: 27.98%  
 Mismatches: 158  
 Indels: 100  
 Query Match: 12.65%  
 RESULT 1018  
 ID ADM02467 standard; cDNA; 2210 BP.  
 DE Human cDNA of the invention SEQ ID NO:1152.  
 PN EP1347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 39.39%  
 Best Local Similarity: 28.88%  
 Mismatches: 180  
 Indels: 100  
 Query Match: 12.65%  
 RESULT 1019  
 ID ADB61928 standard; cDNA; 2683 BP.  
 DE Human cDNA encoding clone BRAC10000510.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 43.07%  
 Best Local Similarity: 29.22%  
 Mismatches: 172  
 Indels: 96  
 Query Match: 12.61%  
 RESULT 1020  
 ID ADQ84237 standard; cDNA; 2811 BP.  
 DE Novel human cDNA sequence #1398.  
 PN EP1440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 42.59%  
 Best Local Similarity: 28.43%  
 Mismatches: 31  
 Indels: 93  
 Query Match: 12.57%  
 RESULT 1021  
 ID ABQ75494 standard; DNA; 30865 BP.  
 DE Human epididymal protein 17 gene sequence SEQ ID NO:2.  
 PN WO200253701-A2.  
 PD 11-JUL-2002.  
 PA (UYVA-) UNIV VANDERBILT.  
 Percent Similarity: 39.11%  
 Best Local Similarity: 27.48%  
 Mismatches: 175  
 Indels: 114  
 Query Match: 12.57%  
 RESULT 1022  
 ID ADN05338 standard; cDNA; 17820 BP.  
 DE Antipsoriatic cDNA sequence #891.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH-) GENENTECH INC.  
 Percent Similarity: 37.55%  
 Best Local Similarity: 32.37%  
 Mismatches: 157  
 Indels: 146  
 Query Match: 12.55%  
 RESULT 1023  
 ID AAL51687 standard; cDNA; 1981 BP.  
 DE Nephila clavipes dragline silk fibronin coding sequence.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 37.64%  
 Best Local Similarity: 27.66%  
 Mismatches: 183  
 Indels: 92  
 Query Match: 12.53%  
 RESULT 1024  
 ID AAQ14184 standard; DNA; 1995 BP.  
 DE N.clavipes dragline silk protein-2 coding sequence.  
 PN EP452925-A.  
 PD 23-OCT-1991.  
 PA (UYWY-) UNIV OF WYOMING.  
 Percent Similarity: 37.64%  
 Best Local Similarity: 27.66%  
 Mismatches: 183  
 Indels: 92  
 Query Match: 12.53%  
 RESULT 1025  
 ID AAV23250 standard; cDNA; 1995 BP.  
 DE Nephila clavipes spider silk protein encoding cDNA.  
 PN US5728810-A.  
 PD 17-MAR-1998.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 37.64%  
 Best Local Similarity: 27.66%  
 Mismatches: 183  
 Indels: 92  
 Query Match: 12.53%  
 RESULT 1026  
 ID AAZ38196 standard; cDNA; 1995 BP.  
 DE N. clavipes spider silk protein 2 encoding cDNA.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 37.64%  
 Best Local Similarity: 27.66%  
 Mismatches: 183  
 Indels: 92  
 Query Match: 12.53%  
 RESULT 1027  
 ID ABA90851 standard; DNA; 2660 BP.  
 DE Bacillus anthracis variable region DNA sequence SEQ ID NO 82.  
 PN WO200181543-A2.  
 PD 01-NOV-2001.  
 PA (REGC-) UNIV CALIFORNIA.

Percent Similarity: 41.67% Conservative: 12  
 Best Local Similarity: 36.40% Mismatches: 87  
 Query Match: 12.53% Indels: 46  
 RESULT 1028  
 ID ADJ75971 standard; DNA; 2779 BP.  
 DE Marker gene SEQ ID NO:1223.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Percent Similarity: 39.74% Conservative: 40  
 Best Local Similarity: 30.91% Mismatches: 175  
 Query Match: 12.51% Indels: 100  
 RESULT 1029  
 ID ADS96695 standard; cDNA; 1761 BP.  
 DE Drosophila melanogaster protein coding sequence, SEQ ID 316.  
 PN WO2004039999-A2.  
 PD 13-MAY-2004.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 36.50% Conservative: 58  
 Best Local Similarity: 25.48% Mismatches: 182  
 Query Match: 12.46% Indels: 152  
 RESULT 1030  
 ID ABL20515 standard; DNA; 2133 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13018.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NV.  
 Percent Similarity: 36.50% Conservative: 58  
 Best Local Similarity: 25.48% Mismatches: 182  
 Query Match: 12.46% Indels: 152  
 RESULT 1031  
 ID ABL12011 standard; cDNA; 2198 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30515.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NV.  
 Percent Similarity: 36.50% Conservative: 58  
 Best Local Similarity: 25.48% Mismatches: 182  
 Query Match: 12.46% Indels: 152  
 RESULT 1032  
 ID ABL28034 standard; DNA; 4329 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35575.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NV.  
 Percent Similarity: 39.78% Conservative: 37  
 Best Local Similarity: 29.56% Mismatches: 139  
 Query Match: 12.46% Indels: 79  
 RESULT 1033  
 ID ABQ61152 standard; cDNA; 13715 BP.  
 DE MUC5B partial gene protein encoding sequence.  
 PN WO200231111-A2.  
 PD 18-APR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.00% Conservative: 28  
 Best Local Similarity: 27.47% Mismatches: 185  
 Query Match: 12.44% Indels: 154  
 RESULT 1034  
 ID AAD55727 standard; DNA; 1692 BP.  
 DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2) DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 35.68% Conservative: 37  
 Best Local Similarity: 27.00% Mismatches: 194  
 Query Match: 12.42% Indels: 80  
 RESULT 1035  
 ID ADA07855 standard; cDNA; 2050 BP.  
 DE cDNA encoding Pinctada margaritifera nacrein.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG P F.  
 PA (LIHH/) LI H.

PA (HSIE/) HSIEH-LI H M.  
 Percent Similarity: 42.58% Conservative: 50  
 Best Local Similarity: 26.45% Mismatches: 125  
 Query Match: 12.42% Indels: 53  
 RESULT 1036  
 ID ABQ39492 standard; DNA; 969 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26083.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Percent Similarity: 37.60% Conservative: 33  
 Best Local Similarity: 28.98% Mismatches: 155  
 Query Match: 12.40% Indels: 84  
 RESULT 1037  
 ID ABQ39493 standard; DNA; 969 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26084.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Percent Similarity: 37.60% Conservative: 33  
 Best Local Similarity: 28.98% Mismatches: 155  
 Query Match: 12.40% Indels: 84  
 RESULT 1038  
 ID ADH47758 standard; DNA; 14859 BP.  
 DE NOV18 coding sequence, SEQ ID 55.  
 PN WO200268647-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 37.53% Conservative: 24  
 Best Local Similarity: 32.49% Mismatches: 153  
 Query Match: 12.40% Indels: 147  
 RESULT 1039  
 ID ADL25641 standard; DNA; 14859 BP.  
 DE Human diagnostic gene, NOV18.  
 PN US2004005557-A1.  
 PD 08-JAN-2004.  
 PA (PADI/) PADIGARU M.  
 PA (ALSO/) ALSOBOOK J P.  
 PA (COLM/) COLMAN S D.  
 PA (SPYT/) SPYTEK K A.  
 PA (BOLD/) BOLDOG F L.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (SHEN/) SHENOY S G.  
 PA (CASM/) CASMAN S J.  
 PA (GUOX/) GUO X.  
 PA (EDIN/) EDINGER S R.  
 PA (MACD/) MACDOUGALL J R.  
 PA (PATT/) PATTURAJAN M.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PENA/) PENNA C E A.  
 PA (TCHE/) TCHERNEV V T.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (MILL/) MILLER I.  
 PA (MILL/) MILLER C E.  
 PA (LEPL/) LEPLY D M.  
 PA (SMIT/) SMITHSON G.  
 PA (BAUM/) BAUMGARTNER J C.  
 PA (HERR/) HERRMANN J L.  
 PA (PEYM/) PEYMAN J A.  
 PA (GORM/) GORMAN L.  
 PA (MEZE/) MEZES P D.  
 PA (KEKU/) KEKUDA R.  
 PA (TAUP/) TAUPIER R J.  
 PA (GERL/) GERLACH V.  
 PA (GROS/) GROSSE W M.  
 PA (LIUX/) LIU X.  
 PA (ELLE/) ELLERMAN K.  
 PA (ROTH/) ROTHENBERG M.  
 PA (STON/) STONE D J.  
 PA (BURG/) BURGESS C E.  
 Percent Similarity: 37.53% Conservative: 24



Best Local Similarity: 32.49% Mismatches: 153  
 Query Match: 12.40% Indels: 147  
 RESULT 1040  
 ID ADH48827 standard; DNA; 15645 BP.  
 DE NOV47 coding sequence, SEQ ID 111.  
 PN WO200268652-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 37.53%  
 Best Local Similarity: 32.49%  
 Query Match: 12.40%  
 RESULT 1041  
 ID AAI64291 standard; DNA; 128139 BP.  
 DE RRV genome nucleotide sequence.  
 PN WO20028040-A2.  
 PD 18-MAY-2000.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Percent Similarity: 39.45%  
 Best Local Similarity: 28.67%  
 Query Match: 12.40%  
 RESULT 1042  
 ID AAC64754 standard; DNA; 133719 BP.  
 DE Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.  
 PN WO20028040-A2.  
 PD 18-MAY-2000.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 Percent Similarity: 39.45%  
 Best Local Similarity: 28.67%  
 Query Match: 12.40%  
 RESULT 1043  
 ID AAH98282 standard; cDNA; 2068 BP.  
 DE Rabbit EST-derived coding sequence SEQ ID NO: 139.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.57%  
 Best Local Similarity: 28.81%  
 Query Match: 12.36%  
 RESULT 1044  
 ID ADI16567 standard; cDNA; 2091 BP.  
 DE Human NOVX cDNA to treat human pathological conditions SeqID103.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.57%  
 Best Local Similarity: 28.81%  
 Query Match: 12.36%  
 RESULT 1045  
 ID AAD27280 standard; cDNA; 2430 BP.  
 DE Human transporter and ion channel-27 (TRICH-27) cDNA.  
 PN WO200192304-A2.  
 PD 06-DEC-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 33.57%  
 Best Local Similarity: 28.81%  
 Query Match: 12.36%  
 RESULT 1046  
 ID AAD55734 standard; DNA; 2740 BP.  
 DE Plectroreus tristis fibroin 1 DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 35.44%  
 Best Local Similarity: 23.42%  
 Query Match: 12.36%  
 RESULT 1047  
 ID ADH22570 standard; cDNA; 3389 BP.  
 DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID68.  
 PN WO2003093444-A2.  
 PD 13-NOV-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 33.57%  
 Best Local Similarity: 28.81%  
 Query Match: 12.36%  
 RESULT 1048  
 ID ADM97705 standard; DNA; 3435 BP.  
 DE Murine MNAR coding sequence.  
 PN WO2004031223-A1.  
 PD 15-APR-2004.  
 PA (AMHP) WYETH.  
 Percent Similarity: 37.75%  
 Best Local Similarity: 27.87%  
 Query Match: 12.36%  
 RESULT 1049  
 ID ADP99220 standard; cDNA; 3524 BP.  
 DE Human transporter and ion channel (TRICH) cDNA - SEQ ID 85.  
 PN WO2004048599-A2.  
 PD 10-JUN-2004.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 33.57%  
 Best Local Similarity: 28.81%  
 Query Match: 12.31%  
 RESULT 1050  
 ID ACH92164 standard; DNA; 2447 BP.  
 DE Human genome derived single exon probe #25359.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Percent Similarity: 36.38%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1051  
 ID AAT18673 standard; cDNA; 2524 BP.  
 DE Human trophinin cDNA.  
 PN WO9610414-A1.  
 PD 11-APR-1996.  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 Percent Similarity: 36.38%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1052  
 ID AAA91964 standard; cDNA; 2524 BP.  
 DE Human trophinin cDNA.  
 PN US6111089-A.  
 PD 29-AUG-2000.  
 PA (BURN-) BURNHAM INST.  
 Percent Similarity: 36.38%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1053  
 ID AAH16656 standard; cDNA; 3677 BP.  
 DE Human cDNA sequence SEQ ID NO:15789.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 36.57%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1054  
 ID AAI93912 standard; cDNA; 3677 BP.  
 DE Human stomach cancer expressed polynucleotide SEQ ID NO 138.  
 PN WO200109317-A1.  
 PD 08-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 36.57%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1055  
 ID AAS34707 standard; DNA; 10598 BP.  
 DE Human DNA for a novel foetal antigen, SEQ ID No 2131.  
 PN WO200155312-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 36.38%  
 Best Local Similarity: 27.62%  
 Query Match: 12.29%  
 RESULT 1056

ID ABZ73802 standard; DNA; 10598 BP.  
DE Secreted protein gene 46 genomic fragment HBMWE61, SEQ ID NO:949.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.38%  
Best Local Similarity: 27.62%  
Query Match: 12.29%  
Indels: 159  
Conservative: 46  
Mismatches: 175  
Indels: 159  
RESULT 1057

ID ABZ67390 standard; DNA; 10598 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 913.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.38%  
Best Local Similarity: 27.62%  
Query Match: 12.29%  
Indels: 159  
Conservative: 46  
Mismatches: 175  
Indels: 159  
RESULT 1058

ID AAV44439 standard; DNA; 985 BP.  
DE Mycobacterium tuberculosis antigen XP25 3' DNA.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.78%  
Best Local Similarity: 29.52%  
Query Match: 12.27%  
Indels: 86  
Conservative: 26  
Mismatches: 110  
Indels: 86  
RESULT 1059

ID AAV64548 standard; DNA; 985 BP.  
DE M. tuberculosis immunogenic polypeptide XP25 3'-end DNA.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.78%  
Best Local Similarity: 29.52%  
Query Match: 12.27%  
Indels: 86  
Conservative: 26  
Mismatches: 110  
Indels: 86  
RESULT 1060

ID AAZ19137 standard; DNA; 985 BP.  
DE M. tuberculosis recombinant antigen DNA encoding 3' XP25.  
PN WO9942118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.78%  
Best Local Similarity: 29.52%  
Query Match: 12.27%  
Indels: 86  
Conservative: 26  
Mismatches: 110  
Indels: 86  
RESULT 1061

ID AAZ19349 standard; DNA; 985 BP.  
DE M. tuberculosis antigen 3' XP25 DNA sequence.  
PN WO9942076-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 37.78%  
Best Local Similarity: 29.52%  
Query Match: 12.27%  
Indels: 86  
Conservative: 26  
Mismatches: 110  
Indels: 86  
RESULT 1062

ID AAS94858 standard; DNA; 14835 BP.  
DE Human DNA sequence #113 expressed during foam cell differentiation.  
PN WO200177389-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 33.40%  
Best Local Similarity: 25.19%  
Query Match: 12.27%  
Indels: 168  
Conservative: 43  
Mismatches: 181  
Indels: 168  
RESULT 1063

ID ADN95229 standard; DNA; 128361 BP.  
DE Human BCC/LEC-related gene sequence SeqID151.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Percent Similarity: 33.07%  
Best Local Similarity: 26.26%  
Query Match: 12.27%  
Indels: 154  
Conservative: 35  
Mismatches: 191  
Indels: 154  
RESULT 1064

ID AAX34250 standard; DNA; 1164 BP.  
DE Mycobacterium species nucleic acid sequence 50C.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Percent Similarity: 40.96%  
Best Local Similarity: 30.38%  
Query Match: 12.23%  
Indels: 42  
Conservative: 31  
Mismatches: 131  
Indels: 42  
RESULT 1065

ID AAX34249 standard; DNA; 1165 BP.  
DE Mycobacterium species nucleic acid sequence 50B.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Percent Similarity: 40.96%  
Best Local Similarity: 30.38%  
Query Match: 12.23%  
Indels: 42  
Conservative: 31  
Mismatches: 131  
Indels: 42  
RESULT 1066

ID AAX34248 standard; DNA; 1166 BP.  
DE Mycobacterium species nucleic acid sequence 50A.  
PN WO9909186-A2.  
PD 25-FEB-1999.  
PA (INSP ) INST PASTEUR.  
Percent Similarity: 40.96%  
Best Local Similarity: 30.38%  
Query Match: 12.23%  
Indels: 42  
Conservative: 31  
Mismatches: 131  
Indels: 42  
RESULT 1067

ID ABQ52497 standard; DNA; 600 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39088.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 36.09%  
Best Local Similarity: 32.33%  
Query Match: 12.19%  
Indels: 72  
Conservative: 10  
Mismatches: 98  
Indels: 72  
RESULT 1068

ID ABQ52496 standard; DNA; 600 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 39087.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 36.09%  
Best Local Similarity: 32.33%  
Query Match: 12.19%  
Indels: 72  
Conservative: 10  
Mismatches: 98  
Indels: 72  
RESULT 1069

ID ABN96892 standard; DNA; 6457 BP.  
DE Gene #3390 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 31.71%  
Best Local Similarity: 24.58%  
Query Match: 12.19%  
Indels: 180  
Conservative: 38  
Mismatches: 184  
Indels: 180  
RESULT 1070

ID ADJ75164 standard; DNA; 6457 BP.  
DE Marker Gene SEQ ID NO:416.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 31.71%  
Best Local Similarity: 24.58%  
Query Match: 12.19%  
Indels: 180  
Conservative: 38  
Mismatches: 184  
Indels: 180  
RESULT 1071

ID ADQ85501 standard; cDNA; 6458 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2315.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.71%  
Best Local Similarity: 24.58%  
Query Match: 12.19%  
Indels: 180  
Conservative: 38  
Mismatches: 184  
Indels: 180  
RESULT 1072

ID ADQ85501 standard; cDNA; 6458 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2315.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.71%  
Best Local Similarity: 24.58%  
Query Match: 12.19%  
Indels: 180  
Conservative: 38  
Mismatches: 184  
Indels: 180  
RESULT 1073

ID ADQ85501 standard; cDNA; 6458 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2315.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.71%  
Best Local Similarity: 24.58%  
Query Match: 12.19%  
Indels: 180  
Conservative: 38  
Mismatches: 184  
Indels: 180  
RESULT 1074

RESULT 1072  
ID ADQ86626 standard; cDNA; 6458 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3500.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WU/DI) WU T D.  
PA (ZHOU) ZHOU Y.  
Percent Similarity: 31.74%  
Best Local Similarity: 24.58%  
Conservative: 38  
Mismatches: 184  
Indels: 180  
Query Match: 12.19%  
RESULT 1073  
ID ACN54596 standard; cDNA; 588 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D5, SEQ:9377.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK) DEIKMAN J.  
PA (FENG) FENG P C C.  
PA (FINC) FINCHER K L.  
PA (ZIEG) ZIEGLER T E.  
Percent Similarity: 31.52%  
Best Local Similarity: 29.18%  
Conservative: 6  
Mismatches: 92  
Indels: 84  
Query Match: 12.15%  
RESULT 1074  
ID AAK51489 standard; cDNA; 2209 BP.  
DE Human polynucleotide SEQ ID NO 34.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.61%  
Best Local Similarity: 27.36%  
Conservative: 35  
Mismatches: 153  
Indels: 120  
Query Match: 12.15%  
RESULT 1075  
ID ADP68293 standard; DNA; 14922 BP.  
DE Human NOV18a DNA encoding an ARL like protein SeqID 55.  
PN WO200281510-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 37.24%  
Best Local Similarity: 31.49%  
Conservative: 25  
Mismatches: 199  
Indels: 76  
Query Match: 12.12%  
RESULT 1076  
ID ADM97694 standard; DNA; 3391 BP.  
DE Human MNAR coding sequence.  
PN WO2004031223-A1.  
PD 15-APR-2004.  
PA (AMHP) WYETH.  
Percent Similarity: 34.69%  
Best Local Similarity: 26.32%  
Conservative: 35  
Mismatches: 141  
Indels: 132  
Query Match: 12.10%  
RESULT 1077  
ID AAL07261 standard; DNA; 3894 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9949.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.40%  
Best Local Similarity: 25.10%  
Conservative: 59  
Mismatches: 187  
Indels: 148  
Query Match: 12.10%  
RESULT 1078  
ID AAL03061 standard; DNA; 3894 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5749.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.40%  
Best Local Similarity: 25.10%  
Conservative: 59  
Mismatches: 187  
Indels: 148  
Query Match: 12.10%  
RESULT 1079  
ID ABL98807 standard; DNA; 3894 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3459.  
PN WO200155317-A2.  
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.40%  
Best Local Similarity: 25.10%  
Conservative: 59  
Mismatches: 187  
Indels: 148  
Query Match: 12.10%  
RESULT 1080  
ID ABL97397 standard; DNA; 3894 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2049.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.40%  
Best Local Similarity: 25.10%  
Conservative: 59  
Mismatches: 187  
Indels: 148  
Query Match: 12.10%  
RESULT 1081  
ID ABL07173 standard; cDNA; 6353 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 35.31%  
Best Local Similarity: 24.31%  
Conservative: 52  
Mismatches: 198  
Indels: 108  
Query Match: 12.10%  
RESULT 1082  
ID ABL07172 standard; cDNA; 8429 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 35.31%  
Best Local Similarity: 24.31%  
Conservative: 52  
Mismatches: 198  
Indels: 108  
Query Match: 12.10%  
RESULT 1083  
ID ACN44822 standard; DNA; 39344 BP.  
DE Human genomic sequence hCG31099.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.60%  
Best Local Similarity: 29.86%  
Conservative: 20  
Mismatches: 196  
Indels: 80  
Query Match: 12.10%  
RESULT 1084  
ID AA157831 standard; cDNA; 4176 BP.  
DE Human polynucleotide SEQ ID NO 34.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.40%  
Best Local Similarity: 27.11%  
Conservative: 32  
Mismatches: 168  
Indels: 174  
Query Match: 12.06%  
RESULT 1085  
ID ADE07797 standard; DNA; 4278 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #863.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 39.90%  
Best Local Similarity: 26.60%  
Conservative: 56  
Mismatches: 177  
Indels: 76  
Query Match: 12.04%  
RESULT 1086  
ID ABL61045 standard; DNA; 831 BP.  
DE N. clavipes spiderin synthetic homologue SFI.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 42.07%  
Best Local Similarity: 29.89%  
Conservative: 33  
Mismatches: 133  
Indels: 24  
Query Match: 12.02%  
RESULT 1087  
ID ADJ92742 standard; cDNA; 2061 BP.  
DE Human HCLI variant (HCLI.v2) cDNA.  
PN US2004009915-A1.  
PD 15-JAN-2004.  
PA (CHAN/) CHANG H.

PA (FEDE/) FEDER J N.  
PA (LEEL/) LEE L M.  
PA (RICH/) RICH A.  
Percent Similarity: 33.33% Conservative: 20  
Best Local Similarity: 28.57% Mismatches: 178  
Query Match: 12.02% Indels: 103  
RESULT 1088  
ID ACC48787 standard; DNA; 16098 BP.  
DE Human Evin-1 gene.  
PN EP1279733-A1.  
PD 29-JAN-2003.  
PA (INSP ) INSTM PASTEUR.  
PA (INRM ) INSTM INST NAT SANTE & RECH MEDICALE.  
Percent Similarity: 38.01% Conservative: 35  
Best Local Similarity: 30.09% Mismatches: 168  
Query Match: 12.02% Indels: 106  
RESULT 1089  
ID ADQ64137 standard; cDNA; 2130 BP.  
DE Novel human cDNA sequence #1298.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 35.06% Conservative: 53  
Best Local Similarity: 25.23% Mismatches: 195  
Query Match: 11.98% Indels: 159  
RESULT 1090  
ID AAA91976 standard; DNA; 3483 BP.  
DE Mouse trophinin DNA.  
PN US6111089-A.  
PD 29-AUG-2000.  
PA (BURN-) BURNHAM INST.  
Percent Similarity: 37.04% Conservative: 28  
Best Local Similarity: 29.63% Mismatches: 154  
Query Match: 11.98% Indels: 84  
RESULT 1091  
ID ACF04823 standard; DNA; 4071 BP.  
DE M lichenicola melithiazol synthesis gene Mel F.  
PN WO2003080828-A2.  
PD 02-OCT-2003.  
PA (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.  
Percent Similarity: 35.87% Conservative: 57  
Best Local Similarity: 25.80% Mismatches: 188  
Query Match: 11.98% Indels: 175  
RESULT 1092  
ID ACF04818 standard; DNA; 51855 BP.  
DE Melithiazol biosynthetic gene cluster.  
PN WO2003080828-A2.  
PD 02-OCT-2003.  
PA (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.  
Percent Similarity: 35.87% Conservative: 57  
Best Local Similarity: 25.80% Mismatches: 188  
Query Match: 11.98% Indels: 175  
RESULT 1093  
ID ADC32422 standard; cDNA; 4650 BP.  
DE Human novel cDNA contig sequence, SEQ ID NO:2504.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.44% Conservative: 39  
Best Local Similarity: 28.20% Mismatches: 181  
Query Match: 11.93% Indels: 85  
RESULT 1094  
ID AAD55721 standard; DNA; 1336 BP.  
DE Argiope trifasciata major ampullate spidroin 2 (MasSp2) DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Percent Similarity: 36.81% Conservative: 45  
Best Local Similarity: 26.16% Mismatches: 178  
Query Match: 11.91% Indels: 96  
RESULT 1095  
ID ABL21716 standard; DNA; 2714 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16621.

PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Percent Similarity: 40.00% Conservative: 28  
Best Local Similarity: 32.53% Mismatches: 142  
Query Match: 11.91% Indels: 83  
RESULT 1096  
ID ADP98694 standard; DNA; 3291 BP.  
DE C. albicans specific gene, CAYMR047C, DNA sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Percent Similarity: 35.63% Conservative: 48  
Best Local Similarity: 26.68% Mismatches: 184  
Query Match: 11.89% Indels: 161  
RESULT 1097  
ID ACH87042 standard; DNA; 7019 BP.  
DE Human genome derived single exon probe #20237.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 35.81% Conservative: 38  
Best Local Similarity: 28.57% Mismatches: 200  
Query Match: 11.89% Indels: 138  
RESULT 1098  
ID ADP85918 standard; DNA; 500 BP.  
DE Synthetic construct #2.  
PN US2004110205-A1.  
PD 10-JUN-2004.  
PA (WANG/) WANG H.  
Percent Similarity: 29.08% Conservative: 0  
Best Local Similarity: 29.08% Mismatches: 93  
Query Match: 11.87% Indels: 85  
RESULT 1099  
ID AAK51488 standard; cDNA; 2179 BP.  
DE Human polynucleotide SEQ ID NO 33.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.12% Conservative: 37  
Best Local Similarity: 26.23% Mismatches: 150  
Query Match: 11.87% Indels: 159  
RESULT 1100  
ID AAV44424 standard; DNA; 1439 BP.  
DE Mycobacterium tuberculosis antigen XP17 DNA.  
PN WO9816645-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 38.35% Conservative: 32  
Best Local Similarity: 29.26% Mismatches: 106  
Query Match: 11.85% Indels: 111  
RESULT 1101  
ID AAV64533 standard; DNA; 1439 BP.  
DE M. tuberculosis immunogenic polypeptide XP17 5'-end DNA.  
PN WO9816646-A2.  
PD 23-APR-1998.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 38.35% Conservative: 32  
Best Local Similarity: 29.26% Mismatches: 106  
Query Match: 11.85% Indels: 111  
RESULT 1102  
ID AAZ19122 standard; DNA; 1439 BP.  
DE M. tuberculosis recombinant antigen DNA encoding 5' XP17.  
PN WO9942118-A2.  
PD 26-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 38.35% Conservative: 32  
Best Local Similarity: 29.26% Mismatches: 106  
Query Match: 11.85% Indels: 111  
RESULT 1103

ID AAZ19334 standard; DNA; 1439 BP.  
 DE M. tuberculosis antigen 5' XP17 DNA sequence.  
 PN WO9942076-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 38.35% Conservative: 32  
 Best Local Similarity: 29.28% Mismatches: 106  
 Query Match: 11.85% Indels: 111  
 RESULT 1104  
 ID ACN91616 standard; DNA; 2163 BP.  
 DE Breast cancer related marker, seq id 12766.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 38.08% Conservative: 29  
 Best Local Similarity: 31.31% Mismatches: 149  
 Query Match: 11.85% Indels: 121  
 RESULT 1105  
 ID ADC87060 standard; DNA; 3163 BP.  
 DE Human GPCR gene SEQ ID NO:1513.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 Percent Similarity: 28.57% Conservative: 10  
 Best Local Similarity: 26.15% Mismatches: 171  
 Query Match: 11.85% Indels: 125  
 RESULT 1106  
 ID ACS58766 standard; cDNA; 5215 BP.  
 DE Decorin-modified pro-alpha chain.  
 PN WO2003035892-A2.  
 PD 01-MAY-2003.  
 PA (UVNA-) UNIV VICTORIA MANCHESTER.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1107  
 ID AAT16508 standard; cDNA; 5460 BP.  
 DE Vector pAC3A1 contg. human collagen type III alpha-1 chain gene.  
 PN JP08023979-A.  
 PD 30-JAN-1996.  
 PA (TERU) TERUMO CORP.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1108  
 ID ABA83117 standard; DNA; 5460 BP.  
 DE Collagen type III alpha-1 ovarian tumour marker gene, SEQ ID NO:71.  
 PN WO200175177-A2.  
 PD 11-OCT-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1109  
 ID ABL92101 standard; cDNA; 5460 BP.  
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 225.  
 PN WO200210217-A2.  
 PD 07-FEB-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1110  
 ID ACC50110 standard; cDNA; 5460 BP.  
 DE Breast cancer associated cDNA sequence SEQ ID NO:67.  
 PN WO2003004989-A2.  
 PD 16-JAN-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1111

ID ABX72026 standard; DNA; 5460 BP.  
 DE DNA encoding human tumour endothelial marker TEM 15.  
 PN WO200283874-A2.  
 PD 24-OCT-2002.  
 PA (UYJO) UNIV JOHNS HOPKINS.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1112  
 ID ADK60971 standard; DNA; 5460 BP.  
 DE Ovarian cancer-related DNA #126 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PD 21-AUG-2003.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1113  
 ID ADP65589 standard; DNA; 5460 BP.  
 DE Human mRNA for pro-alpha-1 type 3 collagen DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1114  
 ID ADP65501 standard; DNA; 5460 BP.  
 DE Human mRNA for pro-alpha-1 type 3 collagen DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1115  
 ID ADR24567 standard; DNA; 5460 BP.  
 DE Breast cancer prognosis marker #428.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1116  
 ID ADT93873 standard; DNA; 5460 BP.  
 DE Non-small cell lung cancer associated gene #15.  
 PN CA2461828-A1.  
 PD 25-SEP-2004.  
 PA (METR-) METRIGENIX INC.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1117  
 ID AAS79378 standard; cDNA; 5466 BP.  
 DE DNA encoding novel human diagnostic protein #15182.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1118  
 ID ABX04154 standard; cDNA; 5489 BP.  
 DE Human mRNA differentially expressed in mesenchymal cells #1.  
 PN WO200271927-A2.  
 PD 19-SEP-2002.  
 PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL INC.  
 Percent Similarity: 33.85% Conservative: 33  
 Best Local Similarity: 27.43% Mismatches: 180  
 Query Match: 11.85% Indels: 160  
 RESULT 1119

RESULT 1119  
ID ADP65050 standard; DNA; 5489 BP.  
DE Human collagen, type III, alpha 1 (Ehlers-Danlos syndrome) DNA sequence.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1120  
ID ADP65012 standard; DNA; 5489 BP.  
DE Human collagen, type III, alpha 1 (Ehlers-Danlos syndrome) DNA sequence.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1121  
ID ADQ29610 standard; DNA; 5489 BP.  
DE Human colorectal cancer-associated protein coding sequence #32.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1122  
ID ACN37799 standard; cDNA; 5489 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324197, SEQ ID NO:921.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1123  
ID ADR67152 standard; DNA; 5489 BP.  
DE Human bladder cancer associated nucleotide sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAU B.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1124  
ID ADS09743 standard; DNA; 5525 BP.  
DE Novel DNA-related contig nucleotide sequence #465.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1125  
ID ACH03802 standard; cDNA; 5615 BP.  
DE Human cDNA differentially expressed in lung cancer #7.  
PN US2003065157-A1.  
PD 03-APR-2003.  
PA (LASE/) LASEK A W.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1126  
ID ADQ23288 standard; DNA; 5755 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6108.  
PN WO2004048938-A2.

PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1127  
ID ACN88799 standard; DNA; 8664 BP.  
DE Breast cancer related marker, seq id 9949.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 33.85% Conservative: 33  
Best Local Similarity: 27.43% Mismatches: 180  
Query Match: 11.85% Indels: 160  
RESULT 1128  
ID ABL66291 standard; DNA; 14800 BP.  
DE Lung cancer related gene sequence SEQ ID NO:4628.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 37.31% Conservative: 40  
Best Local Similarity: 28.48% Mismatches: 184  
Query Match: 11.85% Indels: 100  
RESULT 1129  
ID ADP13447 standard; DNA; 14800 BP.  
DE Renal cell carcinoma differentially expressed gene #183.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Percent Similarity: 37.31% Conservative: 40  
Best Local Similarity: 28.48% Mismatches: 184  
Query Match: 11.85% Indels: 100  
RESULT 1130  
ID ABL21717 standard; DNA; 714 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16624.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 44.49% Conservative: 16  
Best Local Similarity: 38.19% Mismatches: 93  
Query Match: 11.83% Indels: 48  
RESULT 1131  
ID ABS73272 standard; DNA; 1824 BP.  
DE DNA encoding human translocation (12; 16)(q13; p11) protein #2.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONP-) CONFORMA THERAPEUTICS CORP.  
Percent Similarity: 35.53% Conservative: 29  
Best Local Similarity: 27.89% Mismatches: 118  
Query Match: 11.79% Indels: 127  
RESULT 1132  
ID ABK84149 standard; cDNA; 1824 BP.  
DE Human cDNA differentially expressed in granulocytic cells #720.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.53% Conservative: 29  
Best Local Similarity: 27.89% Mismatches: 118  
Query Match: 11.79% Indels: 127  
RESULT 1133  
ID ADI26116 standard; cDNA; 1824 BP.  
DE Human cDNA encoding protein that promotes STAT6 activation #41.  
PN WO2003104277-A2.  
PD 18-DEC-2003.  
PA (ASAH ) ASAH KASEI KK.  
Percent Similarity: 35.53% Conservative: 29  
Best Local Similarity: 27.89% Mismatches: 118

Query Match: 11.79% Indels: 127  
RESULT 1134  
ID ADJ62768 standard; cDNA; 1824 BP.  
DE Human cDNA differentially expressed in response to docetaxel #58.  
PN US2004018527-A1.  
PD 29-JAN-2004.  
PA (CHAN//) CHANG J C.  
PA (OCON//) O'CONNELL P.  
Percent Similarity: 35.53%  
Best Local Similarity: 27.89%  
Conservative: 29  
Mismatches: 118  
Indels: 127  
Query Match: 11.79%  
RESULT 1135  
ID ACN39977 standard; cDNA; 1824 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326146, SEQ ID NO:4465.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 35.53%  
Best Local Similarity: 27.89%  
Conservative: 29  
Mismatches: 118  
Indels: 127  
Query Match: 11.79%  
RESULT 1136  
ID ADC87176 standard; cDNA; 1972 BP.  
DE Human GPCR gene SEQ ID NO:1629.  
PN EPI270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Percent Similarity: 28.81%  
Best Local Similarity: 24.01%  
Conservative: 23  
Mismatches: 210  
Indels: 132  
Query Match: 11.79%  
RESULT 1137  
ID AAC42350 standard; cDNA; 2259 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35220.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 38.67%  
Best Local Similarity: 28.08%  
Conservative: 43  
Mismatches: 159  
Indels: 90  
Query Match: 11.79%  
RESULT 1138  
ID ABL09667 standard; cDNA; 7002 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23483.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 35.78%  
Best Local Similarity: 26.29%  
Conservative: 44  
Mismatches: 167  
Indels: 131  
Query Match: 11.79%  
RESULT 1139  
ID AAK72613 standard; cDNA; 8298 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27425.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 31.04%  
Best Local Similarity: 25.83%  
Conservative: 22  
Mismatches: 192  
Indels: 101  
Query Match: 11.79%  
RESULT 1140  
ID ABL09666 standard; cDNA; 10637 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23480.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 35.78%  
Best Local Similarity: 26.29%  
Conservative: 44  
Mismatches: 167  
Indels: 131  
Query Match: 11.79%  
RESULT 1141  
ID ACA64816 standard; cDNA; 3234 BP.  
DE Human collagen III alpha 1 DNA corresponding to X15332.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHOARRAY GMBH.  
Percent Similarity: 33.85%  
Best Local Similarity: 27.43%  
Conservative: 33  
Mismatches: 180

Query Match: 11.76% Indels: 160  
RESULT 1142  
ID ACN38666 standard; cDNA; 5084 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324972, SEQ ID NO:2321.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 36.20%  
Best Local Similarity: 30.27%  
Conservative: 29  
Mismatches: 192  
Indels: 120  
Query Match: 11.76%  
RESULT 1143  
ID AAH98343 standard; cDNA; 5467 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 200.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.85%  
Best Local Similarity: 27.43%  
Conservative: 33  
Mismatches: 180  
Indels: 160  
Query Match: 11.76%  
RESULT 1144  
ID AAH98411 standard; cDNA; 5468 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 268.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.85%  
Best Local Similarity: 27.43%  
Conservative: 33  
Mismatches: 180  
Indels: 160  
Query Match: 11.76%  
RESULT 1145  
ID AAD30228 standard; cDNA; 53522 BP.  
DE Human PKD1 gene.  
PN WO200206529-A2.  
PD 24-JAN-2002.  
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Percent Similarity: 33.41%  
Best Local Similarity: 26.08%  
Conservative: 34  
Mismatches: 198  
Indels: 112  
Query Match: 11.76%  
RESULT 1146  
ID AAT94101 standard; cDNA; 53526 BP.  
DE Human PKD1 gene.  
PN WO9744457-A1.  
PD 27-NOV-1997.  
PA (GENZ) GENZYME CORP.  
Percent Similarity: 33.41%  
Best Local Similarity: 26.08%  
Conservative: 34  
Mismatches: 198  
Indels: 112  
Query Match: 11.76%  
RESULT 1147  
ID AAT18551 standard; cDNA; 53577 BP.  
DE Human polycystic kidney disease normal PKD1 gene.  
PN WO9612033-A1.  
PD 25-APR-1996.  
PA (IGIG-) IG LAB INC.  
Percent Similarity: 33.41%  
Best Local Similarity: 26.08%  
Conservative: 34  
Mismatches: 198  
Indels: 112  
Query Match: 11.76%  
RESULT 1148  
ID AAT94108 standard; cDNA; 53577 BP.  
DE Human PKD1 locus between chromosomal markers ATP6C and D16S84.  
PN WO9744457-A1.  
PD 27-NOV-1997.  
PA (GENZ) GENZYME CORP.  
Percent Similarity: 33.41%  
Best Local Similarity: 26.08%  
Conservative: 34  
Mismatches: 198  
Indels: 112  
Query Match: 11.76%  
RESULT 1149  
ID ACA43990 standard; cDNA; 711 BP.  
DE Prokaryotic essential gene #25647.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 36.43%  
Best Local Similarity: 30.71%  
Query Match: 11.72%  
Conservative: 16  
Mismatches: 88  
Indels: 90  
RESULT 1151  
ID ABL67071 standard; DNA; 4139 BP.  
DE Thyroid cancer related gene sequence SEQ ID NO:5408.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1152  
ID ABL67544 standard; DNA; 4139 BP.  
DE Thyroid cancer related gene sequence SEQ ID NO:5881.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1153  
ID ABL68884 standard; DNA; 4139 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:7221.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1154  
ID ABK0797 standard; cDNA; 4139 BP.  
DE Human ovarian tumour protein encoding cDNA #330.  
PN WO200190154-A2.  
PD 29-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1155  
ID ABN95623 standard; DNA; 4139 BP.  
DE Gene #2121 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1156  
ID ACC50234 standard; cDNA; 4139 BP.  
DE Breast cancer associated cDNA sequence SEQ ID NO:310.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1157  
ID ACF12907 standard; cDNA; 4139 BP.  
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:157.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1158  
ID ADH17156 standard; cDNA; 4139 BP.  
DE Human mucin 1 cDNA.  
PN WO2003097854-A2.  
PD 27-NOV-2003.

PA (SUGE-) SUGEN INC.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1159  
ID ADQ29627 standard; DNA; 4139 BP.  
DE Human colorectal cancer-associated protein coding sequence #49.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB-) BAYER HEALTHCARE LLC.  
Percent Similarity: 35.84%  
Best Local Similarity: 28.54%  
Query Match: 11.72%  
Conservative: 32  
Mismatches: 182  
Indels: 100  
RESULT 1160  
ID ADR44006 standard; DNA; 4139 BP.  
DE Human breast tumour associated gene clone-19 SEQ ID NO:16.  
PN WO2004074506-A2.  
PD 02-SEP-2004.  
PA (MERG-) MERGEN LTD.  
Percent Similarity: 34.95%  
Best Local Similarity: 27.69%  
Query Match: 11.72%  
Conservative: 33  
Mismatches: 183  
Indels: 114  
RESULT 1161  
ID ADM02721 standard; cDNA; 2529 BP.  
DE Human cDNA of the invention SEQ ID NO:1406.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.16%  
Best Local Similarity: 28.15%  
Query Match: 11.70%  
Conservative: 40  
Mismatches: 162  
Indels: 117  
RESULT 1162  
ID ADB58728 standard; DNA; 4474 BP.  
DE Toxicity-related gene, SEQ ID 3754.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 36.67%  
Best Local Similarity: 30.42%  
Query Match: 11.70%  
Conservative: 30  
Mismatches: 181  
Indels: 123  
RESULT 1163  
ID ABT42284 standard; DNA; 4474 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1986.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 36.67%  
Best Local Similarity: 30.42%  
Query Match: 11.70%  
Conservative: 30  
Mismatches: 181  
Indels: 123  
RESULT 1164  
ID ADQ26946 standard; cDNA; 6786 BP.  
DE Human myosin heavy chain cDNA.  
PN DE10260633-A1.  
PD 24-JUN-2004.  
PA (RAUT/) RAUTENSTRAUSS B.  
Percent Similarity: 32.95%  
Best Local Similarity: 25.97%  
Query Match: 11.70%  
Conservative: 36  
Mismatches: 179  
Indels: 167  
RESULT 1165  
ID AAQ13868 standard; cDNA; 1548 BP.  
DE Insert from clone WPRP1.  
PN WO9113991-A.  
PD 19-SEP-1991.  
PA (ADTE-) ADV TECHN CAMBRIDGE.  
Percent Similarity: 32.95%  
Best Local Similarity: 25.97%  
Query Match: 11.70%  
Conservative: 36  
Mismatches: 179  
Indels: 167  
RESULT 1166  
ID ABQ54916 standard; cDNA; 2438 BP.



DE Human ovarian antigen HNBV053 cDNA, SEQ-ID NO:796.  
PN WO200200677-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 35.43%  
Best Local Similarity: 27.14%  
Query Match: 11.68%  
Conservative: 33  
Mismatches: 147  
Indels: 110  
RESULT 1167  
ID AAL12510 standard; cDNA; 3120 BP.  
DE cDNA encoding a human collagen 1 (alpha2) protein helical region.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USU) US SURGICAL CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1168  
ID AAL12511 standard; cDNA; 3120 BP.  
DE cDNA encoding a human collagen 1 (alpha2) protein helical region.  
PN EP992586-A2.  
PD 12-APR-2000.  
PA (USU) US SURGICAL CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1169  
ID ADC99117 standard; cDNA; 3713 BP.  
DE Human KPP cDNA - SEQ ID 70.  
PN WO2003033680-A2.  
PD 24-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 35.43%  
Best Local Similarity: 27.14%  
Query Match: 11.68%  
Conservative: 33  
Mismatches: 147  
Indels: 110  
RESULT 1170  
ID ADK70306 standard; cDNA; 4608 BP.  
DE Respiratory disease differentially expressed cDNA #42.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1171  
ID ADJ56198 standard; cDNA; 4812 BP.  
DE Human cDNA differentially expressed in MYCN activated cells seqID 4.  
PN US2003119009-A1.  
PD 26-JUN-2003.  
PA (STUA/) STUART S G.  
PA (NUCH/) NUCHTERN J G.  
PA (PLON/) PLON S E.  
PA (SHOH/) SHOHET J M.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1172  
ID ADQ29602 standard; DNA; 5084 BP.  
DE Human colorectal cancer-associated protein coding sequence #24.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1173  
ID ADR99020 standard; DNA; 5084 BP.  
DE Collagen, type 1, alpha 2, COL1A2, coding sequence, SEQ ID 26.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB) BAYER PHARM CORP.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1174  
ID ABL62185 standard; DNA; 5086 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:522.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1175  
ID ABL62730 standard; DNA; 5086 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1067.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1176  
ID ABL92095 standard; cDNA; 5086 BP.  
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 213.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1177  
ID ABL92105 standard; cDNA; 5086 BP.  
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 233.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1178  
ID ABL92121 standard; cDNA; 5086 BP.  
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 264.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1179  
ID AB234912 standard; cDNA; 5086 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 24.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1180  
ID ABK64850 standard; DNA; 5086 BP.  
DE Human benign prostatic hyperplasia gene #745.  
PN WO200212440-A2.  
PD 14-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NTSB) JAPAN TOBACCO INC.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1181  
ID ABN97452 standard; DNA; 5086 BP.  
DE Gene#3950 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136

Query Match: 11.68% Indels: 136  
RESULT 1182  
ID ACF12846 standard; cDNA; 5086 BP.  
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:37.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1183  
ID ABX72046 standard; DNA; 5086 BP.  
DE DNA encoding human tumour endothelial marker TEM 40.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1184  
ID ABX72020 standard; DNA; 5086 BP.  
DE DNA encoding human tumour endothelial marker TEM 10.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1185  
ID ABX72030 standard; DNA; 5086 BP.  
DE DNA encoding human tumour endothelial marker TEM 20.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1186  
ID ABX63022 standard; cDNA; 5432 BP.  
DE Human cDNA #22 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1187  
ID ABV24693 standard; cDNA; 5564 BP.  
DE Human prostate expression marker cDNA 24684.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Percent Similarity: 36.22%  
Best Local Similarity: 29.78%  
Query Match: 11.68%  
Conservative: 32  
Mismatches: 181  
Indels: 136  
RESULT 1188  
ID ADJ39032 standard; cDNA; 1450 BP.  
DE Plant cDNA #32.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 37.64%  
Best Local Similarity: 28.64%  
Conservative: 39  
Mismatches: 171

Query Match: 11.66% Indels: 99  
RESULT 1189  
ID ABL09967 standard; cDNA; 2989 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24383.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.63%  
Best Local Similarity: 24.63%  
Query Match: 11.66%  
Conservative: 54  
Mismatches: 197  
Indels: 156  
RESULT 1190  
ID ADI57666 standard; cDNA; 4144 BP.  
DE Human breast specific nucleic acid (BSNA) #37.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 34.66%  
Best Local Similarity: 27.94%  
Query Match: 11.66%  
Conservative: 32  
Mismatches: 195  
Indels: 117  
RESULT 1191  
ID ABL09966 standard; cDNA; 5190 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24380.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.63%  
Best Local Similarity: 24.63%  
Query Match: 11.66%  
Conservative: 54  
Mismatches: 197  
Indels: 156  
RESULT 1192  
ID ACH89664 standard; DNA; 628 BP.  
DE Human genome derived single exon probe #22859.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENK/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 38.99%  
Best Local Similarity: 32.11%  
Query Match: 11.64%  
Conservative: 15  
Mismatches: 77  
Indels: 56  
RESULT 1193  
ID ABS73275 standard; DNA; 1822 BP.  
DE DNA encoding human translocation (12; 16)(q13; p11) protein #5.  
PN WO200269900-A2.  
PD 12-SEP-2002.  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
Percent Similarity: 35.62%  
Best Local Similarity: 27.70%  
Query Match: 11.64%  
Conservative: 30  
Mismatches: 118  
Indels: 126  
RESULT 1194  
ID ADRI4648 standard; DNA; 1822 BP.  
DE Human NF-kappaB pathway-associated gene SeqID649.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Percent Similarity: 35.62%  
Best Local Similarity: 27.70%  
Query Match: 11.64%  
Conservative: 30  
Mismatches: 118  
Indels: 126  
RESULT 1195  
ID ABD11177 standard; DNA; 1860 BP.  
DE Pseudomonas aeruginosa polynucleotide #9781.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.17%  
Best Local Similarity: 25.63%  
Query Match: 11.64%  
Conservative: 44  
Mismatches: 180  
Indels: 160  
RESULT 1196  
ID AAL62184 standard; cDNA; 2372 BP.  
DE Human collagen 1A2 cDNA.  
PN WO2003048362-A2.  
PD 12-JUN-2003.  
PA (QUEB-) QUEEN ELIZABETH COLLEGE DUBLIN.  
Percent Similarity: 36.02%  
Conservative: 31

Best Local Similarity: 29.78% Mismatches: 182  
 Query Match: 11.64% Indels: 136  
 RESULT 1197  
 ID AAS3800 standard; DNA; 7720 BP.  
 DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.  
 PN WO200046247-A1.  
 PD 10-AUG-2000.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 31.21% Conservative: 25  
 Best Local Similarity: 25.51% Mismatches: 203  
 Query Match: 11.64% Indels: 101  
 RESULT 1198  
 ID ADD18472 standard; DNA; 5418 BP.  
 DE Human prostate cancer diagnosis related DNA sequence SeqID44.  
 PN WO2003012067-A2.  
 PD 13-FEB-2003.  
 PA (UNMI) UNIV MICHIGAN.  
 Percent Similarity: 36.44% Conservative: 28  
 Best Local Similarity: 30.51% Mismatches: 183  
 Query Match: 11.62% Indels: 117  
 RESULT 1199  
 ID ADN35280 standard; DNA; 4037 BP.  
 DE Synthetic collagen used as sealant tissue DNA.  
 PN WO20004028404-A2.  
 PD 08-APR-2004.  
 PA (FIBR-) FIBROGEN INC.  
 Percent Similarity: 33.66% Conservative: 33  
 Best Local Similarity: 27.24% Mismatches: 181  
 Query Match: 11.60% Indels: 160  
 RESULT 1200  
 ID ACF05731 standard; DNA; 7201 BP.  
 DE Plasmid pEAK12d-IPAAA44548-6His.  
 PN WO2003055913-A2.  
 PD 10-JUL-2003.  
 PA (ARES-) ARES TRADING SA.  
 Percent Similarity: 33.73% Conservative: 24  
 Best Local Similarity: 27.99% Mismatches: 160  
 Query Match: 11.60% Indels: 119  
 RESULT 1201  
 ID ACF06299 standard; DNA; 7231 BP.  
 DE Plasmid pEAK12D-IPAAA26841-6His nucleotide sequence.  
 PN WO2003054012-A2.  
 PD 03-JUL-2003.  
 PA (ARES-) ARES TRADING SA.  
 Percent Similarity: 33.73% Conservative: 24  
 Best Local Similarity: 27.99% Mismatches: 160  
 Query Match: 11.60% Indels: 119  
 RESULT 1202  
 ID ACF06300 standard; DNA; 7297 BP.  
 DE SigtdIPAAA268418-6His nucleotide sequence.  
 PN WO2003054012-A2.  
 PD 03-JUL-2003.  
 PA (ARES-) ARES TRADING SA.  
 Percent Similarity: 33.73% Conservative: 24  
 Best Local Similarity: 27.99% Mismatches: 160  
 Query Match: 11.60% Indels: 119  
 RESULT 1203  
 ID ACF05558 standard; DNA; 7429 BP.  
 DE Plasmid pEAK12d-IPAAA24020-6His.  
 PN WO2003055912-A2.  
 PD 10-JUL-2003.  
 PA (ARES-) ARES TRADING SA.  
 Percent Similarity: 33.73% Conservative: 24  
 Best Local Similarity: 27.99% Mismatches: 160  
 Query Match: 11.60% Indels: 119  
 RESULT 1204  
 ID ACF06298 standard; DNA; 7456 BP.  
 DE Plasmid pEAK12D-IPAAA26841long-6His nucleotide sequence.  
 PN WO2003054012-A2.  
 PD 03-JUL-2003.  
 PA (ARES-) ARES TRADING SA.  
 Percent Similarity: 33.73% Conservative: 25  
 Best Local Similarity: 28.67% Mismatches: 111  
 Query Match: 11.57% Indels: 63  
 RESULT 1210  
 ID ADF59971 standard; cDNA; 1794 BP.

Query Match: 11.60% Indels: 119  
 RESULT 1205  
 ID AAD17184 standard; DNA; 65140 BP.  
 DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.  
 PN WO2000159126-A2.  
 PD 16-AUG-2001.  
 PA (UTNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAEV E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Percent Similarity: 31.96% Conservative: 29  
 Best Local Similarity: 26.54% Mismatches: 197  
 Query Match: 11.60% Indels: 169  
 RESULT 1206  
 ID AAD17186 standard; DNA; 125401 BP.  
 DE Streptomyces noursei nystatin PKS gene cluster DNA.  
 PN WO2000159126-A2.  
 PD 16-AUG-2001.  
 PA (UTNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAEV E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Percent Similarity: 31.96% Conservative: 29  
 Best Local Similarity: 26.54% Mismatches: 197  
 Query Match: 11.60% Indels: 169  
 RESULT 1207  
 ID ACH19519 standard; cDNA; 508 BP.  
 DE Human adult lung cDNA #522.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRNA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Percent Similarity: 45.31% Conservative: 1  
 Best Local Similarity: 44.53% Mismatches: 3  
 Query Match: 11.57% Indels: 67  
 RESULT 1208  
 ID ADG73745 standard; cDNA; 1498 BP.  
 DE Aspergillus niger Arsa-7 cDNA.  
 PN US2003215950-A1.  
 PD 20-NOV-2003.  
 PA (LASU/) LASURE L L.  
 PA (DAIZ/) DAI Z.  
 Percent Similarity: 40.00% Conservative: 40  
 Best Local Similarity: 29.87% Mismatches: 158  
 Query Match: 11.57% Indels: 80  
 RESULT 1209  
 ID AAS78187 standard; cDNA; 1794 BP.  
 DE DNA encoding novel human diagnostic protein #13991.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE/) HYSEQ INC.  
 Percent Similarity: 37.63% Conservative: 25  
 Best Local Similarity: 28.67% Mismatches: 111  
 Query Match: 11.57% Indels: 63  
 RESULT 1210  
 ID ADF59971 standard; cDNA; 1794 BP.





RESULT 1238  
 ID ADE77078 standard; cDNA; 3763 BP.  
 DE Human cDNA differentially expressed in a liver disorder #178.  
 PN US2003108871-A1.  
 PD 12-JUN-2003.  
 PA (KASE/) KASER M R.  
 Percent Similarity: 32.79% Conservative: 31  
 Best Local Similarity: 26.52% Mismatches: 174  
 Query Match: 11.51% Indels: 158  
 RESULT 1239  
 ID ACH03803 standard; cDNA; 4360 BP.  
 DE Human cDNA differentially expressed in lung cancer #8.  
 PN US2003065157-A1.  
 PD 03-APR-2003.  
 PA (LASE/) LASEK A W.  
 Percent Similarity: 33.98% Conservative: 33  
 Best Local Similarity: 27.57% Mismatches: 179  
 Query Match: 11.51% Indels: 161  
 RESULT 1240  
 ID ADL12911 standard; cDNA; 5185 BP.  
 DE Human steroid-induced C3A liver cell cDNA #640.  
 PN US6673549-B1.  
 PD 06-JAN-2004.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 32.79% Conservative: 31  
 Best Local Similarity: 26.52% Mismatches: 174  
 Query Match: 11.51% Indels: 158  
 RESULT 1241  
 ID AAD47687 standard; DNA; 28438 BP.  
 DE Human kinase protein gene.  
 PN WO200279431-A2.  
 PD 10-OCT-2002.  
 PA (PEKE-) PE CORP NY.  
 Percent Similarity: 35.42% Conservative: 31  
 Best Local Similarity: 28.24% Mismatches: 168  
 Query Match: 11.51% Indels: 112  
 RESULT 1242  
 ID ACA0512 standard; DNA; 1113 BP.  
 DE Prokaryotic essential gene #22169.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.08% Conservative: 28  
 Best Local Similarity: 29.77% Mismatches: 126  
 Query Match: 11.43% Indels: 116  
 RESULT 1243  
 ID ADA07856 standard; cDNA; 1811 BP.  
 DE cDNA encoding Pinctada maxima nacrein.  
 PN US2003027258-A1.  
 PD 06-FEB-2003.  
 PA (CHAN/) CHANG F F.  
 Percent Similarity: 41.50% Conservative: 44  
 Best Local Similarity: 27.12% Mismatches: 101  
 Query Match: 11.43% Indels: 78  
 RESULT 1244  
 ID ABL26762 standard; DNA; 2922 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31759.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Percent Similarity: 39.45% Conservative: 33  
 Best Local Similarity: 29.36% Mismatches: 129

Query Match: 11.45% Indels: 69  
 RESULT 1247  
 ID AAO30849 standard; cDNA; 3690 BP.  
 DE Type III procollagen (prior art).  
 PN WO219754-A1.  
 PD 12-NOV-1992.  
 PA (UYJB-) UNIV JEFFERSON THOMAS.  
 Percent Similarity: 36.60% Conservative: 34  
 Best Local Similarity: 29.36% Mismatches: 161  
 Query Match: 11.43% Indels: 138  
 RESULT 1248  
 ID AAD06578 standard; cDNA; 4428 BP.  
 DE Porcine alpha1(III) collagen cDNA.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Percent Similarity: 28.62% Conservative: 32  
 Best Local Similarity: 23.47% Mismatches: 208  
 Query Match: 11.43% Indels: 236  
 RESULT 1249  
 ID ABK84534 standard; cDNA; 6483 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #1105.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 42.63% Conservative: 9  
 Best Local Similarity: 37.89% Mismatches: 61  
 Query Match: 11.43% Indels: 48  
 RESULT 1250  
 ID ABN97204 standard; DNA; 6483 BP.  
 DE Gene #3702 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 42.63% Conservative: 9  
 Best Local Similarity: 37.89% Mismatches: 61  
 Query Match: 11.43% Indels: 48  
 RESULT 1251  
 ID ADH13175 standard; DNA; 6483 BP.  
 DE Human malignant neoplasia-related gene SeqID24.  
 PN EPI365034-A2.  
 PD 26-NOV-2003.  
 PA (FARB-) BAYER AG.  
 Percent Similarity: 42.63% Conservative: 9  
 Best Local Similarity: 37.89% Mismatches: 61  
 Query Match: 11.43% Indels: 48  
 RESULT 1252  
 ID AAI24125 standard; DNA; 887 BP.  
 DE Probe #14058 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65% Conservative: 22  
 Best Local Similarity: 34.77% Mismatches: 123  
 Query Match: 11.40% Indels: 40  
 RESULT 1255  
 ID ABA69248 standard; DNA; 887 BP.  
 DE Human foetal liver single exon nucleic acid probe #17553.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65% Conservative: 22  
 Best Local Similarity: 34.77% Mismatches: 123  
 Query Match: 11.40% Indels: 40  
 RESULT 1256

ID AAI19421 standard; DNA; 887 BP.  
 DE Probe #18107 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1257  
 ID ABA51240 standard; DNA; 887 BP.  
 DE Human breast cell single exon nucleic acid probe #9935.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1258  
 ID ABA316164 standard; DNA; 887 BP.  
 DE Probe #14630 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1259  
 ID AAK43350 standard; DNA; 887 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 17907.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1260  
 ID AAK17542 standard; DNA; 887 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 17533.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1261  
 ID ABS42971 standard; DNA; 887 BP.  
 DE Human liver single exon probe, SEQ ID No 17961.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1262  
 ID AAI09639 standard; DNA; 887 BP.  
 DE Probe #9690 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1263  
 ID ABS17431 standard; DNA; 887 BP.  
 DE Human genome-derived single exon probe ORP from lung SEQ ID No 17422.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 42.65%  
 Best Local Similarity: 34.77%  
 Query Match: 11.40%  
 RESULT 1264  
 ID AAD55715 standard; DNA; 1083 BP.

DE Latrodectus geometricus major ampullate spideroin 1 (MspI) DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 34.36%  
 Best Local Similarity: 25.12%  
 Query Match: 11.40%  
 RESULT 1265  
 ID AAI14937 standard; DNA; 1981 BP.  
 DE Probe #4870 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1266  
 ID ABA56674 standard; DNA; 1981 BP.  
 DE Human foetal liver single exon nucleic acid probe #4979.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1267  
 ID AAI36292 standard; DNA; 1981 BP.  
 DE Probe #4978 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1268  
 ID ABA46128 standard; DNA; 1981 BP.  
 DE Human breast cell single exon nucleic acid probe #4823.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1269  
 ID ABA26279 standard; DNA; 1981 BP.  
 DE Probe #4745 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1270  
 ID AAK30333 standard; DNA; 1981 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 4890.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1271  
 ID AAK04811 standard; DNA; 1981 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 4802.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1272  
 ID ABS29973 standard; DNA; 1981 BP.  
 DE Human liver single exon probe, SEQ ID No 4963.

PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1273  
 ID AAI04714 standard; DNA; 1981 BP.  
 DE Probe #4705 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1274  
 ID ABS04920 standard; DNA; 1981 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID NO 4911.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.06%  
 Best Local Similarity: 33.44%  
 Query Match: 11.40%  
 RESULT 1275  
 ID ABT19135 standard; DNA; 3003 BP.  
 DE Aspergillus fumigatus essential gene #1493.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 27.62%  
 Query Match: 11.40%  
 RESULT 1276  
 ID ABT18541 standard; DNA; 3039 BP.  
 DE Aspergillus fumigatus essential gene #899.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 27.62%  
 Query Match: 11.40%  
 RESULT 1277  
 ID ABT17947 standard; DNA; 5039 BP.  
 DE Aspergillus fumigatus essential gene #305.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 27.62%  
 Query Match: 11.40%  
 RESULT 1278  
 ID ABL26763 standard; DNA; 819 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31762.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 29.87%  
 Query Match: 11.38%  
 RESULT 1279  
 ID ACF04821 standard; DNA; 9855 BP.  
 DE M lichenicola melithiazol synthesis gene Mel D.  
 PN WO2003080828-A2.  
 PD 02-OCT-2003.  
 PA (GBFB) GBF GFS BIOTECH FORSCHUNG GMBH.  
 Percent Similarity: 35.35%  
 Best Local Similarity: 27.07%  
 Query Match: 11.36%  
 RESULT 1280  
 ID AAC98196 standard; cDNA; 5145 BP.  
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:206.  
 PN WO200055351-A1.

PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 36.81%  
 Best Local Similarity: 30.00%  
 Query Match: 11.34%  
 RESULT 1281  
 ID ABD33300 standard; cDNA; 5294 BP.  
 DE Human cancer-associated (CA) cDNA HR07-053.  
 PN WO2004058146-A2.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 36.65%  
 Best Local Similarity: 30.08%  
 Query Match: 11.34%  
 RESULT 1282  
 ID ABZ35486 standard; cDNA; 5451 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 597.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 36.69%  
 Best Local Similarity: 29.84%  
 Query Match: 11.34%  
 RESULT 1283  
 ID ADQ23105 standard; DNA; 2409 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5925.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 37.12%  
 Best Local Similarity: 30.37%  
 Query Match: 11.32%  
 RESULT 1284  
 ID ABA83119 standard; DNA; 5416 BP.  
 DE Collagen type I alpha-2 ovarian tumour marker gene, SEQ ID NO:75.  
 PN WO200175177-A2.  
 PD 11-OCT-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Percent Similarity: 36.23%  
 Best Local Similarity: 30.30%  
 Query Match: 11.32%  
 RESULT 1285  
 ID ABL65476 standard; DNA; 5416 BP.  
 DE Lung cancer related gene sequence SEQ ID NO:3813.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Percent Similarity: 36.23%  
 Best Local Similarity: 30.30%  
 Query Match: 11.32%  
 RESULT 1286  
 ID ABL62092 standard; DNA; 5416 BP.  
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:429.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Percent Similarity: 36.23%  
 Best Local Similarity: 30.30%  
 Query Match: 11.32%  
 RESULT 1287  
 ID ABL62655 standard; DNA; 5416 BP.  
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:992.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Percent Similarity: 36.23%  
 Best Local Similarity: 30.30%  
 Query Match: 11.32%  
 RESULT 1288  
 ID ABT10868 standard; cDNA; 5416 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 1002.  
 PN WO200259271-A2.  
 PD 01-AUG-2002.



PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 36.23% Conservative: 28  
Best Local Similarity: 30.30% Mismatches: 184  
Query Match: 11.32% Indels: 117  
RESULT 1289  
ID ABK64492 standard; DNA; 5416 BP.  
DE Human benign prostatic hyperplasia gene #387.  
PN WO200212440-A2.  
PD 14-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISR) JAPAN TOBACCO INC.  
Percent Similarity: 36.23% Conservative: 28  
Best Local Similarity: 30.30% Mismatches: 184  
Query Match: 11.32% Indels: 117  
RESULT 1290  
ID ABN95596 standard; DNA; 5416 BP.  
DE Gene #2094 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 36.23% Conservative: 28  
Best Local Similarity: 30.30% Mismatches: 184  
Query Match: 11.32% Indels: 117  
RESULT 1291  
ID AAQ13864 standard; DNA; 3526 BP.  
DE PRP 378 gene and regulatory region.  
PN WO9113991-A.  
PD 19-SEP-1991.  
PA (ADTE-) ADV TECHN CAMBRIDGE.  
PA (AGRI-) AGRIC GENETICS CO.  
PA (BIOT-) BIOTAL LTD.  
PA (BRE-) BP NUTRITION LTD.  
Percent Similarity: 37.25% Conservative: 31  
Best Local Similarity: 30.38% Mismatches: 187  
Query Match: 11.30% Indels: 98  
RESULT 1292  
ID ADC30636 standard; cDNA; 6058 BP.  
DE Human novel cDNA sequence, SEQ ID NO:718.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.39% Conservative: 33  
Best Local Similarity: 27.87% Mismatches: 211  
Query Match: 11.30% Indels: 123  
RESULT 1293  
ID AAD08215 standard; DNA; 114793 BP.  
DE Human genome from BAC clone, hbm168.  
PN WO200142434-A1.  
PD 14-JUN-2001.  
PA (MERI) MERCK & CO INC.  
Percent Similarity: 37.10% Conservative: 43  
Best Local Similarity: 27.38% Mismatches: 172  
Query Match: 11.30% Indels: 108  
RESULT 1294  
ID AAS84219 standard; cDNA; 3250 BP.  
DE DNA encoding novel human diagnostic protein #20023.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.27% Conservative: 39  
Best Local Similarity: 25.77% Mismatches: 173  
Query Match: 11.28% Indels: 175  
RESULT 1295  
ID ADC32560 standard; cDNA; 3250 BP.  
DE Human novel cDNA contig sequence, SEQ ID NO:2642.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 33.27% Conservative: 39  
Best Local Similarity: 25.77% Mismatches: 173  
Query Match: 11.28% Indels: 175  
RESULT 1296  
ID ABL14811 standard; cDNA; 1186 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38915.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.35% Conservative: 18  
Best Local Similarity: 31.93% Mismatches: 142  
Query Match: 11.26% Indels: 66  
RESULT 1297  
ID ABL14810 standard; cDNA; 3254 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38912.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.35% Conservative: 18  
Best Local Similarity: 31.93% Mismatches: 142  
Query Match: 11.26% Indels: 66  
RESULT 1298  
ID ABL14138 standard; cDNA; 22948 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 36896.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.35% Conservative: 18  
Best Local Similarity: 31.93% Mismatches: 142  
Query Match: 11.26% Indels: 66  
RESULT 1299  
ID AAAL4651 standard; DNA; 77536 BP.  
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
PN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Percent Similarity: 35.89% Conservative: 33  
Best Local Similarity: 29.05% Mismatches: 188  
Query Match: 11.24% Indels: 121  
RESULT 1302  
Percent Similarity: 39.78% Conservative: 50  
Best Local Similarity: 28.79% Mismatches: 165  
Query Match: 11.24% Indels: 109  
RESULT 1303  
ID AAS12490 standard; DNA; 1794 BP.  
DE DNA sequence for Mycobacterium tuberculosis clone mTCC#3.  
PN WO200162893-A2.  
PD 30-AUG-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 36.99% Conservative: 48  
Best Local Similarity: 28.07% Mismatches: 186  
Query Match: 11.21% Indels: 153  
RESULT 1304  
ID AAS68014 standard; cDNA; 2416 BP.  
DE DNA encoding novel human diagnostic protein #3818.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 36.70% Conservative: 30  
Best Local Similarity: 30.26% Mismatches: 150  
Query Match: 11.21% Indels: 107  
RESULT 1305  
ID ABL19674 standard; DNA; 21222 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10495.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 36.21% Conservative: 23

Best Local Similarity: 29.60% Mismatches: 101  
 Query Match: 11.21% Indels: 121  
 RESULT 1306  
 Percent Similarity: 36.99% Conservative: 48  
 Best Local Similarity: 28.07% Mismatches: 186  
 Query Match: 11.21% Indels: 153  
 RESULT 1307  
 Percent Similarity: 36.99% Conservative: 48  
 Best Local Similarity: 28.07% Mismatches: 186  
 Query Match: 11.21% Indels: 153  
 RESULT 1308  
 ID AAV62694 standard; DNA; 1611 BP.  
 DE Phenolic acid esterase encoding DNA.  
 PN GB2324302-A.  
 PD 21-OCT-1998.  
 PA (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.  
 PA (UYNE-) UNIV NEWCASTLE-UPON-TYNE.  
 Percent Similarity: 38.83% Conservative: 28  
 Best Local Similarity: 29.77% Mismatches: 120  
 Query Match: 11.19% Indels: 69  
 RESULT 1309  
 ID ABL19675 standard; DNA; 2015 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10499.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.87% Conservative: 25  
 Best Local Similarity: 28.46% Mismatches: 116  
 Query Match: 11.19% Indels: 139  
 RESULT 1310  
 ID ABK32842 standard; DNA; 2307 BP.  
 DE DNA encoding human homologue of MPT1 antifungal target.  
 PN WO200202055-A2.  
 PD 10-JAN-2002.  
 PA (ANAD-) ANADYS PHARM INC.  
 Percent Similarity: 35.96% Conservative: 38  
 Best Local Similarity: 27.15% Mismatches: 184  
 Query Match: 11.19% Indels: 94  
 RESULT 1311  
 ID AAT59268 standard; cDNA; 2898 BP.  
 DE Streptomyces pristinaespiralis papA and papM intergenic region.  
 PN WO9601901-A1.  
 PD 25-JAN-1996.  
 PA (RHON ) RHONE POULENC RORER SA.  
 Percent Similarity: 34.06% Conservative: 36  
 Best Local Similarity: 26.93% Mismatches: 179  
 Query Match: 11.19% Indels: 157  
 RESULT 1312  
 ID ABD33153 standard; DNA; 247461 BP.  
 DE Murine cancer-associated (CA) gene MD07-020.  
 PN WO2004058146-A2.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 51.52% Conservative: 11  
 Best Local Similarity: 44.85% Mismatches: 57  
 Query Match: 11.19% Indels: 23  
 RESULT 1313  
 ID ADC32443 standard; cDNA; 4826 BP.  
 DE Human novel cDNA contig sequence, SEQ ID NO:2525.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 37.45% Conservative: 34  
 Best Local Similarity: 30.23% Mismatches: 181  
 Query Match: 11.15% Indels: 116  
 RESULT 1314  
 ID ADK00602 standard; DNA; 3903 BP.  
 DE HOMO protein encoding sequence #7.  
 PN WO2004014946-A1.  
 PD 19-FEB-2004.  
 PA (NEWO-) NEWORGEN LTD.  
 Percent Similarity: 33.13% Conservative: 32  
 Best Local Similarity: 26.67% Mismatches: 171

Query Match: 11.13% Indels: 161  
 RESULT 1315  
 ID ADQ97167 standard; DNA; 176771 BP.  
 DE Human cancer associated sequence HD2-08-009, SEQ ID 143.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 34.41% Conservative: 35  
 Best Local Similarity: 27.36% Mismatches: 157  
 Query Match: 11.13% Indels: 171  
 RESULT 1316  
 ID ADQ86582 standard; cDNA; 2171 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3455.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 37.12% Conservative: 23  
 Best Local Similarity: 30.06% Mismatches: 82  
 Query Match: 11.11% Indels: 123  
 RESULT 1317  
 ID AAD06574 standard; cDNA; 4428 BP.  
 DE Bovine alphas(IIII) collagen cDNA #1.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Percent Similarity: 31.34% Conservative: 25  
 Best Local Similarity: 26.35% Mismatches: 207  
 Query Match: 11.11% Indels: 137  
 RESULT 1318  
 ID AAD06575 standard; cDNA; 4428 BP.  
 DE Bovine alphas(IIII) collagen cDNA #2.  
 PN WO200134647-A2.  
 PD 17-MAY-2001.  
 PA (FIBR-) FIBROGEN INC.  
 Percent Similarity: 31.34% Conservative: 25  
 Best Local Similarity: 26.35% Mismatches: 207  
 Query Match: 11.11% Indels: 137  
 RESULT 1319  
 Percent Similarity: 38.93% Conservative: 54  
 Best Local Similarity: 27.87% Mismatches: 185  
 Query Match: 11.11% Indels: 113  
 RESULT 1320  
 Percent Similarity: 38.93% Conservative: 54  
 Best Local Similarity: 27.87% Mismatches: 185  
 Query Match: 11.11% Indels: 113  
 RESULT 1321  
 ID AAL51689 standard; cDNA; 1789 BP.  
 DE Synthetic spider silk protein coding sequence #2.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 35.50% Conservative: 34  
 Best Local Similarity: 27.61% Mismatches: 206  
 Query Match: 11.09% Indels: 73  
 RESULT 1322  
 ID ACA40519 standard; DNA; 2037 BP.  
 DE Prokaryotic essential gene #22176.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.95% Conservative: 46  
 Best Local Similarity: 27.35% Mismatches: 187  
 Query Match: 11.09% Indels: 115  
 RESULT 1323  
 ID AAA64661 standard; cDNA; 2126 BP.  
 DE cDNA encoding TBP associated factor (TAFII68).  
 PN WO200050595-A2.  
 PD 31-AUG-2000.  
 PA (GOUT/) GOUT I.  
 PA (RODN/) RODNIN N.  
 PA (FILO/) FILOENKO V.

PA (MATS/) MATSUKA G.  
PA (SCAN/) SCANLAN M.  
PA (OLD/) OLD L.  
PA (BILY/) BILYNSKY B.  
Percent Similarity: 32.48%  
Best Local Similarity: 25.69%  
Indels: 171  
Indels: 147  
Query Match:  
RESULT 1324  
ID ACN44634 standard; DNA; 24525 BP.  
DE Human genomic sequence hCG21734.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 31.63%  
Best Local Similarity: 24.91%  
Indels: 160  
Indels: 229  
Query Match:  
RESULT 1325  
Percent Similarity: 36.95%  
Best Local Similarity: 27.35%  
Indels: 187  
Indels: 115  
Query Match:  
RESULT 1326  
ID ABL05326 standard; cDNA; 2972 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10460.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.71%  
Best Local Similarity: 31.50%  
Indels: 100  
Indels: 119  
Query Match:  
RESULT 1327  
ID ABL04337 standard; cDNA; 6776 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7493.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 42.71%  
Best Local Similarity: 28.90%  
Indels: 54  
Indels: 152  
Query Match:  
RESULT 1328  
ID ACN44282 standard; DNA; 23380 BP.  
DE Human genomic sequence hCG25303.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 32.88%  
Best Local Similarity: 27.08%  
Indels: 205  
Indels: 143  
Query Match:  
RESULT 1329  
ID AAF45087 standard; cDNA; 740 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 26.  
PN WO200077023-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 43.42%  
Best Local Similarity: 30.92%  
Indels: 38  
Indels: 92  
Query Match:  
RESULT 1330  
ID ADN99087 standard; cDNA; 1899 BP.  
DE Novel human cDNA sequence #687.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 36.84%  
Best Local Similarity: 30.59%  
Indels: 19  
Indels: 73  
Query Match:  
RESULT 1331  
ID ADO00656 standard; cDNA; 1899 BP.  
DE Novel human cDNA sequence #1471.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 36.84%  
Best Local Similarity: 30.59%  
Indels: 19  
Indels: 73  
Query Match:  
RESULT 1332  
ID ADR85784 standard; DNA; 3150 BP.  
DE Aspergillus fumigatus essential gene open reading frame #421.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.08%  
Best Local Similarity: 23.93%  
Indels: 49  
Indels: 184  
Query Match:  
RESULT 1333  
ID ACN92690 standard; DNA; 5274 BP.  
DE Breast cancer related marker, seq id 13840.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 36.61%  
Best Local Similarity: 29.24%  
Indels: 36  
Indels: 191  
Query Match:  
RESULT 1334  
ID ACH87046 standard; DNA; 597 BP.  
DE Human genome derived single exon probe #20241.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 39.23%  
Best Local Similarity: 32.69%  
Indels: 17  
Indels: 85  
Query Match:  
RESULT 1335  
ID ABL12649 standard; cDNA; 2487 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.10%  
Best Local Similarity: 26.50%  
Indels: 43  
Indels: 188  
Query Match:  
RESULT 1336  
ID ADE07564 standard; DNA; 2529 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #630.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.48%  
Best Local Similarity: 29.52%  
Indels: 25  
Indels: 75  
Query Match:  
RESULT 1337  
ID ADQ08605 standard; DNA; 4037 BP.  
DE Ciona intestinalis nervous system associated gene SeqID7.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Percent Similarity: 35.61%  
Best Local Similarity: 28.57%  
Indels: 33  
Indels: 189  
Query Match:  
RESULT 1338  
ID ABL12648 standard; cDNA; 4487 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32426.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.10%  
Best Local Similarity: 26.50%  
Indels: 43  
Indels: 188  
Query Match:  
RESULT 1339  
ID ABL08505 standard; cDNA; 7396 BP.  
DE Human novel protein NOV11 coding sequence SEQ ID NO: 35.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.

Query Match: 11.05% Indels: 119  
RESULT 1332  
ID ADR85784 standard; DNA; 3150 BP.  
DE Aspergillus fumigatus essential gene open reading frame #421.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.08%  
Best Local Similarity: 23.93%  
Indels: 49  
Indels: 184  
Query Match: 11.05% Indels: 174  
RESULT 1333  
ID ACN92690 standard; DNA; 5274 BP.  
DE Breast cancer related marker, seq id 13840.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 36.61%  
Best Local Similarity: 29.24%  
Indels: 36  
Indels: 191  
Query Match: 11.05% Indels: 119  
RESULT 1334  
ID ACH87046 standard; DNA; 597 BP.  
DE Human genome derived single exon probe #20241.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 39.23%  
Best Local Similarity: 32.69%  
Indels: 17  
Indels: 85  
Query Match: 11.02% Indels: 73  
RESULT 1335  
ID ABL12649 standard; cDNA; 2487 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.10%  
Best Local Similarity: 26.50%  
Indels: 43  
Indels: 188  
Query Match: 11.02% Indels: 185  
RESULT 1336  
ID ADE07564 standard; DNA; 2529 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #630.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.48%  
Best Local Similarity: 29.52%  
Indels: 25  
Indels: 75  
Query Match: 11.02% Indels: 75  
RESULT 1337  
ID ADQ08605 standard; DNA; 4037 BP.  
DE Ciona intestinalis nervous system associated gene SeqID7.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Percent Similarity: 35.61%  
Best Local Similarity: 28.57%  
Indels: 33  
Indels: 189  
Query Match: 11.02% Indels: 113  
RESULT 1338  
ID ABL12648 standard; cDNA; 4487 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32426.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.10%  
Best Local Similarity: 26.50%  
Indels: 43  
Indels: 188  
Query Match: 11.02% Indels: 185  
RESULT 1339  
ID ABL08505 standard; cDNA; 7396 BP.  
DE Human novel protein NOV11 coding sequence SEQ ID NO: 35.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.

Percent Similarity: 31.05% Conservative: 43  
 Best Local Similarity: 23.67% Mismatches: 197  
 Query Match: 11.02% Indels: 205  
 RESULT 1340  
 ID AAV33277 standard; cDNA; 1548 BP.  
 DE Nucleotide sequence encoding Chlamydomonas protein RSP3.  
 PN WO9826094-A1.  
 PD 18-JUN-1998.  
 PA (JARV/) JARVIK J W.  
 Percent Similarity: 34.55% Conservative: 27  
 Best Local Similarity: 27.53% Mismatches: 164  
 Query Match: 11.00% Indels: 88  
 RESULT 1341  
 ID AAV33278 standard; cDNA; 1581 BP.  
 DE Nucleotide sequence encoding tagged Chlamydomonas protein RSP3.  
 PN WO9826094-A1.  
 PD 18-JUN-1998.  
 PA (JARV/) JARVIK J W.  
 Percent Similarity: 34.55% Conservative: 27  
 Best Local Similarity: 27.53% Mismatches: 164  
 Query Match: 11.00% Indels: 88  
 RESULT 1342  
 ID ADI26206 standard; cDNA; 2144 BP.  
 DE Human cDNA encoding protein that promotes STAT6 activation #86.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH ) ASAH KASEI KK.  
 Percent Similarity: 32.48% Conservative: 32  
 Best Local Similarity: 25.69% Mismatches: 171  
 Query Match: 11.00% Indels: 147  
 RESULT 1343  
 ID ABK84369 standard; cDNA; 2153 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #940.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 32.48% Conservative: 32  
 Best Local Similarity: 25.69% Mismatches: 171  
 Query Match: 11.00% Indels: 147  
 RESULT 1344  
 ID ADI26208 standard; cDNA; 2153 BP.  
 DE Human cDNA encoding protein that promotes STAT6 activation #87.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH ) ASAH KASEI KK.  
 Percent Similarity: 32.48% Conservative: 32  
 Best Local Similarity: 25.69% Mismatches: 171  
 Query Match: 11.00% Indels: 147  
 RESULT 1345  
 ID ABL22542 standard; cDNA; 2213 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 19099.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 36.90% Conservative: 9  
 Best Local Similarity: 33.33% Mismatches: 83  
 Query Match: 11.00% Indels: 76  
 RESULT 1346  
 ID AAD5725 standard; cDNA; 1196 BP.  
 DE Latrodectus geometricus major ampullate epidroidin 2 (MaSp2) DNA #2.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Percent Similarity: 36.07% Conservative: 32  
 Best Local Similarity: 27.32% Mismatches: 135  
 Query Match: 10.98% Indels: 99  
 RESULT 1347  
 ID ADO09868 standard; cDNA; 7396 BP.  
 DE Human NOV11 cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.

PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERRHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHH/) TCHERNEV V T.  
 PA (SIJU/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Percent Similarity: 31.23% Conservative: 45  
 Best Local Similarity: 23.50% Mismatches: 196  
 Query Match: 10.98% Indels: 205  
 RESULT 1348  
 ID AAF82982 standard; DNA; 17150 BP.  
 DE Human DNA methyltransferase, DNMT3L genomic sequence.  
 PN WO200127249-A1.  
 PD 19-APR-2001.  
 PA (FIIM-) FINNISH IMMUNOTECHNOLOGY LTD.  
 PA (KROH/) KROHN K.  
 PA (AAPO/) AAPOLA U.  
 PA (SCOT/) SCOTT H.  
 PA (ANTO/) ANTONARAKIS S.  
 PA (SHIM/) SHIMIZU N.  
 PA (KUDO/) KUDOH.  
 PA (PETE/) PETERSON P.  
 Percent Similarity: 36.62% Conservative: 34  
 Best Local Similarity: 29.17% Mismatches: 196  
 Query Match: 10.98% Indels: 93  
 RESULT 1349  
 ID ABA17086 standard; DNA; 30032 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 9417.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 36.09% Conservative: 29  
 Best Local Similarity: 29.43% Mismatches: 164  
 Query Match: 10.98% Indels: 116  
 RESULT 1350  
 ID ACA27418 standard; DNA; 1896 BP.  
 DE Prokaryotic essential gene #9075.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.67% Conservative: 29  
 Best Local Similarity: 29.58% Mismatches: 132  
 Query Match: 10.98% Indels: 127  
 RESULT 1351  
 ID ADE77157 standard; cDNA; 1939 BP.  
 DE Human cDNA differentially expressed in a liver disorder #240.  
 PN US2003108871-A1.  
 PD 12-JUN-2003.  
 PA (KASE/) KASER M R.  
 Percent Similarity: 34.91% Conservative: 28  
 Best Local Similarity: 27.56% Mismatches: 120  
 Query Match: 10.96% Indels: 129  
 RESULT 1352  
 Percent Similarity: 31.83% Conservative: 14  
 Best Local Similarity: 27.33% Mismatches: 115  
 Query Match: 10.98% Indels: 98  
 RESULT 1353

ID ABS73274 standard; DNA; 1678 BP.  
 DE DNA encoding human translocation (12; 16) (q13; p11) protein #4.  
 PN WO200269900-A2.  
 PD 12-SEP-2002.  
 PA (CONP-) CONFORMA THERAPEUTICS CORP.  
 Percent Similarity: 40.82% Conservative: 20  
 Best Local Similarity: 32.65% Mismatches: 92  
 Query Match: 10.94% Indels: 53  
 RESULT 1354  
 ID ABK94148 standard; cDNA; 1692 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #719.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 40.82% Conservative: 20  
 Best Local Similarity: 32.65% Mismatches: 92  
 Query Match: 10.94% Indels: 53  
 RESULT 1355  
 ID ACA64957 standard; DNA; 1682 BP.  
 DE Human TLS/CHOP DNA corresponding to SC2138.  
 PN DE10127572-A1.  
 PD 05-DEC-2002.  
 PA (PATH-) PATHOARRAY GMBH.  
 Percent Similarity: 40.82% Conservative: 20  
 Best Local Similarity: 32.65% Mismatches: 92  
 Query Match: 10.94% Indels: 53  
 RESULT 1356  
 ID ADB31366 standard; cDNA; 1692 BP.  
 DE Bicalutamide regulated prostate cancer gene #43.  
 PN US6506607-B1.  
 PD 14-JAN-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 40.82% Conservative: 20  
 Best Local Similarity: 32.65% Mismatches: 92  
 Query Match: 10.94% Indels: 53  
 RESULT 1357  
 ID ADR26011 standard; DNA; 1682 BP.  
 DE Breast cancer prognosis marker #1872.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 Percent Similarity: 40.82% Conservative: 20  
 Best Local Similarity: 32.65% Mismatches: 92  
 Query Match: 10.94% Indels: 53  
 RESULT 1358  
 ID ADO13830 standard; DNA; 71138 BP.  
 DE dbv gene cluster.  
 PN EP1413626-A1.  
 PD 28-APR-2004.  
 PA (VICU-) VICURON PHARM INC.  
 Percent Similarity: 31.36% Conservative: 29  
 Best Local Similarity: 25.46% Mismatches: 197  
 Query Match: 10.94% Indels: 141  
 RESULT 1359  
 ID ADQ89963 standard; DNA; 103052 BP.  
 DE Antagonist of cell cycle progression nucleotide sequence #197.  
 PN WO2004063362-A2.  
 PD 29-JUL-2004.  
 PA (CYCL-) CYCLACEL LTD.  
 Percent Similarity: 37.87% Conservative: 40  
 Best Local Similarity: 29.36% Mismatches: 189  
 Query Match: 10.94% Indels: 105  
 RESULT 1360  
 ID AAC1802 standard; DNA; 1047 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33190.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Percent Similarity: 36.57% Conservative: 20  
 Best Local Similarity: 30.10% Mismatches: 102  
 Query Match: 10.92% Indels: 94  
 RESULT 1361  
 ID ADI26112 standard; cDNA; 1832 BP.  
 DE Human secreted protein 5' EST SEQ ID NO:194.  
 PN WO9906548-A2.  
 DE Human cDNA encoding protein that promotes STAT6 activation #39.  
 PN WO2003104277-A2.  
 PD 18-DEC-2003.  
 PA (ASAH) ASAH KASEI KK.  
 Percent Similarity: 34.74% Conservative: 37  
 Best Local Similarity: 26.06% Mismatches: 162  
 Query Match: 10.92% Indels: 116  
 RESULT 1362  
 ID ADH48847 standard; DNA; 5896 BP.  
 DE NOV57 coding sequence, SEQ ID 131.  
 PN WO200268652-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.20% Conservative: 37  
 Best Local Similarity: 25.66% Mismatches: 178  
 Query Match: 10.92% Indels: 150  
 RESULT 1363  
 ID AAF30757 standard; DNA; 47981 BP.  
 DE Micromonospora megalomycin megalomicin biosynthetic gene cluster.  
 PN WO200268652-A2.  
 PD 06-SEP-2002.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Percent Similarity: 40.89% Conservative: 30  
 Best Local Similarity: 29.74% Mismatches: 112  
 Query Match: 10.90% Indels: 47  
 RESULT 1364  
 ID ABL61036 standard; DNA; 705 BP.  
 DE N. clavipes spideroin synthetic homologue SE1.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Percent Similarity: 40.89% Conservative: 30  
 Best Local Similarity: 29.74% Mismatches: 112  
 Query Match: 10.90% Indels: 47  
 RESULT 1365  
 ID ADR85197 standard; DNA; 3820 BP.  
 DE Aspergillus fumigatus essential gene with introns #421.  
 PN WO2004067709-A2.  
 PD 12-AUG-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.43% Conservative: 44  
 Best Local Similarity: 25.36% Mismatches: 192  
 Query Match: 10.90% Indels: 127  
 RESULT 1366  
 ID ADR4610 standard; DNA; 5820 BP.  
 DE Aspergillus fumigatus essential gene genomic sequence #421.  
 PN WO2004067709-A2.  
 PD 12-AUG-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.43% Conservative: 44  
 Best Local Similarity: 25.36% Mismatches: 192  
 Query Match: 10.90% Indels: 127  
 RESULT 1367  
 ID ACN88799 standard; DNA; 8664 BP.  
 DE Breast cancer related marker, seq id 9949.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 34.73% Conservative: 29  
 Best Local Similarity: 28.32% Mismatches: 186  
 Query Match: 10.90% Indels: 109  
 RESULT 1368  
 ID ABD32827 standard; DNA; 129381 BP.  
 DE Human cancer-associated genomic DNA HD17-008.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 31.60% Conservative: 32  
 Best Local Similarity: 24.06% Mismatches: 147  
 Query Match: 10.90% Indels: 143  
 RESULT 1369  
 ID AAX41250 standard; cDNA; 272 BP.  
 DE Human secreted protein 5' EST SEQ ID NO:194.  
 PN WO9906548-A2.



Query Match: 10.81% Indels: 119  
 RESULT 1385  
 ID ADC60733 standard; DNA; 50000 BP.  
 DE Human elingshot-related DNA 7.  
 PN JP2003102483-A.  
 PD 08-APR-2003.  
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
 Percent Similarity: 36.76% Conservative: 29  
 Best Local Similarity: 30.14% Mismatches: 178  
 Query Match: 10.81% Indels: 100  
 RESULT 1386  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 30.48% Conservative: 32  
 Best Local Similarity: 24.78% Mismatches: 207  
 Query Match: 10.81% Indels: 186  
 RESULT 1387  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 30.48% Conservative: 32  
 Best Local Similarity: 24.78% Mismatches: 207  
 Query Match: 10.81% Indels: 186  
 RESULT 1388  
 ID ABL06790 standard; cDNA; 9051 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14852.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NV.  
 Percent Similarity: 36.11% Conservative: 52  
 Best Local Similarity: 25.00% Mismatches: 197  
 Query Match: 10.79% Indels: 102  
 RESULT 1389  
 ID ADN73798 standard; cDNA; 1113 BP.  
 DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1693.  
 PN WO2004035798-A2.  
 PD 29-APR-2004.  
 PA (CROP-) CROPPDESIGN NV.  
 Percent Similarity: 39.07% Conservative: 36  
 Best Local Similarity: 29.82% Mismatches: 150  
 Query Match: 10.77% Indels: 87  
 RESULT 1390  
 ID ACC70864 standard; DNA; 10494 BP.  
 DE Oncolytic microorganism-related DNA sequence.  
 PN WO2003031602-A1.  
 PD 17-APR-2003.  
 PA (HANG-) HANGZHOU CONQUER BIOTECH CO LTD.  
 Percent Similarity: 33.94% Conservative: 16  
 Best Local Similarity: 29.77% Mismatches: 129  
 Query Match: 10.77% Indels: 125  
 RESULT 1391  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Percent Similarity: 37.32% Conservative: 21  
 Best Local Similarity: 29.71% Mismatches: 116  
 Query Match: 10.77% Indels: 58  
 RESULT 1392  
 ID ABL04336 standard; cDNA; 3791 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7490.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NV.  
 Percent Similarity: 37.53% Conservative: 38  
 Best Local Similarity: 27.76% Mismatches: 134  
 Query Match: 10.75% Indels: 109

RESULT 1393  
 ID ADC21545 standard; DNA; 4464 BP.  
 DE Human type II collagen gene sequence.  
 PN WO2003006603-A2.  
 PD 23-JAN-2003.  
 PA (AREX-) AREXIS AB.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1394  
 ID ADJ56239 standard; cDNA; 4837 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 45.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 PA (PLON/) PLON S E.  
 PA (SHOH/) SHOHET J M.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1395  
 ID ADQ84507 standard; cDNA; 4853 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1321.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1396  
 ID ACN39417 standard; cDNA; 4853 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA325637, SEQ ID NO:3545.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1397  
 ID ACN42212 standard; cDNA; 4865 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1087.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1398  
 ID ABK92176 standard; DNA; 5060 BP.  
 DE Prostate cancer-associated DNA sequence #62.  
 PN WO2002020268-A2.  
 PD 18-APR-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Percent Similarity: 34.33% Conservative: 35  
 Best Local Similarity: 27.38% Mismatches: 197  
 Query Match: 10.75% Indels: 134  
 RESULT 1399  
 ID AAH78668 standard; cDNA; 6200 BP.  
 DE Human COL5A3 cDNA sequence encoding pro-alpha-3(V) polypeptide.  
 PN WO200164871-A2.  
 PD 07-SEP-2001.  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 Percent Similarity: 35.06% Conservative: 34  
 Best Local Similarity: 27.71% Mismatches: 182  
 Query Match: 10.75% Indels: 118  
 RESULT 1400  
 ID ADQ19840 standard; DNA; 6200 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2659.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 34  
 Percent Similarity: 35.06%  
 Best Local Similarity: 27.71%  
 Query Match: 10.75%  
 RESULT 1401  
 ID AEN59647 standard; cDNA; 6368 BP.  
 DE Novel human coding sequence SEQ ID NO: 58.  
 PN WO200222660-A2.  
 PD 21-MAR-2002.  
 PA (HYSE-) HYSEQ INC. Conservative: 34  
 Percent Similarity: 35.06%  
 Best Local Similarity: 27.71%  
 Query Match: 10.75%  
 RESULT 1402  
 ID ADQ23958 standard; DNA; 6617 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6778.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 34  
 Percent Similarity: 35.06%  
 Best Local Similarity: 27.71%  
 Query Match: 10.75%  
 RESULT 1403  
 ID ADC87242 standard; DNA; 38918 BP.  
 DE Human GPCR gene SEQ ID NO:1695.  
 PN RPI270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. Conservative: 32  
 Percent Similarity: 37.99%  
 Best Local Similarity: 29.05%  
 Query Match: 10.73%  
 RESULT 1405  
 ID AAS92830 standard; cDNA; 1371 BP.  
 DE DNA encoding novel human diagnostic protein #28634.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC. Conservative: 9  
 Percent Similarity: 44.44%  
 Best Local Similarity: 39.18%  
 Query Match: 10.73%  
 RESULT 1406  
 ID ADQ23091 standard; DNA; 5827 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5911.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 31  
 Percent Similarity: 35.56%  
 Best Local Similarity: 28.16%  
 Query Match: 10.73%  
 RESULT 1407  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON. Conservative: 38  
 Percent Similarity: 32.43%  
 Best Local Similarity: 25.05%  
 Query Match: 10.73%  
 RESULT 1408  
 ID ACH87193 standard; DNA; 461 BP.  
 DE Human genome derived single exon probe #20388.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.

PA (PENN/) PENN S G. Conservative: 6  
 Percent Similarity: 36.93%  
 Best Local Similarity: 33.52%  
 Query Match: 10.71%  
 RESULT 1409  
 ID AAS92206 standard; cDNA; 1543 BP.  
 DE DNA encoding novel human diagnostic protein #28010.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC. Conservative: 29  
 Percent Similarity: 35.95%  
 Best Local Similarity: 27.19%  
 Query Match: 10.71%  
 RESULT 1410  
 ID ABZ21589 standard; DNA; 3651 BP.  
 DE Bombyx mori sericin encoding DNA SEQ ID NO 3.  
 PN WO200286133-A1.  
 PD 31-OCT-2002.  
 PA (SEIR-) SEIREN CO LTD. Conservative: 46  
 Percent Similarity: 38.97%  
 Best Local Similarity: 28.17%  
 Query Match: 10.71%  
 RESULT 1411  
 ID ABL07399 standard; cDNA; 3823 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16679.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY. Conservative: 31  
 Percent Similarity: 32.91%  
 Best Local Similarity: 26.33%  
 Query Match: 10.71%  
 RESULT 1412  
 ID ACI9443 standard; cDNA; 5634 BP.  
 DE CDNA encoding novel human protein #123.  
 PN WO2003023002-A2.  
 PD 20-MAR-2003.  
 PA (CURA-) CURAGEN CORP. Conservative: 26  
 Percent Similarity: 34.86%  
 Best Local Similarity: 27.84%  
 Query Match: 10.71%  
 RESULT 1413  
 ID ADQ91713 standard; DNA; 22533 BP.  
 DE Polyketide synthase ORF17, SEQ ID 36.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC. Conservative: 45  
 Percent Similarity: 38.84%  
 Best Local Similarity: 29.55%  
 Query Match: 10.71%  
 RESULT 1414  
 ID ABK3567 standard; cDNA; 112460 BP.  
 DE Human CDNA differentially expressed in granulocytic cells #138.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC. Conservative: 34  
 Percent Similarity: 32.64%  
 Best Local Similarity: 25.52%  
 Query Match: 10.71%  
 RESULT 1415  
 ID ADQ91695 standard; DNA; 164051 BP.  
 DE Polyketide synthase related DNA contig 2, SEQ ID 18.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC. Conservative: 45  
 Percent Similarity: 38.84%  
 Best Local Similarity: 29.55%  
 Query Match: 10.71%  
 RESULT 1416  
 ID ABK98331 standard; cDNA; 1485 BP.  
 DE Arabidopsis CDNA for periaxin #2.  
 PN WO200251981-A2.



PD 04-JUL-2002.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 39.95%  
 Best Local Similarity: 30.93%  
 Query Match: 10.69%  
 Indels: 85  
 RESULT 1417  
 ID AAD21684 standard; DNA; 2849 BP.  
 DE Human retinitis pigmentosa GTPase regulator (RPGR) exon ORF15 DNA.  
 PN WO200177380-A2.  
 PD 18-OCT-2001.  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 Percent Similarity: 32.61%  
 Best Local Similarity: 26.13%  
 Query Match: 10.69%  
 Indels: 81  
 RESULT 1418  
 ID ADG37080 standard; DNA; 28198 BP.  
 DE Mouse plakoglobin polynucleotide seq id 2.  
 PN JP2003189850-A.  
 PD 08-JUL-2003.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Percent Similarity: 29.22%  
 Best Local Similarity: 25.00%  
 Query Match: 10.69%  
 Indels: 120  
 RESULT 1419  
 ID AAL51697 standard; cDNA; 681 BP.  
 DE Argiope trifasciata spider silk protein coding sequence #2.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYMY-) UNIV WYOMING.  
 Percent Similarity: 39.85%  
 Best Local Similarity: 28.04%  
 Query Match: 10.66%  
 Indels: 74  
 RESULT 1420  
 ID ACN40095 standard; cDNA; 3465 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326253, SEQ ID NO:4663.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 35.89%  
 Best Local Similarity: 27.23%  
 Query Match: 10.66%  
 Indels: 121  
 RESULT 1421  
 ID ADJ92727 standard; cDNA; 3641 BP.  
 DE Human intracellular chloride ion channel-related protein HCL1 cDNA.  
 PN US2004009915-A1.  
 PD 15-JAN-2004.  
 PA (CHAN/) CHANG H.  
 PA (FEDE/) FEDER J N.  
 PA (LEEL/) LEE L M.  
 PA (RICH/) RICH A.  
 Percent Similarity: 35.64%  
 Best Local Similarity: 29.70%  
 Query Match: 10.66%  
 Indels: 101  
 RESULT 1422  
 ID ABL3813 standard; cDNA; 15009 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35921.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE ) PE CORP NY.  
 Percent Similarity: 32.35%  
 Best Local Similarity: 25.04%  
 Query Match: 10.66%  
 Indels: 219  
 RESULT 1423  
 ID ABL61041 standard; DNA; 672 BP.  
 DE N. clavipes spideroin synthetic homologue PA2.  
 PN DE10113781-A1.  
 PD 13-DEC-2001.  
 PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
 Percent Similarity: 41.60%  
 Best Local Similarity: 33.21%  
 Query Match: 10.64%  
 Indels: 53  
 RESULT 1424  
 ID ADE77158 standard; cDNA; 1684 BP.

DE Human cDNA differentially expressed in a liver disorder #241.  
 PN US2003108871-A1.  
 PD 12-JUN-2003.  
 PA (KASE/) KASER M R.  
 Percent Similarity: 36.66%  
 Best Local Similarity: 29.90%  
 Query Match: 10.64%  
 Indels: 105  
 RESULT 1425  
 ID AAH67497 standard; DNA; 1755 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 2532.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 26.26%  
 Query Match: 10.64%  
 Indels: 147  
 RESULT 1426  
 ID ABZ13886 standard; DNA; 2283 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1691.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 26.71%  
 Query Match: 10.64%  
 Indels: 93  
 RESULT 1427  
 ID ADR31451 standard; DNA; 4826 BP.  
 DE Streptomyces aureofaciens NRRL2209 Sau3A I genomic DNA fragment.  
 PN US2004157303-A1.  
 PD 12-AUG-2004.  
 PA (MAHI/) MAHISHI L H.  
 PA (TRIP/) TRIPATHI G.  
 PA (RAMC/) RAMCHANDER T V N.  
 PA (RAWA/) RAWAL S K.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 24.91%  
 Query Match: 10.64%  
 Indels: 161  
 RESULT 1428  
 ID AAH68531 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 7066.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 26.26%  
 Query Match: 10.64%  
 Indels: 147  
 RESULT 1429  
 ID AAH68532 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 7067.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 26.26%  
 Query Match: 10.64%  
 Indels: 147  
 RESULT 1430  
 ID ADB53942 standard; DNA; 5721 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4484.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 36.36%  
 Best Local Similarity: 27.70%  
 Query Match: 10.62%  
 Indels: 108  
 RESULT 1431  
 ID ADP73027 standard; DNA; 5721 BP.  
 DE Renal toxin progression gene marker #1616.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 36.36%  
 Best Local Similarity: 27.70%  
 Query Match: 10.64%  
 Indels: 108  
 RESULT 1432  
 ID ADE77158 standard; cDNA; 1684 BP.

Query Match: 10.62% Indels: 108  
RESULT 1432  
ID AAI19102 standard; DNA; 985 BP.  
DE Probe #9035 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.00%  
Best Local Similarity: 33.88%  
Conservative: 15  
Mismatch: 82  
Indels: 67  
Query Match: 10.60%  
RESULT 1433  
ID ABA31265 standard; DNA; 985 BP.  
DE Probe #9731 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.00%  
Best Local Similarity: 33.88%  
Conservative: 15  
Mismatch: 82  
Indels: 67  
Query Match: 10.60%  
RESULT 1434  
ID AAK12588 standard; DNA; 985 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 12579.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.00%  
Best Local Similarity: 33.88%  
Conservative: 15  
Mismatch: 82  
Indels: 67  
Query Match: 10.60%  
RESULT 1435  
ID AAK12588 standard; DNA; 985 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 12579.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.00%  
Best Local Similarity: 33.88%  
Conservative: 15  
Mismatch: 82  
Indels: 67  
Query Match: 10.60%  
RESULT 1436  
ID ABS12355 standard; DNA; 985 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 12346.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.00%  
Best Local Similarity: 33.88%  
Conservative: 15  
Mismatch: 82  
Indels: 67  
Query Match: 10.60%  
RESULT 1437  
ID ABQ68452 standard; DNA; 1327 BP.  
DE Listeria monocytogenes 4b contig DNA sequence #1218.  
PN WO200228891-A2.  
PD 11-APR-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Percent Similarity: 37.95%  
Best Local Similarity: 31.25%  
Conservative: 15  
Mismatch: 114  
Indels: 26  
Query Match: 10.60%  
RESULT 1438  
ID ADQ83371 standard; cDNA; 2507 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #185.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Percent Similarity: 43.44%  
Best Local Similarity: 36.20%  
Conservative: 16  
Mismatch: 93  
Indels: 33  
Query Match: 10.60%  
RESULT 1439  
ID RAS81477 standard; cDNA; 2109 BP.  
DE DNA encoding novel human diagnostic protein #17281.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Percent Similarity: 32.53% Conservative: 12  
Best Local Similarity: 28.92% Mismatches: 140  
Query Match: 10.58% Indels: 87  
RESULT 1440  
ID AAC5842 standard; DNA; 53500 BP.  
DE Complete nucleotide sequence of the mitomycin biosynthetic genes.  
PN WO200053737-A2.  
PD 14-SEP-2000.  
PA (MINU) UNIV MINNESOTA.  
PA (SHER) SHERMAN D H.  
PA (MAOY) MAO Y.  
PA (HEMM) HE M.  
PA (SHEL) SHELDON P C.  
Percent Similarity: 33.21% Conservative: 43  
Best Local Similarity: 25.36% Mismatches: 158  
Query Match: 10.58% Indels: 210  
RESULT 1441  
ID ADE10261 standard; DNA; 53500 BP.  
DE S. lavendulae mitomycin biosynthetic genes complete sequence.  
PN US2003134398-A1.  
PD 17-JUL-2003.  
PA (SHER) SHERMAN D H.  
PA (MAOY) MAO Y.  
PA (VARO) VAROGLU M.  
PA (HEMM) HE M.  
PA (SHEL) SHELDON P.  
Percent Similarity: 33.21% Conservative: 43  
Best Local Similarity: 25.36% Mismatches: 158  
Query Match: 10.58% Indels: 210  
RESULT 1442  
ID AAI23276 standard; DNA; 446 BP.  
DE Probe #13209 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.85% Conservative: 4  
Best Local Similarity: 28.86% Mismatches: 72  
Query Match: 10.56% Indels: 67  
RESULT 1443  
ID ABA68382 standard; DNA; 446 BP.  
DE Human foetal liver single exon nucleic acid probe #16687.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.85% Conservative: 4  
Best Local Similarity: 28.86% Mismatches: 72  
Query Match: 10.56% Indels: 67  
RESULT 1444  
ID AAI48596 standard; DNA; 446 BP.  
DE Probe #17282 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.85% Conservative: 4  
Best Local Similarity: 28.86% Mismatches: 72  
Query Match: 10.56% Indels: 67  
RESULT 1445  
ID ABA50433 standard; DNA; 446 BP.  
DE Human breast cell single exon nucleic acid probe #9128.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.85% Conservative: 4  
Best Local Similarity: 28.86% Mismatches: 72  
Query Match: 10.56% Indels: 67  
RESULT 1446  
ID ABA35379 standard; DNA; 446 BP.  
DE Probe #13845 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.85% Conservative: 4  
Best Local Similarity: 28.86% Mismatches: 72  
Query Match: 10.56% Indels: 67

Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1447					
ID AAK42529 standard; DNA; 446 BP.					
DE Human bone marrow expressed single exon probe SEQ ID NO: 17086.					
PN WO200157276-A2.					
PD 03-AUG-2001.					
PA (MOLE-) MOLECULAR DYNAMICS INC.					
Percent Similarity: 30.85%	Conservative: 4				
Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1448					
ID AAK16757 standard; DNA; 446 BP.					
DE Human brain expressed single exon probe SEQ ID NO: 16748.					
PN WO200157275-A2.					
PD 09-AUG-2001.					
PA (MOLE-) MOLECULAR DYNAMICS INC.					
Percent Similarity: 30.85%	Conservative: 4				
Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1449					
ID ABS42140 standard; DNA; 446 BP.					
DE Human liver single exon probe, SEQ ID NO 17130.					
PN WO200157273-A2.					
PD 03-AUG-2001.					
PA (MOLE-) MOLECULAR DYNAMICS INC.					
Percent Similarity: 30.85%	Conservative: 4				
Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1450					
ID AAI08921 standard; DNA; 446 BP.					
DE Probe #8912 used to measure gene expression in human breast sample.					
PN WO200157270-A2.					
PD 09-AUG-2001.					
PA (MOLE-) MOLECULAR DYNAMICS INC.					
Percent Similarity: 30.85%	Conservative: 4				
Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1451					
ID ABS16574 standard; DNA; 446 BP.					
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 16565.					
PN WO200186003-A2.					
PD 15-NOV-2001.					
PA (MOLE-) MOLECULAR DYNAMICS INC.					
Percent Similarity: 30.85%	Conservative: 4				
Best Local Similarity: 28.86%	Mismatches: 72				
Query Match: 10.56%	Indels: 67				
RESULT 1452					
ID ACA29408 standard; DNA; 2007 BP.					
DE Prokaryotic essential gene #11065.					
PN WO200277183-A2.					
PD 03-OCT-2002.					
PA (ELIT-) ELITRA PHARM INC.					
Percent Similarity: 53.69%	Conservative: 15				
Best Local Similarity: 43.62%	Mismatches: 36				
Query Match: 10.56%	Indels: 33				
RESULT 1453					
ID ADJ67344 standard; DNA; 2110 BP.					
DE Human ovarian specific gene SEQ ID NO:58.					
PN WO2004013311-A2.					
PD 12-FEB-2004.					
PA (DIAD-) DIADEXUS INC.					
Percent Similarity: 33.92%	Conservative: 24				
Best Local Similarity: 27.85%	Mismatches: 190				
Query Match: 10.56%	Indels: 71				
RESULT 1454					
ID ADQ22244 standard; DNA; 2548 BP.					
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5064.					
PN WO2004048938-A2.					
PD 10-JUN-2004.					
PA (PROT-) PROTEIN DESIGN LABS INC.					
Percent Similarity: 43.44%	Conservative: 16				
Best Local Similarity: 36.20%	Mismatches: 93				
RESULT 1455					
ID ADF69260 standard; cDNA; 1612 BP.					
DE Human lung specific nucleotide sequence SEQ ID NO:17.					
PN WO2003102137-A2.					
PD 11-DEC-2003.					
PA (DIAD-) DIADEXUS INC.					
Percent Similarity: 33.56%	Conservative: 20				
Best Local Similarity: 28.94%	Mismatches: 177				
Query Match: 10.54%	Indels: 111				
RESULT 1456					
ID ADF69261 standard; cDNA; 1690 BP.					
DE Human lung specific nucleotide sequence SEQ ID NO:18.					
PN WO2003102137-A2.					
PD 11-DEC-2003.					
PA (DIAD-) DIADEXUS INC.					
Percent Similarity: 33.56%	Conservative: 20				
Best Local Similarity: 28.94%	Mismatches: 177				
Query Match: 10.54%	Indels: 111				
RESULT 1457					
ID ABL29942 standard; DNA; 5205 BP.					
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41299.					
PN WO200171042-A2.					
PD 27-SEP-2001.					
PA (PEKE ) PE CORP NY.					
Percent Similarity: 38.78%	Conservative: 15				
Best Local Similarity: 32.65%	Mismatches: 84				
Query Match: 10.54%	Indels: 66				
RESULT 1458					
ID ABQ77243 standard; DNA; 57130 BP.					
DE Human MARK DNA.					
PN WO2003194704-A1.					
PD 16-OCT-2003.					
PA (RANK/) RANK S G.					
Percent Similarity: 38.90%	Conservative: 42				
Best Local Similarity: 28.88%	Mismatches: 184				
Query Match: 10.54%	Indels: 74				
RESULT 1459					
ID ACH92753 standard; DNA; 666 BP.					
DE Human genome derived single exon probe #25948.					
PN US2003194704-A1.					
PD 16-OCT-2003.					
PA (RANK/) RANK S G.					
Percent Similarity: 38.21%	Conservative: 18				
Best Local Similarity: 30.89%	Mismatches: 85				
Query Match: 10.52%	Indels: 67				
RESULT 1460					
ID ABL06387 standard; cDNA; 1619 BP.					
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13643.					
PN WO200171042-A2.					
PD 27-SEP-2001.					
PA (PEKE ) PE CORP NY.					
Percent Similarity: 32.19%	Conservative: 31				
Best Local Similarity: 24.57%	Mismatches: 171				
Query Match: 10.52%	Indels: 105				
RESULT 1461					
ID AAK52472 standard; cDNA; 2213 BP.					
DE Human polynucleotide SEQ ID NO 2001.					
PN WO200157190-A2.					
PD 09-AUG-2001.					
PA (HYSE-) HYSEQ INC.					
Percent Similarity: 34.30%	Conservative: 42				
Best Local Similarity: 25.57%	Mismatches: 145				
Query Match: 10.52%	Indels: 171				
RESULT 1462					
ID AAK52473 standard; cDNA; 2213 BP.					
DE Human polynucleotide SEQ ID NO 2002.					
PN WO200157190-A2.					
PD 09-AUG-2001.					
PA (HYSE-) HYSEQ INC.					
Percent Similarity: 34.30%	Conservative: 42				
Best Local Similarity: 25.57%	Mismatches: 145				
Query Match: 10.52%	Indels: 171				
RESULT 1463					
ID AAK52473 standard; cDNA; 2213 BP.					
DE Human polynucleotide SEQ ID NO 2002.					
PN WO200157190-A2.					
PD 09-AUG-2001.					
PA (HYSE-) HYSEQ INC.					
Percent Similarity: 34.30%	Conservative: 42				
Best Local Similarity: 25.57%	Mismatches: 145				
Query Match: 10.52%	Indels: 171				

ID ABQ17270 standard; DNA; 966 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 3861.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Percent Similarity: 38.57%  
Best Local Similarity: 34.13%  
Query Match: 10.50%  
RESULT 1464  
ID ABQ17271 standard; DNA; 966 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 3862.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Percent Similarity: 38.57%  
Best Local Similarity: 34.13%  
Query Match: 10.50%  
RESULT 1465  
ID ABL24448 standard; DNA; 3010 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24817.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.81%  
Best Local Similarity: 31.10%  
Query Match: 10.50%  
RESULT 1466  
ID AQ087119 standard; cDNA; 5883 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3995.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1467  
ID AQ084854 standard; cDNA; 5883 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1668.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1468  
ID ACN40924 standard; cDNA; 5883 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326958, SEQ ID NO:6025.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1469  
ID ADJ56352 standard; cDNA; 6354 BP.  
DE Chicken cDNA differentially expressed in MYCN activated cells SeqID 158.  
PN US2003119009-A1.  
PD 26-JUN-2003.  
PA (STUA/) STUART S G.  
PA (NUCH/) NUCHTERN J G.  
PA (FLOH/) FLOH S E.  
PA (SHOH/) SHOHET J M.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1470  
ID AAS65903 standard; cDNA; 6432 BP.  
DE DNA encoding novel human diagnostic protein #1707.  
PN WO200175067-A2.

PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1471  
ID ADN60282 standard; cDNA; 7274 BP.  
DE Human non-muscle myosin heavy chain 9 encoding cDNA.  
PN WO2004039955-A2.  
PD 13-MAY-2004.  
PA (RIGR-) RIGEL PHARM INC.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1472  
ID AAK51987 standard; cDNA; 7516 BP.  
DE Human polynucleotide SEQ ID NO 532.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 30.46%  
Best Local Similarity: 23.58%  
Query Match: 10.50%  
RESULT 1473  
ID ABD33518 standard; DNA; 34261 BP.  
DE Murine Cancer-associated (CA) gene MD07-102.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 37.98%  
Best Local Similarity: 27.47%  
Query Match: 10.50%  
RESULT 1474  
ID ABQ88150 standard; cDNA; 40668 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 57.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.45%  
Best Local Similarity: 24.61%  
Query Match: 10.50%  
RESULT 1475  
ID ABZ35980 standard; cDNA; 1937 BP.  
DE Human secretory polynucleotide SPTM SEQ ID NO 144.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 31.93%  
Best Local Similarity: 25.05%  
Query Match: 10.47%  
RESULT 1476  
ID AAZ43800 standard; cDNA; 1974 BP.  
DE Human adult skin cDNA clone vdl\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Percent Similarity: 31.93%  
Best Local Similarity: 25.05%  
Query Match: 10.47%  
RESULT 1477  
ID ACC44572 standard; cDNA; 3285 BP.  
DE Alpha-amylase/glucosylase fusion nucleotide sequence SEQ ID NO:46.  
PN WO2003018766-A2.  
PD 06-MAR-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 32.63%  
Best Local Similarity: 25.00%  
Query Match: 10.47%  
RESULT 1478  
ID AAH78667 standard; cDNA; 6109 BP.  
DE Murine Col5a3 cDNA sequence encoding pro-alpha-3(V) procollagen.  
PN WO200164871-A2.

PD 07-SEP-2001.  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 Percent Similarity: 35.50% Conservative: 44  
 Best Local Similarity: 26.57% Mismatches: 181  
 Query Match: 10.47% Indels: 137  
 RESULT 1479  
 ID AAK52971 standard; cDNA; 8486 BP.  
 DE Human polynucleotide SEQ ID NO 2500.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 30.58% Conservative: 40  
 Best Local Similarity: 23.71% Mismatches: 204  
 Query Match: 10.47% Indels: 200  
 RESULT 1480  
 ID ACA40315 standard; DNA; 9903 BP.  
 DE Prokaryotic essential gene #21972.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 32.02% Conservative: 45  
 Best Local Similarity: 23.97% Mismatches: 155  
 Query Match: 10.47% Indels: 225  
 RESULT 1481  
 Percent Similarity: 32.02% Conservative: 45  
 Best Local Similarity: 23.97% Mismatches: 155  
 Query Match: 10.47% Indels: 225  
 RESULT 1483  
 ID ADA29351 standard; DNA; 2928 BP.  
 DE DNA encoding Acinetobacter baumannii protein #638.  
 PN US6562958-B1.  
 PD 13-MAY-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.82% Conservative: 54  
 Best Local Similarity: 24.32% Mismatches: 175  
 Query Match: 10.45% Indels: 160  
 RESULT 1484  
 ID ACN92102 standard; DNA; 6753 BP.  
 DE Breast cancer related marker, seq id 13252.  
 PN US2003099374-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 34.69% Conservative: 36  
 Best Local Similarity: 26.98% Mismatches: 205  
 Query Match: 10.45% Indels: 100  
 RESULT 1485  
 ID AAV44437 standard; DNA; 538 BP.  
 DE Mycobacterium tuberculosis antigen XP22 3' DNA.  
 PN WO9816645-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 44.71% Conservative: 25  
 Best Local Similarity: 32.69% Mismatches: 77  
 Query Match: 10.43% Indels: 38  
 RESULT 1486  
 ID AAV64546 standard; DNA; 538 BP.  
 DE M. tuberculosis immunogenic polypeptide XP22 3'-end DNA.  
 PN WO9816646-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 44.71% Conservative: 25  
 Best Local Similarity: 32.69% Mismatches: 77  
 Query Match: 10.43% Indels: 38  
 RESULT 1487  
 ID AA219135 standard; DNA; 538 BP.  
 DE M. tuberculosis recombinant antigen DNA encoding 3' XP22.  
 PN WO9942118-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.

Percent Similarity: 44.71% Conservative: 25  
 Best Local Similarity: 32.69% Mismatches: 77  
 Query Match: 10.43% Indels: 38  
 RESULT 1488  
 ID AA219347 standard; DNA; 538 BP.  
 DE M. tuberculosis antigen 3' XP22 DNA sequence.  
 PN WO9942076-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 44.71% Conservative: 25  
 Best Local Similarity: 32.69% Mismatches: 77  
 Query Match: 10.43% Indels: 38  
 RESULT 1489  
 ID ABL20514 standard; DNA; 5870 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13015.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 37.78% Conservative: 35  
 Best Local Similarity: 27.84% Mismatches: 113  
 Query Match: 10.43% Indels: 106  
 RESULT 1490  
 ID ABL12010 standard; cDNA; 6128 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30512.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 37.78% Conservative: 35  
 Best Local Similarity: 27.84% Mismatches: 113  
 Query Match: 10.43% Indels: 106  
 RESULT 1491  
 ID ABL26493 standard; DNA; 1341 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30952.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.65% Conservative: 18  
 Best Local Similarity: 29.38% Mismatches: 186  
 Query Match: 10.41% Indels: 94  
 RESULT 1492  
 ID ABL26492 standard; DNA; 3042 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30949.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.65% Conservative: 18  
 Best Local Similarity: 29.38% Mismatches: 186  
 Query Match: 10.41% Indels: 94  
 RESULT 1493  
 ID AAA12503 standard; cDNA; 3171 BP.  
 DE cDNA encoding a human collagen 1 (alpha) protein helical region.  
 PN EP992586-A2.  
 PD 12-APR-2000.  
 PA (USU) US SURGICAL CORP.  
 Percent Similarity: 36.27% Conservative: 32  
 Best Local Similarity: 29.71% Mismatches: 175  
 Query Match: 10.41% Indels: 137  
 RESULT 1494  
 ID AA299843 standard; DNA; 3174 BP.  
 DE DNA encoding human type 1 (alpha) collagen polypeptide.  
 PN WO200014201-A1.  
 PD 16-MAR-2000.  
 PA (PAOL/) PAOLELLA D N.  
 PA (GRUS/) GRUSKIN E A.  
 PA (BUEC/) BUECHTER D D.  
 Percent Similarity: 36.27% Conservative: 32  
 Best Local Similarity: 29.71% Mismatches: 175  
 Query Match: 10.41% Indels: 137  
 RESULT 1495  
 ID AAV62176 standard; DNA; 117213 BP.  
 DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
 PN WO9942118-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.

Best Local Similarity: 29.25% Mismatches: 190  
Query Match: 10.41% Indels: 57  
RESULT 1496  
ID ADR96635 standard; DNA; 1062 BP.  
DE M. tuberculosis antigen Rv2353c DNA SEQ ID NO:61.  
FN WO2004083448-A2.  
PD 30-SEP-2004.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (STAT-) STATENS SERUM INST.  
Percent Similarity: 34.57% Conservative: 39  
Best Local Similarity: 26.04% Mismatches: 126  
Query Match: 10.39% Indels: 173  
RESULT 1497  
ID ADB59228 standard; DNA; 2217 BP.  
DE Toxicity-related gene, SEQ ID 4254.  
FN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 31.87% Conservative: 16  
Best Local Similarity: 27.72% Mismatches: 136  
Query Match: 10.39% Indels: 127  
RESULT 1498  
ID ABR42483 standard; DNA; 2217 BP.  
DE Toxicity modelling related rat gene SEQ ID No 2185.  
FN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 31.87% Conservative: 16  
Best Local Similarity: 27.72% Mismatches: 136  
Query Match: 10.39% Indels: 127  
RESULT 1499  
ID AAD06576 standard; cDNA; 4425 BP.  
DE Porcine alpha1(I) collagen cDNA.  
FN WO200134647-A2.  
PD 17-MAY-2001.  
PA (FIBR-) FIBROGEN INC.  
Percent Similarity: 35.77% Conservative: 33  
Best Local Similarity: 28.87% Mismatches: 190  
Query Match: 10.39% Indels: 117  
RESULT 1500  
ID ADF45427 standard; DNA; 5487 BP.  
DE Human vasodilator-responsive gene #24.  
FN JP2003310272-A.  
PD 05-NOV-2003.  
PA (TANA/) TANAKA T.  
PA (ASAH ) ASAH KASEI KK.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Percent Similarity: 39.81% Conservative: 39  
Best Local Similarity: 30.68% Mismatches: 157  
Query Match: 10.39% Indels: 102

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 15, 2005, 06:04:34 ; Search time 3439 Seconds  
(without alignments)  
4870.101 Million cell updates/sec

Title: US-10-063-699-52  
Perfect score: 2363  
Sequence: 1 MKFGPLACLLALCLSGE.....KLGFINWDAINKQRRSRIP 440

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_gpool\_p/US10063699/runat\_12052005\_103528\_15784/app\_query.fasta\_1.583  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODES=LOCAL  
-OUTFMT=ptc -NORM=ext -HAPSIZES=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10063699 @CGN 1 15180 @runat\_12052005\_103528\_15784 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hcc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gse1:\*  
9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	48.8	868	4	BG680112
2	1077.5	45.6	2065	3	AK081753
3	1038	43.9	863	4	BG679557
4	967	40.9	792	4	BG681553
5	829.5	35.1	969	4	BG675558
6	793	33.6	634	6	CA446785
7	712	30.1	878	6	CB193179
8	673	28.5	900	6	CA489311
9	664	28.1	532	2	BF829704

10	664	28.1	843	4	BI8223399
11	663	28.1	761	7	CK128355
12	635	26.9	752	7	CO384272
13	601.5	25.5	415	4	BG676132
14	594	25.1	515	7	CN369384
15	549.5	23.3	712	7	CV113267
16	495.5	21.0	925	5	BQ936377
17	495.5	21.0	956	5	BQ935815
18	494.5	20.9	746	7	CN369385
19	492	20.8	581	5	BP293011
20	492	20.8	945	6	CD247582
21	490.5	20.8	596	1	AU296351
22	483	20.4	737	7	CV126149
23	470.5	19.9	658	7	CO681303
24	469	19.8	742	2	BB649423
25	453.5	19.2	607	7	CO680280
26	453.5	19.2	611	7	CO680457
27	453.5	19.2	617	7	CO695910
28	451.5	19.1	600	7	CO690216
29	450.5	19.1	626	7	CO682918
30	448.5	19.0	601	7	CO680520
31	446	18.9	531	7	CO681087
32	446	18.9	538	7	CO680087
33	446	18.9	615	7	CO688917
34	441	18.7	520	7	CO688807
35	441	18.7	921	5	BQ935633
36	438	18.5	528	7	CO681703
37	437	18.5	514	7	CO716268
38	435	18.4	547	4	BM712887
39	426.5	18.0	659	7	CF763278
40	425	18.0	525	7	CO684145
41	423	17.9	2152	8	CC283954
42	420	17.8	1560	9	CL081488
43	416	17.6	2244	8	CC255272
44	415	17.6	1256	9	CL082735
45	413.5	17.5	1245	9	CL082775
46	413.5	17.5	1668	8	CC338091
47	413	17.5	1578	8	CC303267
48	413	17.5	1585	8	CC294035
49	413	17.5	1700	8	CC298790
50	412.5	17.5	1872	8	CC269714
51	412	17.4	1400	9	AG425855
52	411.5	17.4	1788	8	CC320563
53	411	17.4	1695	8	CC290874
54	411	17.4	2287	9	AG341484
55	409.5	17.3	561	4	BM557961
56	409.5	17.3	1767	8	CC294031
57	407	17.2	496	6	CD174636
58	407	17.2	841	5	BU927828
59	407	17.2	1403	8	CC290252
60	406	17.2	2104	8	CC202398
61	405	17.1	1427	9	AG333458
62	405	17.1	1484	9	CL079800
63	404.5	17.1	1612	9	CL076947
64	403	17.1	528	7	CO684434
65	403	17.1	633	7	CO690630
66	403	17.1	1284	9	CL082747
67	402.5	17.0	1100	6	CB905637
68	402.5	17.0	1100	7	CF877318
69	402	17.0	1593	8	CC255263
70	401.5	17.0	1722	8	CC279933
71	400.5	16.9	1380	9	CL058490
72	399	16.9	1397	9	CL105166
73	399	16.9	1448	7	CC220110
74	398.5	16.9	1086	7	CV520645
75	398.5	16.9	1693	8	CC207296
76	397.5	16.8	1114	9	CR030904
77	397.5	16.8	1816	8	CC210902
78	397	16.8	1971	8	CC207340
79	396.5	16.8	743	9	BX173549
80	396.5	16.8	1598	9	CL078355
81	394.5	16.7	1082	2	BE455154
82	394.5	16.7	1129	9	CL045106

83	394.5	16.7	1432	8	CC250857	CH261-166	c 156	375	15.9	1175	9	AG448201	Mus muscu
84	393.5	16.7	1319	8	CC243775	CH261-20P	c 157	375	15.9	1200	8	CC187380	CH261-33E
c 85	392.5	16.6	1363	9	AG332071	Mus muscu	c 158	374.5	15.8	1161	2	BP256588	HVSMF001
c 86	392	16.6	1771	8	CC254257	CH261-106	c 159	374.5	15.8	1250	9	CL509322	SAIL_811
c 87	391.5	16.6	1318	7	CF874345	tric006xn	c 160	374	15.8	1736	9	CL104572	ISBI_43D1
c 88	391.5	16.6	1404	9	AG441902	Mus muscu	c 161	374	15.8	844	6	BI003515	MR3-HN012
c 89	391.5	16.6	1674	9	CL078342	CH216-149	c 162	374	15.8	805	6	CB907084	tric081xe
c 90	391	16.5	335	5	BP430945	BP430945	c 163	374	15.8	845	6	BH148610	ENTP267TR
c 91	390.5	16.5	1107	4	BI416477	hasp001xa	c 164	374	15.8	1319	8	AG448157	Mus muscu
c 92	390.5	16.5	1571	9	CL082695	CH216-169	c 165	374	15.8	1324	8	CC284084	CH261-167
c 93	390	16.5	546	1	AA756812	vv72c05.r	c 166	373.5	15.8	1204	8	CC284084	CH216-58E
c 94	390	16.5	1463	9	CL515327	SAIL_89 C	c 167	373.5	15.8	1548	9	CL043588	DKP2p779M
c 95	389.5	16.5	1191	5	BQ410366	GA_Ed003	c 168	373	15.8	400	5	BI139650	K-EST0192
c 96	389	16.5	651	2	BE562709	BE562709	c 169	373	15.8	515	7	CB139650	K-EST0192
c 97	389	16.5	1211	8	CC295933	AA727274	c 170	373	15.8	557	6	CB163124	K-EST0223
c 98	387.5	16.4	532	1	AA727274	vv98h01.r	c 171	373	15.8	582	5	BP292786	BP292786
c 99	387.5	16.4	611	6	CL175431	AGENCOURT	c 172	373	15.8	583	5	BP292786	BP292786
c 100	387.5	16.4	1083	7	CV520573	0089P0047	c 173	373	15.8	601	6	CD635038	56088965H
c 101	387.5	16.4	1222	8	BH146899	ENTQW47TF	c 174	373	15.8	602	6	CD635038	56088965H
c 102	386	16.3	502	7	CO691245	AG324452	c 175	373	15.8	655	4	BM715676	UI-B-EJ0-
c 103	386	16.3	1214	9	AG324452	GA_Eb004	c 176	373	15.8	691	2	BF031291	601460818
c 104	386	16.3	1077	4	BQ447302	GA_Eb004	c 177	373	15.8	692	7	CN369396	170006000
c 105	385.5	16.3	1215	4	BI416650	hasp001xm	c 178	373	15.8	713	7	CN369393	170005331
c 106	385.5	16.3	1042	4	BI416535	hasp001xe	c 179	373	15.8	844	2	BE562668	601336120
c 107	385	16.3	1399	9	CL104926	ISBI_43N2	c 180	373	15.8	889	6	CD249548	AGENCOURT
c 108	384.5	16.3	1565	9	AG340866	Mus muscu	c 181	373	15.8	967	6	CB906742	tric080xc
c 109	384	16.3	1379	9	CL079001	CH216-154	c 182	373	15.8	967	6	CB906742	tric080xc
c 110	383.5	16.2	974	9	CNS06P21	T7 end of	c 183	373	15.8	994	6	CB907117	tric081xg
c 111	383.5	16.2	1296	7	CF873646	tric005xi	c 184	373	15.8	994	6	CB907117	tric081xg
c 112	383.5	16.2	1360	9	CL469817	SAIL_133	c 185	373	15.8	994	6	CB907117	tric081xg
c 113	383.5	16.2	1406	9	AG441598	Mus muscu	c 186	373	15.8	1016	5	BM923917	AGENCOURT
c 114	382.5	16.2	2198	9	AG332729	Forward s	c 187	373	15.8	1253	5	CL082653	CH216-169
c 115	382	16.2	975	9	CR002932	Forward s	c 188	373	15.8	1327	5	BM913920	AGENCOURT
c 116	382	16.2	1502	9	CL082604	CH216-168	c 189	373	15.8	1396	9	AG332686	Mus muscu
c 117	382	16.2	1558	9	CL023806	CH216-17J	c 190	373	15.8	1506	9	AG442117	Mus muscu
c 118	381.5	16.1	1691	9	AG341104	Mus muscu	c 191	373	15.8	1566	9	CL080066	CH216-157
c 119	381	16.1	486	1	BA607750	vo8e06.r	c 192	373	15.8	1619	8	CC306715	TAM32-181
c 120	381	16.1	1135	8	BZ574895	msht_4207	c 193	372.5	15.8	1093	7	CB905750	tric075xp
c 121	381	16.1	1235	9	CL495365	SAIL_609	c 194	372.5	15.8	1093	7	CB905750	tric075xp
c 122	381	16.1	1242	8	BZ695377	SP_Ba006	c 195	372	15.7	1294	2	BF256749	HVSMF001
c 123	380.5	16.1	1134	8	CC245095	CH261-13G	c 196	372	15.7	1314	9	CG748456	CH261-143
c 124	380.5	16.1	1160	9	CL505495	SAIL_751	c 197	372	15.7	1354	8	CC186289	CH261-143
c 125	380.5	16.1	1751	9	AG333042	Mus muscu	c 198	371.5	15.7	907	9	CR117058	Forward s
c 126	380	16.1	1350	2	BE455228	HVSMH009	c 199	371.5	15.7	1099	9	CL463584	SAIL_1188
c 127	380	16.1	1446	8	CL082756	CH216-170	c 200	371.5	15.7	1116	2	BF256617	HVSMF001
c 128	380	16.1	1785	8	CC219595	Mus muscu	c 201	371.5	15.7	1223	4	BI416573	hasp001xg
c 129	379.5	16.1	1523	9	AG448267	tric006xm	c 202	371.5	15.7	1945	8	CC251395	CH261-157
c 130	379	16.0	1313	7	CF874294	tric006xm	c 203	371.5	15.7	2296	5	BQ306472	MR0-BT300
c 131	379	16.0	1328	2	BE455227	HVSMH009	c 204	371	15.7	337	5	BQ306472	MR0-BT300
c 132	378.5	16.0	1106	6	CB905422	tric074xf	c 205	370.5	15.7	2041	9	AG363808	Mus muscu
c 133	378.5	16.0	1132	7	CF876941	tric074xf	c 206	370.5	15.7	877	4	BI416653	hasp001xm
c 134	378.5	16.0	1132	9	CL090899	ISBI-19F1	c 207	370.5	15.7	970	9	AG417486	Pan trogl
c 135	378.5	16.0	1288	8	CC220182	CH261-23J	c 208	370.5	15.7	974	9	AG071677	tric074xh
c 136	378.5	16.0	1264	2	BE455159	HVSMH009	c 209	370.5	15.7	988	6	CB905440	tric074xh
c 137	378	16.0	1275	9	AG442214	Mus muscu	c 210	370.5	15.7	988	6	CF876954	tric074xh
c 138	378	16.0	1591	9	CL077232	CH216-143	c 211	370.5	15.7	1066	6	CB905393	tric074xh
c 139	377.5	16.0	500	7	CO690072	DG11-2690	c 212	370.5	15.7	1066	7	CF876920	tric074xh
c 140	377.5	16.0	1150	8	CC216742	CH261-165	c 213	370.5	15.7	1412	9	CL505072	SAIL_744
c 141	377.5	16.0	1151	6	CB905418	tric074xf	c 214	370.5	15.7	1430	9	CL515395	hasp001xg
c 142	377.5	16.0	1151	7	CF876938	tric074xf	c 215	370	15.7	979	8	CC243776	CH261-20P
c 143	377	16.0	596	7	CO679552	DG11-102n	c 216	369.5	15.6	1305	8	BZ694620	SP_Ba004
c 144	377	16.0	1100	8	CC262597	CH261-167	c 217	369	15.6	289	2	BE184234	QW0-HT067
c 145	377	16.0	1282	9	CL081061	CH216-160	c 218	369	15.6	289	2	BE184234	QW0-HT067
c 146	377	16.0	1349	9	AG441910	Mus muscu	c 219	369	15.6	997	6	CB905724	tric075xn
c 147	377	16.0	1417	2	BF257444	HVSMF001	c 220	369	15.6	1224	4	BI416537	hasp001xe
c 148	376.5	15.9	2131	8	CC296269	CH261-104	c 221	369	15.6	1342	2	BE455093	HVSMH009
c 149	376	15.9	1120	5	BQ686415	AGENCOURT	c 222	369	15.6	1391	2	BE455155	HVSMH009
c 150	376	15.9	1326	8	BZ697030	SP_Ba009	c 223	369	15.6	1398	9	CL965096	Reverse s
c 151	376	15.9	1450	8	AG429738	Mus muscu	c 224	368.5	15.6	935	8	BX998174	Reverse s
c 152	375.5	15.9	559	7	CNS369398	170006001	c 225	368.5	15.6	1173	8	CC275658	CH261-133
c 153	375.5	15.9	1296	9	CL474234	SAIL_215	c 226	368	15.6	999	4	BI416539	hasp001xe
c 154	375	15.9	1036	2	BF254665	HVSMF000	c 227	368	15.6	1616	9	CG753270	P048-2-CO
c 155	375	15.9	1072	7	CV520572	0089P0047	c 228	367.5	15.6	1001	9	AG369874	Mus muscu



c 229 367.5 15.6 1031 9 CL492176 SAIL 564\_ 360.5 15.3 302 360.5 15.3 1471 9 CG748176 P042-1-A0  
c 230 367.5 15.6 1038 9 CL478560 SAIL 292 360 15.2 382 7 CW786707 170004247  
231 367.5 15.6 1099 2 BF256465 HVSMF001 304 360 15.2 488 2 AW786707 120102 MA  
232 367.5 15.6 1287 6 CD388578 AGNSCOURT 305 360 15.2 985 6 CB905748 tr1c075xp  
233 367.5 15.6 1287 2 BF256624 HVSMF001 306 360 15.2 985 7 CF877399 tr1c075xp  
234 367.5 15.6 1489 9 AG448218 Mus muscu 307 360 15.2 992 4 BI416571 hasp001xg  
235 367.5 15.6 1672 9 AG430445 Mus muscu 308 360 15.2 993 9 CL468466 SAIL 1287  
236 367 634 6 CB127790 K-EST0177 309 360 15.2 1647 9 AG361024 Mus muscu  
237 366.5 15.5 1074 2 BF257201 HVSMF001 311 359.5 15.2 803 4 BI416474 hasp001xa  
238 366.5 15.5 1189 2 BE455091 HVSMF001 312 359.5 15.2 1225 6 CD501543 CDA51-D09  
c 239 366.5 15.5 1460 8 CC189146 CH261-147 313 359.5 15.2 1301 9 AG363665 Mus muscu  
240 366 731 6 BX160732 Danio rer 314 359.5 15.2 1806 9 AG333016 Mus muscu  
241 366 1087 6 CB908860 tr1c086x1 315 359 15.2 1806 9 CL063000 CH216-99D  
242 366 15.5 1087 7 CF882340 tr1c086x1 316 358.5 15.2 439 7 CO684087 DG11-1780  
243 366 15.5 1142 6 CB905439 Mus muscu 317 358.5 15.2 1122 9 AG441585 Mus muscu  
244 366 15.5 1142 7 CF876953 tr1c074xh 318 358 15.2 1052 4 BI416480 hasp001xa  
c 245 366 15.5 1193 8 CC300050 CH261-107 319 358 15.2 1181 4 BI869996  
246 366 1365 9 CG745655 P038-3-F0 320 357.5 15.1 901 9 AG131311 Pan trogl  
247 365.5 15.5 717 2 BE889405 603512522 321 357.5 15.1 937 4 BI416476 hasp001xa  
248 365.5 15.5 908 8 AZ191473 SP\_1019 B 322 357.5 15.1 1192 6 CB905423 tr1c074xf  
249 365.5 15.5 1014 9 AG162131 Pan trogl 323 357.5 15.1 1192 7 CF876942 tr1c074xf  
250 365.5 15.5 1047 6 CB905697 tr1c075x1 324 357 15.1 706 9 BX199436 Danio rer  
251 365.5 15.5 1047 7 CF877361 tr1c075x1 325 357 15.1 993 5 BQ411388 GA\_Ed003  
252 365.5 15.5 1117 6 CB905666 tr1c075x1 326 357 15.1 1364 9 CG754835 P050-2-F0  
253 365.5 15.5 1117 7 CF877340 tr1c075x1 327 356.5 15.1 1090 7 CK410624 AUF\_Iphdk  
254 365.5 15.5 1918 9 AG340926 Mus muscu 328 356.5 15.1 1161 5 BM912505 AGNSCOURT  
255 365 15.4 1107 6 CB905729 tr1c075xn 329 356.5 15.1 1296 9 CG461074 SAIL 113  
256 365 15.4 1107 4 BF877385 tr1c075xn 330 356.5 15.1 1839 9 CG747711 P041-2-E0  
257 365 15.4 1197 7 BI416470 hasp001xa 331 356.5 15.1 1910 9 AG382199 Mus muscu  
c 258 364.5 15.4 996 9 CC921441 t051k04ba 332 356 15.1 739 9 BX238932 Danio rer  
259 364.5 15.4 1013 6 CB905417 tr1c074xf 333 356 15.1 800 9 CC530667 CH240 407  
260 364.5 15.4 1013 7 CF876937 tr1c074xf 334 356 15.1 931 4 BI416575 hasp001xg  
261 364.5 15.4 1082 8 CC300639 CH261-68J 335 356 15.1 1292 8 CC208790 CH261-36P  
262 364.5 15.4 1090 9 CG749024 P043-1-E0 336 356 15.1 1328 4 BG441224 GA\_Ea001  
263 364.5 15.4 1223 9 AG441637 Mus muscu 337 355.5 15.0 984 4 BG441224 GA\_Ea001  
264 364.5 15.4 1351 8 CC312666 TAW32-32D 338 355.5 15.0 1088 2 BF256580 HVSMF001  
265 364.5 15.4 1556 9 CL460740 SAIL 10 B 339 355.5 15.0 1389 4 BM019473 603647660  
266 364 15.4 1087 7 CV520644 0089P0048 340 355.5 15.0 1578 9 AG448781 Mus muscu  
267 364 15.4 1195 4 BI416506 hasp001xc 341 355 15.0 869 6 CD671002 OeMR423 5  
c 268 364 15.4 1201 9 CL082769 CH216-171 342 355 15.0 884 6 CD789701 EST661062  
269 364 1317 9 CL082603 CH216-168 343 355 15.0 915 8 CG947840 MBEM30TR  
270 363.5 15.4 909 9 AG125251 Pan trogl 344 355 15.0 1197 8 CC234867 CH261-153  
271 363.5 15.4 1068 9 AG429516 Mus muscu 345 354.5 15.0 830 6 CA033345 EST663692  
272 363.5 15.4 1176 9 CL974133 OBIFCC042 346 354.5 15.0 957 6 CD792331 EST663692  
273 363.5 15.4 1293 2 BF256498 HVSMF001 347 354.5 15.0 991 9 AG387759 Mus muscu  
274 363.5 15.4 1397 9 CL118478 ISB1-7001 348 354.5 15.0 1204 9 CL077707 CH216-146  
275 363 15.4 1011 6 CB905602 tr1c075xf 349 354.5 15.0 1249 6 CB905420 tr1c074xf  
276 363 15.4 1011 7 CF877292 tr1c075xf 350 354.5 15.0 1262 9 CL496190 SAIL 620  
277 363 15.4 1077 9 CL945097 OBIFSB002 351 354.5 15.0 1331 8 CC300018 CH261-107  
c 278 363 15.4 1125 9 CC905389 t020m09ba 352 354.5 15.0 1425 9 AG441757 Mus muscu  
279 363 1435 9 CL079025 CH216-154 353 354 15.0 324 5 BQ308097 MRO-BT300  
280 363 15.4 1648 9 AG390465 Mus muscu 354 354 15.0 797 9 CR043527 Reverse s  
281 362.5 15.3 891 9 CR133966 Forward s 355 354 15.0 864 9 AG060559 Pan trogl  
282 362.5 15.3 896 9 CR151764 Reverse s 356 354 15.0 873 9 AG136937 Pan trogl  
283 362.5 15.3 1266 9 CG747089 P040-3-B1 357 354 15.0 898 6 CB905663 tr1c075x1  
284 362 1299 2 BE455157 HVSMF001 358 354 15.0 898 7 CF877337 tr1c075x1  
c 285 362.5 15.3 1686 8 CC189908 CH261-611 359 354 15.0 1237 8 CC232156 CH261-162  
286 362 1023 9 AG405483 Mus muscu 360 354 15.0 1252 9 CL082583 CH216-168  
287 362 15.3 1111 9 AG384981 Mus muscu 361 354 15.0 1284 9 CL078799 CH216-153  
c 288 362 15.3 1116 8 BZ557923 pac61-60 362 353.5 15.0 1518 8 CC220681 CH261-183  
289 362 1313 1289 9 CL147104 ISB1-156E 363 353.5 15.0 1777 9 CR106035 Forward s  
290 361 15.3 1249 2 BE455160 HVSMF001 364 353.5 15.0 1178 9 CG751365 P045-4-D0  
291 361 15.3 1284 9 CL081493 CH216-162 365 353.5 15.0 1231 9 AG363910 Mus muscu  
292 361 15.3 1381 8 CC261242 CH261-541 366 353.5 15.0 1284 9 CL078799 CH216-153  
c 293 361 15.3 1692 9 AG396765 Mus muscu 367 353 14.9 1309 9 CL080508 CH216-158  
294 361 15.3 1862 9 AG442225 Mus muscu 368 352.5 14.9 927 6 CA588496 hab64e04  
295 360.5 15.3 240 7 BF738482 PMI-KT004 369 352.5 14.9 934 6 CD788927 EST660288  
c 296 360.5 15.3 441 7 CO685482 DG11-200C 370 352.5 14.9 1048 9 CL463403 SAIL 1185  
297 360.5 15.3 1138 2 BF256506 HVSMF001 371 352.5 14.9 1048 9 CL463403 SAIL 1185  
298 360.5 15.3 1152 2 BF256631 HVSMF001 372 352.5 14.9 1082 9 CL500589 SAIL 685  
c 299 360.5 15.3 1197 9 CL082672 CH216-169 373 352.5 14.9 1156 8 CC319460 TAW32-17H  
300 360.5 15.3 1286 9 AG448422 Mus muscu 374 352.5 14.9 1222 4 BI416660 hasp001xm  
301 360.5 15.3 1366 2 BF257203 HVSMF001

CG748176 P042-1-A0  
CN369391 170004247  
AW786707 120102 MA  
CB905748 tr1c075xp  
CB907739 tr1c075xp  
BI416571 hasp001xg  
CL468466 SAIL 1287  
AG361024 Mus muscu  
CL085855 ISB1-6A12  
BI416474 hasp001xa  
CD501543 CDA51-D09  
AG363665 Mus muscu  
AG333016 Mus muscu  
CL063000 CH216-99D  
CO684087 DG11-1780  
AG441585 Mus muscu  
BI416480 hasp001xa  
BI869996 603394150  
AG131311 Pan trogl  
BI416476 hasp001xa  
CB905423 tr1c074xf  
CF876942 tr1c074xf  
BX199436 Danio rer  
BQ411388 GA\_Ed003  
CG754835 P050-2-F0  
CK410624 AUF\_Iphdk  
BM912505 AGNSCOURT  
CL461074 SAIL 113  
CG747711 P041-2-E0  
AG382199 Mus muscu  
BX238932 Danio rer  
CC530667 CH240 407  
BI416575 hasp001xg  
CC208790 CH261-36P  
BG441224 GA\_Ea001  
BF256580 HVSMF001  
BM019473 603647660  
AG448781 Mus muscu  
CD671002 OeMR423 5  
CD789701 EST661062  
CC947840 MBEM30TR  
CC234867 CH261-153  
CA033345 EST663692  
CD792331 EST663692  
AG387759 Mus muscu  
CL077707 CH216-146  
CB905420 tr1c074xf  
CF876940 tr1c074xf  
CL496190 SAIL 620  
CC300018 CH261-107  
AG441757 Mus muscu  
BQ308097 MRO-BT300  
CR043527 Reverse s  
AG060559 Pan trogl  
AG136937 Pan trogl  
CB905663 tr1c075x1  
CF877337 tr1c075x1  
CC232156 CH261-162  
CL082583 CH216-168  
CR106035 Forward s  
AG363910 Mus muscu  
AG363910 Mus muscu  
CL078799 CH216-153  
CC220681 CH261-183  
CL080508 CH216-158  
AG423023 Mus muscu  
CA588496 hab64e04  
CD788927 EST660288  
CL463403 SAIL 1185  
CL500589 SAIL 685  
CC319460 TAW32-17H  
BI416660 hasp001xm

375 352.5 14.9 1258 9 AG441605 Mus muscu  
376 352 14.9 292 7 CN369397 170004252  
377 352 14.9 985 7 CK401878 AUF IfInt  
378 352 14.9 1282 9 CL081590 CH216-163  
379 352 14.9 1601 9 CG752479 P047-2-A0  
380 351.5 14.9 786 8 BH018846 L2011a.d  
381 351.5 14.9 898 5 BQ411951 GA\_Ed004  
382 351.5 14.9 1593 9 CL476602 SAIL\_258  
383 351 14.9 909 9 AG392597 Mus muscu  
384 351 14.9 1110 9 CL079755 CH216-156  
385 351 14.9 1328 9 AG441962 Mus muscu  
386 351 14.9 2465 9 AG280392 Mus muscu  
387 350.5 14.8 1235 4 BM475329 AGENCOURT  
388 350.5 14.8 1297 9 CG744520 P037-1-E1  
389 350.5 14.8 1822 9 AG433170 Mus muscu  
390 350 14.8 909 9 CR066599 Reverse s  
391 350 14.8 924 2 BR455162 HVSMH009  
392 350 14.8 1236 5 BM927210 AGENCOURT  
393 350 14.8 1253 8 CL300023 CH261-107  
394 349.5 14.8 814 9 CR138760 Reverse s  
395 349.5 14.8 845 9 CC578225 CH240\_457  
396 349.5 14.8 952 4 BG441341 GA\_Ea001  
397 349.5 14.8 1126 9 CL500314 SAIL\_67 H  
398 349.5 14.8 1170 8 CL291804 CH261-61G  
399 349.5 14.8 1279 9 AG382489 Mus muscu  
400 349.5 14.8 1294 8 CG279571 CH261-151  
401 349 14.8 837 7 CO167031 FLVD1\_66 G  
402 349 14.8 1166 2 BF256751 HVSMH001  
403 349 14.8 1694 7 CR874342 trlc006xm  
404 348.5 14.7 905 9 CR071027 Forward s  
405 348.5 14.7 918 9 AG137554 Pan trogl  
406 348.5 14.7 1200 9 AG435638 Mus muscu  
407 348.5 14.7 1251 2 BR455089 HVSMH009  
408 348.5 14.7 1537 9 AG435682 Mus muscu  
409 348 14.7 556 7 CO690415 DG11-2741  
410 348 14.7 788 9 AG378458 Mus muscu  
411 348 14.7 893 8 AZ199082 SP\_1038 B  
412 348 14.7 928 6 CB905438 trlc074xh  
413 348 14.7 928 7 CR876952 trlc074xh  
414 348 14.7 1277 9 CG753585 P048-3-H1  
415 348 14.7 1288 6 CA974086 AGENCOURT  
416 348 14.7 1303 5 BM908878 AGENCOURT  
417 348 14.7 1308 8 CC229000 CH261-32N  
418 347.5 14.7 724 9 CR171920 Reverse s  
419 347.5 14.7 945 9 AG439533 Mus muscu  
420 347.5 14.7 1029 9 CL478689 SAIL\_294  
421 347.5 14.7 1052 6 CD780545 EST651906  
422 347.5 14.7 1099 9 CL509275 SAIL\_811  
423 347.5 14.7 1179 2 BR455222 HVSMH009  
424 347.5 14.7 1196 2 BF256755 HVSMH001  
425 347.5 14.7 1252 9 CG752943 P047-4-D1  
426 347.5 14.7 1836 9 AG382181 Mus muscu  
427 347 14.7 1070 9 AG367198 Mus muscu  
428 347 14.7 1070 9 AG392454 Mus muscu  
429 347 14.7 1246 9 CL058545 CH216-88E  
430 347 14.7 1737 8 CC251254 CH261-17L  
431 347 14.7 1738 9 CG750956 P045-2-H0  
432 346.5 14.7 927 9 CR244051 Reverse s  
433 346.5 14.7 961 6 CD792011 EST663372  
434 346.5 14.7 1157 5 BQ889194 AGENCOURT  
435 346.5 14.7 1459 9 AG361235 Mus muscu  
436 346.5 14.7 1489 9 AG435090 Mus muscu  
437 346 14.6 748 9 CR125767 Forward s  
438 346 14.6 883 8 AZ186646 SP\_1007 B  
439 346 14.6 1008 9 AG395157 Mus muscu  
440 346 14.6 1158 8 CC251504 CH261-84H  
441 346 14.6 1332 8 CC264642 CH261-28F  
442 345.5 14.6 501 7 CO690948 AGENCOURT  
443 345.5 14.6 888 9 AG392364 Mus muscu  
444 345.5 14.6 911 9 CR116264 Forward s  
445 345.5 14.6 1030 9 CL486328 SAIL\_431  
446 345.5 14.6 1327 8 CC321975 TAM32-31N  
447 345.5 14.6 1382 9 CL078098 CH216-148

AG448338 Mus muscu  
BX986280 Forward s  
CD509648 P041-2-C0  
CG747660 P041-2-D1  
AG289910 Mus muscu  
AG448497 Mus muscu  
BI4116482 hasp001xa  
CD788732 EST660093  
AG132448 Pan trogl  
CD795550 EST666911  
AG396899 Mus muscu  
AG392837 Mus muscu  
BI948944 HVSMH001  
BF256704 HVSMH001  
BF256541 HVSMH001  
CG755163 P050-4-D0  
BG677392 602625212  
AG468082 Mus muscu  
CA341452 pk19d08.x  
CK415613 AUF\_IpIt  
AG417941 Mus muscu  
CL031113 CH216-32A  
AG382169 Mus muscu  
CL078620 CH216-151  
CD795249 EST666610  
CD797147 EST666850  
CD795551 EST666912  
CD790613 EST6661974  
CD788559 EST659920  
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CD908599 t043p13ba  
CL058574 CH216-88F  
CL647465 CH213-139  
CG754720 P050-2-A0  
CD780546 EST651907  
BR455291 HVSMH009  
AG292627 Mus muscu  
CL082667 CH216-169  
CG748472 P042-2-E0  
EST62299 EST663660  
CD795248 EST666609  
CG746709 P040-1-B0  
CG746709 DG11-99d1  
AG387373 Mus muscu  
AG385073 Mus muscu  
CL515456 SAIL\_8\_E1  
CC210170 CH261-131  
AG408002 Mus muscu  
CC224483 CH261-153  
BF256709 HVSMH001  
AG361044 Mus muscu  
CG757066 P052-2-A0  
CB904612 trlc039xa  
AG032994 Pan trogl  
CL507774 SAIL\_788  
CC294165 CH261-130  
CL193928 CH261-95J  
BM914619 AGENCOURT  
CC257347 CH261-331  
CG754979 P050-3-D0  
AG397258 Mus muscu  
CL082802 CH216-191  
AG400277 Mus muscu  
CC921444 t051121ba  
AG392532 Mus muscu  
CB204333 AGENCOURT  
BF256667 HVSMH001  
AG381912 Mus muscu  
AG044893 Pan trogl  
AG531127 Mus muscu  
CR121829 Forward s  
AZ934358 BJ\_Ba000

C 521	340.5	14.4	993	9	CL470505	CL470505 SAIL_143	C 594	335.5	14.2	1143	8	CC217764	CH261-790
522	340.5	14.4	995	5	BQ411334	GA_Ed003	595	335	14.2	635	9	CR008962	Reverse 8
523	340.5	14.4	1021	9	AG378264	Mus muscu	596	335	14.2	765	9	CR172200	Forward 8
524	340.5	14.4	1141	9	CG753070	P048-1-B0	597	335	14.2	837	9	CR074624	Forward 8
525	340.5	14.4	1177	9	AG441911	Mus muscu	598	335	14.2	902	4	BI953312	HVSMEM001
526	340.5	14.4	1283	9	AG435406	Mus muscu	599	335	14.2	905	9	AG395391	Mus muscu
527	340	14.4	945	6	CB589303	AGENCOURT	600	335	14.2	997	9	AG379478	Mus muscu
528	340	14.4	974	5	BQ411403	GA_Ed003	601	335	14.2	1491	8	CC236272	CH261-190
529	340	14.4	976	4	BI416536	hasp001xe	602	334.5	14.2	737	9	CR024844	Reverse 8
530	340	14.4	1152	8	CC307549	TAM32-19F	603	334.5	14.2	896	6	CR0794507	EST665868
531	340	14.4	1188	8	CC209172	CH261-18A	604	334.5	14.2	899	6	CD791099	EST662460
532	340	14.4	1503	9	CL118256	ISB1-70G1	605	334.5	14.2	925	4	BG441241	GA_EA001
533	340	14.4	1679	8	CC237100	CH261-191	606	334.5	14.2	1004	7	CK412777	AUF_Ip011
534	339.5	14.4	885	9	AG050199	Pan trogl	607	334	14.1	846	9	AG381624	Mus muscu
535	339.5	14.4	1155	2	BF256671	HVSMEM001	608	334	14.1	899	9	AG135251	Pan trogl
536	339.5	14.4	1231	2	BE455156	HVSMEM009	609	334	14.1	899	9	AG18751	Mus muscu
537	339.5	14.4	1265	9	CL082651	CH216-168	610	334	14.1	900	6	CD790644	EST662005
538	339	14.3	754	9	CR163306	Forward 8	611	334	14.1	900	6	CD795719	EST667080
539	339	14.3	907	7	CM088196	L24_Ag2_P	612	334	14.1	944	6	CD792268	EST663629
540	339	14.3	913	6	CD789618	EST660979	613	334	14.1	985	9	CL488815	SAIL_514
541	339	14.3	918	8	AQ895329	HS_4832_A	614	334	14.1	1141	9	CL082639	CH216-168
542	339	14.3	932	6	CD794099	EST665460	615	334	14.1	1284	9	CG753544	P048-3-G0
543	339	14.3	1138	9	AG152606	Pan trogl	616	334	14.1	1327	9	CL478195	SAIL_285
544	339	14.3	1159	4	BG848793	1024022G1	617	334	14.1	1793	9	CG754612	P050-1-D0
545	339	14.3	1161	6	CB905725	trico075xn	618	334	14.1	2054	9	AG441640	Mus muscu
546	339	14.3	1269	9	AG435113	Mus muscu	619	333.5	14.1	847	6	CD788960	EST660321
547	339	14.3	1337	8	CC277037	CH261-134	620	333.5	14.1	918	9	AG307388	Mus muscu
548	339	14.3	1522	8	CC183848	CH261-140	621	333.5	14.1	935	4	BI958090	HVSMEM001
549	338.5	14.3	664	9	BX247035	Danio rer	622	333.5	14.1	1042	6	CA963983	CELLO2a07
550	338.5	14.3	884	8	AQ782679	HS_3183_B	623	333.5	14.1	1094	9	AG391420	Mus muscu
551	338.5	14.3	912	9	AG178114	Mus muscu	624	333.5	14.1	1141	9	AG441809	Mus muscu
552	338.5	14.3	1025	9	AG137560	Pan trogl	625	333.5	14.1	1180	8	CC292964	CH261-174
553	338.5	14.3	1270	9	AG365353	Mus muscu	626	333.5	14.1	1280	9	CL063127	CH216-99J
554	338	14.3	872	6	CD780302	EST651663	627	333.5	14.1	1352	8	CC291944	CH261-611
555	338	14.3	881	9	CC912161	t070g08ba	628	333	14.1	711	9	CR109089	Reverse 8
556	337.5	14.3	675	9	CG898392	paetbac07	629	333	14.1	883	9	AG425045	Mus muscu
557	337.5	14.3	901	6	CD789678	EST668507	630	333	14.1	1117	7	CF879253	trico19x1
558	337.5	14.3	1339	4	BM458211	AGENCOURT	631	333	14.1	1174	9	AG408500	Mus muscu
559	338	14.3	1656	9	AG430456	Mus muscu	632	333	14.1	1175	8	CC252641	CH261-166
560	337.5	14.3	676	9	CR152762	Reverse 8	633	333	14.1	1320	9	AG365349	Mus muscu
561	337.5	14.3	746	9	CD538826	paetbac07	634	332.5	14.1	623	9	CR055317	Reverse 8
562	337.5	14.3	901	6	CD789678	EST661040	635	332.5	14.1	860	6	CD794798	EST666159
563	337.5	14.3	904	9	AG049068	Pan trogl	636	332.5	14.1	866	6	CD791084	EST662445
564	337.5	14.3	834	9	BQ411526	GA_Ed004	637	332.5	14.1	881	6	CD796424	EST667785
565	337.5	14.3	988	5	CL088612	ISB1-11E7	638	332.5	14.1	884	6	CD795718	EST667079
566	337.5	14.3	1140	9	CL088612	ISB1-11E7	639	332.5	14.1	950	9	AG129199	Pan trogl
567	337.5	14.3	1300	9	AG346626	Mus muscu	640	332.5	14.1	958	9	AG219891	Lotus cor
568	337.5	14.3	1619	9	AG435648	Mus muscu	641	332.5	14.1	982	9	CL470491	SAIL_143
569	337	14.3	740	9	AG061516	Pan trogl	642	332.5	14.1	1107	9	AG395610	Mus muscu
570	337	14.3	813	3	AY568672	Arabidops	643	332.5	14.1	1109	8	BH168544	VV_SBa000
571	337	14.3	834	9	AG131468	Pan trogl	644	332.5	14.1	1238	9	AG448606	Mus muscu
572	337	14.3	1193	9	AG349830	Mus muscu	645	332.5	14.1	1342	9	AG435407	Mus muscu
573	337	14.3	1232	4	BI948976	HVSMEM001	646	332.5	14.1	1406	7	CK408425	AUF_ILVr
574	337	14.3	1236	9	CL489898	SAIL_662	647	332.5	14.1	1573	8	CC251191	CH261-17J
575	337	14.3	1340	9	CL063195	CH216-99L	648	332	14.0	680	9	CR234856	Forward 8
576	337	14.3	1427	9	CG755119	P050-4-B0	649	332	14.0	851	6	CD795970	EST667331
577	337	14.3	1555	9	CL073978	CH216-131	650	332	14.0	1037	9	AG146864	Pan trogl
578	336.5	14.2	826	7	CF753703	EST-77-2-	651	332	14.0	1080	8	AQ893056	HS_4832_A
579	336.5	14.2	890	9	AG388286	Mus muscu	652	332	14.0	1188	4	BG067996	H3G60F01-
580	336.5	14.2	890	6	CD788333	EST659724	653	332	14.0	1333	9	AG363323	Mus muscu
581	336.5	14.2	1726	9	CL063123	CH216-99I	654	332	14.0	1622	9	CL476695	SAIL_258
582	336.5	14.2	1726	9	CL063151	CH216-99J	655	331.5	14.0	647	9	CR113451	Forward 8
583	336	14.2	682	9	CR157807	Reverse 8	656	331.5	14.0	765	9	AG043737	Pan trogl
584	336	14.2	897	9	AG060530	Pan trogl	657	331.5	14.0	879	9	CL507219	SAIL_779
585	336	14.2	993	9	CNS07DER	T7 end of	658	331.5	14.0	886	6	CD795969	EST667330
586	336	14.2	1159	8	CC210735	CH261-185	659	331.5	14.0	888	6	CD793381	EST664742
587	336	14.2	1188	9	AG435374	Mus muscu	660	331.5	14.0	900	6	CD792300	EST663661
588	336	14.2	1226	9	AG350051	Mus muscu	661	331.5	14.0	1064	7	CK208880	FGAS02060
589	336	14.2	1241	9	AG396661	Mus muscu	662	331.5	14.0	1070	9	CL082694	CH216-169
590	336	14.2	1385	9	CL044197	CH216-60G	663	331.5	14.0	1092	9	AG448376	Mus muscu
591	336	14.2	1521	9	AG365620	Mus muscu	664	331.5	14.0	1159	9	CL045149	CH216-62G
592	335.5	14.2	1722	9	CC549003	CH240_433	665	331.5	14.0	1459	9	AG340896	Mus muscu
593	335.5	14.2	1076	9	CL505483	SAIL_751_	666	331.5	14.0	1586	9	CL481349	SAIL_33_E

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667	331.5	14.0	1675	9	AG360980	Mus muscu	740	327	13.8	1329	9	AG441619	Mus muscu
668	331	14.0	775	9	AG392495	Mus muscu	741	327	13.8	1580	9	CL043898	CH216-59E
669	331	14.0	878	6	CD792274	EST663635	742	326.5	13.8	860	9	AG395407	Mus muscu
670	331	14.0	922	9	AG072035	Pan trogl	743	326.5	13.8	895	9	AG395284	Mus muscu
671	331	14.0	927	5	BQ411332	GA_Ed003	C 744	326.5	13.8	972	9	CL514122	SAIL_883
672	331	14.0	930	9	AG421539	Mus muscu	C 745	326.5	13.8	997	9	CL392400	Mus muscu
673	331	14.0	936	9	CC921440	t051104ba	C 746	326.5	13.8	1035	9	CL086207	ISB1-7A17
674	331	14.0	1205	9	CL505256	SAIL_748	C 747	326.5	13.8	1134	6	CB905366	tric074xb
675	331	14.0	1909	9	CL078604	CH216-151	748	326.5	13.8	1134	7	CF876898	tric074xb
676	331	14.0	2017	9	AG435283	Mus muscu	C 749	326.5	13.8	1142	9	CL501710	SAIL_702
677	330.5	14.0	715	9	AG036665	Pan trogl	C 750	326.5	13.8	1246	9	AG430307	Mus muscu
678	330.5	14.0	759	9	CG697254	MUQO_CH25	C 751	326.5	13.8	1260	9	AG435279	Mus muscu
679	330.5	14.0	928	6	CD796584	EST667945	C 752	326.5	13.8	1276	9	AG363745	Mus muscu
680	330.5	14.0	984	9	CL513555	SAIL_877	C 753	326.5	13.8	1388	2	BE881567	601490281
681	330.5	14.0	1051	9	CL119109	ISB1-75M6	C 754	326.5	13.8	1409	9	AG396691	Mus muscu
682	330.5	14.0	1071	9	AG377116	Mus muscu	755	326	13.8	1409	9	AG110286	Pan trogl
683	330.5	14.0	1160	6	CA966152	CLX05a16	C 756	326	13.8	805	9	AG280718	Mus muscu
684	330.5	14.0	1187	9	CL492283	SAIL_565	757	326	13.8	826	9	AG449819	Mus muscu
685	330.5	14.0	1200	9	CL109992	ISB1-52J1	758	326	13.8	828	6	CD794508	EST665869
686	330.5	14.0	1217	8	CC222933	CH261-40G	C 759	326	13.8	846	6	CD794797	EST666158
687	330	14.0	1154	9	CL055694	CH216-81I	C 760	326	13.8	880	9	AG387938	Mus muscu
688	330	14.0	1155	9	CL471894	SAIL_16_C	C 761	326	13.8	885	6	CD788165	EST665926
689	330	14.0	1537	8	CL082803	CH216-191	C 762	326	13.8	940	9	AG417910	Mus muscu
690	329.5	13.9	583	8	BZ299296	CG4867.r1	C 763	326	13.8	957	9	CL506576	SAIL_769
691	329.5	13.9	1008	9	AG392743	Mus muscu	C 764	326	13.8	981	9	AG060379	Pan trogl
692	329.5	13.9	1011	9	AG062256	AG062256 Pan trogl	C 765	326	13.8	1002	9	CC269751	CH261-90F
693	329.5	13.9	1121	9	CL496797	SAIL_631	C 766	326	13.8	1134	8	CC1269751	ISB1-69N2
694	329.5	13.9	1166	4	B1819986	60303349	C 767	326	13.8	1244	9	CL118045	CH240-369
695	329.5	13.9	1598	9	AG346280	Mus muscu	768	326	13.8	1482	9	CC521571	PH043-1-A0
696	329.5	13.9	1961	8	BZ565482	pac82-164	C 769	325.5	13.8	621	9	CG521571	CH240-369
697	329	13.9	813	6	AG462678	Mus muscu	770	325.5	13.8	660	6	CD434979	EL01N0331
698	329	13.9	846	6	CD792269	EST663630	C 771	325.5	13.8	916	4	AG450259	Mus muscu
699	329	13.9	1005	5	BQ888552	AGENCOURT	772	325.5	13.8	921	9	BI953358	HVSMEn001
700	329	13.9	1013	9	AG421540	Mus muscu	773	325.5	13.8	972	9	AG137966	Mus muscu
701	329	13.9	1311	9	AG383008	Mus muscu	774	325.5	13.8	993	9	CL082609	CH216-168
702	329	13.9	1376	9	CL506511	SAIL_768	C 775	325.5	13.8	1218	9	AG137966	CH216-168
703	328.5	13.9	722	6	CB908416	pastbac07	C 776	325.5	13.8	1233	9	AG341388	Mus muscu
704	328.5	13.9	821	6	CB908416	tric074xf	C 777	325.5	13.8	1283	9	AG430554	Mus muscu
705	328.5	13.9	821	7	CF876936	tric074xf	778	325	13.8	573	9	BI132676	Danio rer
706	328.5	13.9	962	9	AG389471	Mus muscu	779	325	13.8	602	9	CR023579	Reverse s
707	328.5	13.9	973	9	CL515454	SAIL_8_E0	780	325	13.8	643	9	CR097781	Reverse s
708	328.5	13.9	992	9	AG417826	Mus muscu	C 781	325	13.8	846	6	CD792927	EST664288
709	328.5	13.9	1029	8	BZ569266	pac82-164	C 782	325	13.8	870	2	BE258873	601116824
710	328.5	13.9	1157	9	AG363600	Mus muscu	783	325	13.8	870	4	BG847222	1024016D0
711	328.5	13.9	1164	9	CL081895	CH216-164	784	325	13.8	925	9	AG392228	Mus muscu
712	328.5	13.9	1241	8	CC288341	CH261-151	785	325	13.8	963	9	AG421523	Mus muscu
713	328.5	13.9	1691	9	AG333297	Mus muscu	C 786	325	13.8	977	6	CD792010	EST663371
714	328	13.9	811	9	AG395411	Mus muscu	C 787	325	13.8	1000	9	AG234404	Lotus cor
715	328	13.9	845	6	CB900986	tric025xa	C 788	325	13.8	1061	9	AG306566	Mus muscu
716	328	13.9	877	9	AG136839	Pan trogl	789	325	13.8	1292	2	BF255049	HVSMEn000
717	328	13.9	922	4	B1416502	hasp001xc	C 790	325	13.8	1419	9	AG371525	Mus muscu
718	328	13.9	1081	8	CC218526	CH261-135	C 791	325	13.8	1760	5	BU199272	DCBSEB06
719	328	13.9	1094	9	AG134530	Pan trogl	792	324.5	13.7	634	9	CR169910	Reverse s
720	328	13.9	1419	8	CC275971	CH261-172	793	324.5	13.7	719	8	BZ060968	lles3b12.
721	328	13.9	1426	2	BR256712	HVSMEn001	C 794	324.5	13.7	785	9	AG081505	AG081505 Pan trogl
722	327.5	13.9	890	9	AG556888	Mus muscu	C 795	324.5	13.7	795	7	CF259320	322 Trich
723	327.5	13.9	916	6	CB906783	tric080xe	C 796	324.5	13.7	807	5	BQ411568	GA_Ed004
724	327.5	13.9	955	9	AG379392	Mus muscu	C 797	324.5	13.7	900	9	AG380272	Mus muscu
725	327.5	13.9	955	9	AG379392	Mus muscu	C 798	324.5	13.7	938	9	CG220119	OG0AH63TH
726	327.5	13.9	955	9	CL466365	SAIL_1254	799	324.5	13.7	988	9	AG135153	Pan trogl
727	327.5	13.9	1001	6	CD790612	EST661973	800	324.5	13.7	1006	9	AG373580	Mus muscu
728	327.5	13.9	1038	9	CL503616	CH216-95N	801	324.5	13.7	1011	8	AO878632	HS 3121.A
729	327.5	13.9	1229	9	CL063245	Mus muscu	C 802	324.5	13.7	1130	9	CL077291	CH216-144
730	327.5	13.9	1364	9	AG390540	Mus muscu	C 803	324.5	13.7	1349	9	CL508191	CH216-144
731	327.5	13.9	1521	8	CC308197	TAM32-34G	C 804	324.5	13.7	1404	2	BE455290	HVSMEn009
732	327.5	13.9	1609	9	AG396435	Mus muscu	805	324	13.7	771	9	AG060509	Pan trogl
733	327	13.8	812	6	CD794517	EST665878	806	324	13.7	828	8	AZ184464	SP 1003.A
734	327	13.8	890	6	CD789121	ENTR220482	807	324	13.7	925	4	BI958094	HVSMEn001
735	327	13.8	932	8	BH163101	ENTR220482	808	324	13.7	1090	9	AG128386	Pan trogl
736	327	13.8	965	9	AG032944	Pan trogl	809	324	13.7	1216	9	AG387483	Mus muscu
737	327	13.8	1032	5	BQ411400	GA_Ed003	C 810	324	13.7	1245	9	AG430216	Mus muscu
738	327	13.8	1201	8	CC228732	CH261-102	C 811	324	13.7	1328	9	CL082796	CH216-171
739	327	13.8	1236	9	AG448372	Mus muscu	C 812	323.5	13.7	778	9	AG481486	Mus muscu

813	323.5	13.7	792	9	AG449674	Mus muscu	AG449674	Mus muscu	886	320	13.5	878	9	AG142647	Pan trogl
c 814	323.5	13.7	850	6	CD780095	EST651456	CD780095	EST651456	c 887	320	13.5	933	9	AG392892	Mus muscu
c 815	323.5	13.7	967	9	AG387712	Mus muscu	AG387712	Mus muscu	c 888	320	13.5	1162	9	CL081029	CH216-160
c 816	323.5	13.7	1167	9	CL647723	CH213-147	CL647723	CH213-147	c 889	320	13.5	1375	9	AG435314	Mus muscu
c 817	323.5	13.7	1223	9	CL080163	CL080163	CL080163	CL080163	c 890	319.5	13.5	543	9	CR250961	Forward s
c 818	323.5	13.7	1373	9	AG435617	Mus muscu	AG435617	Mus muscu	c 891	319.5	13.5	684	8	BZ579729	msh2 744
c 819	323.5	13.7	1689	8	BZ58582	pa98401_2	BZ58582	pa98401_2	c 892	319.5	13.5	761	9	AG081695	Pan trogl
c 820	323	13.7	644	9	BX971245	Reverse s	BX971245	Reverse s	c 893	319.5	13.5	850	9	AG573155	Mus muscu
c 821	323	13.7	860	6	CB904993	tr1c040xp	CB904993	tr1c040xp	c 894	319.5	13.5	1225	8	CC192432	CH261-6N2
c 822	323	13.7	865	9	AG142641	Pan trogl	AG142641	Pan trogl	c 895	319.5	13.5	1292	9	CL496211	SAIL 620
c 823	323	13.7	954	9	AG387669	Mus muscu	AG387669	Mus muscu	c 896	319.5	13.5	1339	9	CL498952	SAIL 662
c 824	323	13.7	987	7	CK401954	AUP_Ifint	CK401954	AUP_Ifint	c 897	319.5	13.5	1465	9	CL515385	SAIL 89_G
c 825	323	13.7	1237	7	AG435098	Mus muscu	AG435098	Mus muscu	c 898	319.5	13.5	1607	9	CL515305	SAIL 89_A
c 826	323	13.7	1321	8	B08977	F28E19-T7 I	B08977	F28E19-T7 I	c 899	319	13.5	540	1	AI121206	CE90C08_Y
c 827	323	13.7	1350	9	CL461110	SAIL 113	CL461110	SAIL 113	c 900	319	13.5	709	7	CF764444	CE8004052
c 828	323	13.7	1382	9	AG382718	Mus muscu	AG382718	Mus muscu	c 901	319	13.5	730	9	AG076255	Pan trogl
c 829	323	13.7	1689	9	AG390487	Mus muscu	AG390487	Mus muscu	c 902	319	13.5	784	8	BZ474985	BONIK27TR
c 830	323	13.7	1737	9	CG754769	P050-2-C0	CG754769	P050-2-C0	c 903	319	13.5	794	6	CD779417	EST650778
c 831	323	13.7	1792	9	AG279106	Mus muscu	AG279106	Mus muscu	c 904	319	13.5	807	6	CD796585	EST667946
c 832	322.5	13.6	808	6	CD796423	EST667784	CD796423	EST667784	c 905	319	13.5	845	9	AG283249	Mus muscu
c 833	322.5	13.6	868	9	CG345168	OG1B032TV	CG345168	OG1B032TV	c 906	319	13.5	868	9	AG514956	Mus muscu
c 834	322.5	13.6	960	5	B0429353	AGENCOURT	B0429353	AGENCOURT	c 907	319	13.5	943	9	AG416717	Mus muscu
c 835	322.5	13.6	1003	9	CL508278	SAIL 794	CL508278	SAIL 794	c 908	319	13.5	947	6	CB200158	AGENCOURT
c 836	322.5	13.6	1152	7	CK162291	FGA501488	CK162291	FGA501488	c 909	319	13.5	982	9	CL465305	SAIL 1237
c 837	322.5	13.6	1215	8	CC276136	CH261-11L	CC276136	CH261-11L	c 910	319	13.5	986	9	AG534089	Mus muscu
c 838	322.5	13.6	1248	8	CC233708	Mus muscu	CC233708	Mus muscu	c 911	319	13.5	986	9	CL118072	ISB1-6902
c 839	322.5	13.6	1272	9	AG365674	Mus muscu	AG365674	Mus muscu	c 912	319	13.5	993	9	AG081720	Pan trogl
c 840	322.5	13.6	1276	9	AG363492	Mus muscu	AG363492	Mus muscu	c 913	319	13.5	1216	9	AG435140	Mus muscu
c 841	322.5	13.6	1370	9	CL473648	SAIL 204	CL473648	SAIL 204	c 914	319	13.5	1275	9	AG382133	Mus muscu
c 842	322.5	13.6	1509	9	CL476587	SAIL 258	CL476587	SAIL 258	c 915	319	13.5	1352	5	BM913391	AGENCOURT
c 843	322	13.6	636	9	CR079344	Reverse s	CR079344	Reverse s	c 916	318.5	13.5	400	7	CO691099	DG11-284n
c 844	322	13.6	656	9	CR094507	Forward s	CR094507	Forward s	c 917	318.5	13.5	768	9	AG138112	Pan trogl
c 845	322	13.6	684	9	CR158408	Forward s	CR158408	Forward s	c 918	318.5	13.5	795	6	CD793202	EST664563
c 846	322	13.6	692	9	CG898388	pastbac07	CG898388	pastbac07	c 919	318.5	13.5	846	9	AG426621	Mus muscu
c 847	322	13.6	817	6	CD796662	EST668023	CD796662	EST668023	c 920	318.5	13.5	897	4	BI416517	haap001xd
c 848	322	13.6	897	9	AG392363	Mus muscu	AG392363	Mus muscu	c 921	318.5	13.5	931	9	AG387827	Mus muscu
c 849	322	13.6	918	9	AG074987	Pan trogl	AG074987	Pan trogl	c 922	318.5	13.5	942	9	AG120142	Pan trogl
c 850	322	13.6	922	9	AG508565	Mus muscu	AG508565	Mus muscu	c 923	318.5	13.5	953	9	AG395078	Mus muscu
c 851	322	13.6	1320	9	CL118071	ISB1-6902	CL118071	ISB1-6902	c 924	318.5	13.5	992	9	AG276718	Mus muscu
c 852	322	13.6	1356	9	CL119203	ISB1-76L4	CL119203	ISB1-76L4	c 925	318.5	13.5	993	9	AG033032	Pan trogl
c 853	322	13.6	1384	8	CC230110	CH261-192	CC230110	CH261-192	c 926	318.5	13.5	1008	9	AG380577	Mus muscu
c 854	322	13.6	1472	5	BM910703	AGENCOURT	BM910703	AGENCOURT	c 927	318.5	13.5	1039	6	CB905391	tr1c074xd
c 855	321.5	13.6	1068	5	BQ411337	GA_Ed003	BQ411337	GA_Ed003	c 928	318.5	13.5	1090	4	BM015212	603641314
c 856	321.5	13.6	1146	8	CC288118	CH261-130	CC288118	CH261-130	c 929	318.5	13.5	1451	9	CL461116	SAIL 113
c 857	321.5	13.6	1166	9	AG341070	Mus muscu	AG341070	Mus muscu	c 930	318.5	13.5	1502	8	CC290279	CH261-130
c 858	321.5	13.6	1227	9	CG749171	P043-2-C0	CG749171	P043-2-C0	c 931	318.5	13.5	1790	9	AG396847	Mus muscu
c 859	321.5	13.6	1393	8	CC251162	CH261-129	CC251162	CH261-129	c 932	318	13.5	444	7	CO690826	DG11-280g
c 860	321.5	13.6	1961	9	AG435522	Mus muscu	AG435522	Mus muscu	c 933	318	13.5	550	9	CR141028	Forward s
c 861	321	13.6	488	1	AA760019	vv72e05.r	AA760019	vv72e05.r	c 934	318	13.5	815	6	CD795693	EST667054
c 862	321	13.6	624	9	CR021387	Reverse s	CR021387	Reverse s	c 935	318	13.5	830	9	AG497612	Mus muscu
c 863	321	13.6	655	9	CR132677	Forward s	CR132677	Forward s	c 936	318	13.5	858	9	AG282072	Mus muscu
c 864	321	13.6	708	7	CF753914	EST-77-2	CF753914	EST-77-2	c 937	318	13.5	867	4	BI957861	HVSMEn001
c 865	321	13.6	939	9	AG407744	Mus muscu	AG407744	Mus muscu	c 938	318	13.5	880	9	CG912175	t070h10ba
c 866	321	13.6	988	9	CL474288	SAIL 215	CL474288	SAIL 215	c 939	318	13.5	894	9	AG433034	Mus muscu
c 867	321	13.6	1072	9	CL503204	SAIL 720	CL503204	SAIL 720	c 940	318	13.5	979	9	CL470915	SAIL 150
c 868	321	13.6	1274	9	CL078659	CH216-152	CL078659	CH216-152	c 941	318	13.5	1075	9	AG415245	Mus muscu
c 869	321	13.6	1393	9	CL043635	CH216-58H	CL043635	CH216-58H	c 942	318	13.5	1089	4	BM468944	AGENCOURT
c 870	321	13.6	2420	9	CL509247	SAIL 811	CL509247	SAIL 811	c 943	318	13.5	1232	9	AG060687	Pan trogl
c 871	320.5	13.6	869	9	AG543783	Mus muscu	AG543783	Mus muscu	c 944	318	13.5	1254	9	AG355445	Mus muscu
c 872	320.5	13.6	889	9	AG370044	Mus muscu	AG370044	Mus muscu	c 945	318	13.5	1435	2	BF256711	HVSMEnf001
c 873	320.5	13.6	904	9	AG424774	Mus muscu	AG424774	Mus muscu	c 946	317.5	13.4	629	9	CR109987	Reverse s
c 874	320.5	13.6	921	5	BQ411516	GA_Ed004	BQ411516	GA_Ed004	c 947	317.5	13.4	717	9	CL129223	Pan trogl
c 875	320.5	13.6	960	9	AG126398	Pan trogl	AG126398	Pan trogl	c 948	317.5	13.4	771	7	CO166342	FLD1 61 F
c 876	320.5	13.6	1030	9	AG081846	Pan trogl	AG081846	Pan trogl	c 949	317.5	13.4	846	9	AG081511	Pan trogl
c 877	320.5	13.6	1055	9	CL477872	SAIL 281	CL477872	SAIL 281	c 950	317.5	13.4	965	7	CK402072	AUF_Ifint
c 878	320.5	13.6	1110	9	CL072693	CH216-126	CL072693	CH216-126	c 951	317.5	13.4	990	9	AG077124	Pan trogl
c 879	320.5	13.6	1332	8	CC252696	CH261-19C	CC252696	CH261-19C	c 952	317.5	13.4	1047	7	CK210077	FGA502186
c 880	320	13.5	596	9	CR094319	Reverse s	CR094319	Reverse s	c 953	317.5	13.4	1078	5	BQ901025	AGENCOURT
c 881	320	13.5	626	9	CR035227	Reverse s	CR035227	Reverse s	c 954	317.5	13.4	1147	8	BZ557946	pacel-60
c 882	320	13.5	689	9	BX217706	Danio rer	BX217706	Danio rer	c 955	317.5	13.4	1149	5	BM910848	AGENCOURT
c 883	320	13.5	802	6	CD791552	EST662913	CD791552	EST662913	c 956	317.5	13.4	1243	5	BM913931	AGENCOURT
c 884	320	13.5	829	7	CK141363	AGENCOURT	CK141363	AGENCOURT	c 957	317	13.4	527	9	BX200083	Danio rer
c 885	320	13.5	861	9	AG517597	Mus muscu	AG517597	Mus muscu	c 958	317	13.4	585	2	AW335294	S45E8 AGS

959	317	13.4	693	9	AG041030	Pan trogl	1032	314.5	13.3	1056	9	AG367644	Mus muscu
c 960	317	13.4	778	7	CO200256	GE02_6_G1	c1033	314.5	13.3	1060	9	CL466364	SAIL 1254
c 961	317	13.4	801	8	AX197313	SP_1034_A	c1034	314.5	13.3	1092	6	CA975899	AGENCOURT
c 962	317	13.4	826	6	CD791551	EST662912	c1035	314.5	13.3	1295	5	BQ670738	AGENCOURT
963	317	13.4	878	9	AG388963	Mus muscu	c1036	314.5	13.3	1691	9	CL078603	CH216-151
964	317	13.4	936	9	AG395222	Mus muscu	1037	314	13.3	274	1	AA337683	EST42438
965	317	13.4	1016	9	CNS031U9	Tetraodon	1038	314	13.3	293	1	AA336632	EST41246
c 966	317	13.4	1142	7	CK408553	AUF Iflvir	1039	314	13.3	636	9	CR010949	Reverse s
c 967	317	13.4	1142	7	CK408553	AUF Iflvir	1040	314	13.3	707	8	BZ696495	SP_Ba008
c 968	317	13.4	1142	7	CK408553	AUF Iflvir	1041	314	13.3	713	6	CD778199	EST649560
c 969	317	13.4	1176	2	BP256757	HVSMEF001	1042	314	13.3	724	9	AG081478	Pan trogl
970	317	13.4	1314	9	CL959715	OSTFCC003	c1043	314	13.3	806	9	AG427940	Mus muscu
971	317	13.4	1822	9	AG382306	Mus muscu	c1044	314	13.3	842	9	AG556688	Mus muscu
c 972	316.5	13.4	822	9	AG384944	Mus muscu	c1045	314	13.3	903	9	AG542699	Mus muscu
c 973	316.5	13.4	833	8	AQ748616	HS_5573_A	1046	314	13.3	909	9	AG431452	Mus muscu
c 974	316.5	13.4	842	9	AG535123	Mus muscu	1047	314	13.3	914	4	B1956690	HVSMEN000
c 975	316.5	13.4	857	9	AG566696	Mus muscu	1048	314	13.3	925	9	AG416716	Mus muscu
976	316.5	13.4	863	4	B1416699	hasp001xp	1049	314	13.3	929	9	AG136821	Pan trogl
c 977	316.5	13.4	877	4	BM013050	603637860	c1050	314	13.3	1017	9	CL515167	SAIL 898
c 978	316.5	13.4	887	8	AG192949	SP_1022_B	1051	314	13.3	1036	6	CB908131	tric084xi
c 979	316.5	13.4	889	9	AG396213	Mus muscu	c1052	314	13.3	1216	9	CL082698	CH216-169
c 980	316.5	13.4	899	9	AG396213	Mus muscu	1053	314	13.3	1233	9	AG396109	Mus muscu
c 981	316.5	13.4	963	9	CL508181	SAIL_792	c1054	314	13.3	1245	9	AG382040	Mus muscu
982	316.5	13.4	980	9	CG769648	TcB42_4_D	c1055	314	13.3	1245	8	CC314665	TAM32-30M
c 983	316.5	13.4	1083	9	AG388511	Mus muscu	1056	314	13.3	1474	8	CL078558	CH216-151
c 984	316.5	13.4	1132	8	CC287400	CH261-167	1057	313.5	13.3	1790	9	CF768858	CE5001319
c 985	316	13.4	782	4	BG809582	mgct001xa	c1058	313.5	13.3	489	7	AG543421	Mus muscu
c 986	316	13.4	899	9	AG447359	Mus muscu	c1059	313.5	13.3	867	9	AG543421	Mus muscu
c 987	316	13.4	1029	9	CL972941	OSTFCC023	c1060	313.5	13.3	868	9	CD794098	EST665459
c 988	316	13.4	1095	9	AG418501	Pan trogl	1061	313.5	13.3	925	6	CD794098	Mus muscu
c 989	316	13.4	1218	9	AG433262	Mus muscu	1062	313.5	13.3	940	9	AG388463	Mus muscu
c 990	316	13.4	1271	8	CC302539	CH261-43M	1063	313.5	13.3	981	6	CB903399	tric034xg
c 991	316	13.4	1312	9	CL491552	SAIL_558	c1064	313.5	13.3	983	9	AG395443	Mus muscu
c 992	316	13.4	1324	9	AG382082	Mus muscu	c1065	313.5	13.3	1081	9	AG545516	Mus muscu
993	316	13.4	1690	9	AG435238	Mus muscu	1066	313.5	13.3	1183	8	BM911719	AGENCOURT
994	316	13.4	1703	9	CL078618	CH216-151	c1067	313.5	13.3	1184	5	BM911719	AGENCOURT
c 995	316	13.4	1725	9	AG363738	Mus muscu	1068	313.5	13.3	1186	4	BM452726	AGENCOURT
c 996	316	13.4	1769	9	AG396861	Mus muscu	1069	313.5	13.3	1222	9	AG435399	Mus muscu
c 997	315.5	13.4	349	2	AW354159	Danio rer	c1070	313.5	13.3	1284	8	AG435071	Mus muscu
c 998	315.5	13.4	715	9	BX185868	Danio rer	c1071	313.5	13.3	1293	8	CC281425	CH261-25B
c 999	315.5	13.4	875	9	AG471168	Mus muscu	1072	313.5	13.3	1500	8	CC224556	CH261-87B
1000	315.5	13.4	891	9	AG393945	Mus muscu	1073	313	13.2	2260	7	CR291696	CR291696
1001	315.5	13.4	930	9	AG388552	Mus muscu	c1074	313	13.2	618	9	BX977072	Forward s
1002	315.5	13.4	980	4	BG786274	SEAUMC006	1075	313	13.2	787	9	AG557945	Mus muscu
c1003	315.5	13.4	989	9	CL468473	SAIL_1287	1076	313	13.2	797	9	AG396219	Mus muscu
1004	315.5	13.4	1012	7	CK206734	FGAS01834	c1077	313	13.2	854	9	AG417911	Mus muscu
c1005	315.5	13.4	1028	7	CK240409	AUF Ip8to	c1078	313	13.2	862	9	AG528548	Mus muscu
c1006	315.5	13.4	1057	9	CL471756	SAIL_167	1079	313	13.2	882	9	AG126234	Pan trogl
c1007	315.5	13.4	1115	8	CC219063	CH261-165	1080	313	13.2	935	9	AG080623	Pan trogl
c1008	315.5	13.4	1157	8	CC227732	CH261-156	1081	313	13.2	946	9	AG384972	Mus muscu
c1009	315.5	13.4	1178	8	CC233291	CH261-20F	c1082	313	13.2	1010	9	AG340610	Mus muscu
c1010	315.5	13.4	1206	8	CC233291	CH261-20F	c1083	313	13.2	1244	9	AG340610	Mus muscu
1011	315.5	13.4	1268	8	BZ694881	SP_Ba005	c1084	313	13.2	1256	5	BU163430	AGENCOURT
1012	315	13.3	724	9	AG044843	Pan trogl	c1085	313	13.2	1293	8	CC225154	HVSMEN009
1013	315	13.3	759	9	AG391330	Mus muscu	1086	312.5	13.2	1429	8	CC225154	CH261-154
c1014	315	13.3	830	8	BH966848	odh13db06	1087	312.5	13.2	746	7	CF343413	AGENCOURT
c1015	315	13.3	842	9	AG492633	EST667165	1088	312.5	13.2	819	9	AG128554	Pan trogl
c1016	315	13.3	873	6	CD795804	EST667165	c1089	312.5	13.2	931	9	AG128554	Pan trogl
c1017	315	13.3	934	9	AG046262	Pan trogl	1090	312.5	13.2	956	9	AG530430	Mus muscu
c1018	315	13.3	1007	9	AG134493	Mus muscu	c1091	312.5	13.2	960	9	AG060752	Pan trogl
c1019	315	13.3	1092	9	AG395657	Mus muscu	1092	312.5	13.2	1074	9	AG397178	Mus muscu
c1020	315	13.3	1256	5	BQ422680	AGENCOURT	c1093	312.5	13.2	1080	4	B1416623	hasp001xk
c1021	315	13.3	1440	9	AG365352	Mus muscu	1094	312.5	13.2	1137	4	BM415579	OP20656 M
c1022	314.5	13.3	638	9	AG076816	Pan trogl	c1095	312.5	13.2	1387	9	CG745005	P037-4-B0
c1023	314.5	13.3	794	9	AG526306	Mus muscu	1096	312	13.2	1411	4	BM549073	AGENCOURT
c1024	314.5	13.3	810	9	CG907974	t038p01ba	1097	312	13.2	563	9	CR039368	Reverse s
c1025	314.5	13.3	848	6	CB901245	tric025xp	1098	312	13.2	585	9	CR152671	Forward s
c1026	314.5	13.3	848	7	CB901245	tric025xp	1099	312	13.2	705	9	AG392596	Mus muscu
c1027	314.5	13.3	900	4	BG440857	GA_Ea001	1100	312	13.2	811	5	BU576031	TGESTzyb9
c1028	314.5	13.3	913	9	AG414928	Mus muscu	1101	312	13.2	821	8	AG893474	HS_4832_A
c1029	314.5	13.3	927	9	AG472543	Mus muscu	1102	312	13.2	869	6	CD779008	EST50369
c1030	314.5	13.3	931	6	CD795803	EST667164	c1103	312	13.2	876	9	AG143831	Pan trogl
1031	314.5	13.3	978	9	AG377077	Mus muscu	c1104	312	13.2	1001	9	CL465285	SAIL 1237
										1020	7	CK165933	FGAS04996

cl105	312	13.2	1066	9	CL461337	CL461337 SAIL 1145	cl178	309	13.1	548	9	EX121682	EX121682
cl106	312	13.2	1269	9	CL971215	CL971215 OslfCC041	1179	309	13.1	643	9	AG123077	Danio rer
cl107	312	13.2	1661	8	CC321442	TAM32-34D	cl180	309	13.1	749	9	AG375372	Pan trogl
cl108	311.5	13.2	559	8	CR121735	Reverse s	1181	309	13.1	799	9	AG049309	Mus muscu
cl109	311.5	13.2	809	8	B2726483	OGFCH42TM	1182	309	13.1	801	9	AG391102	Mus muscu
cl110	311.5	13.2	811	9	AG081698	AG081698 Pan trogl	1183	309	13.1	804	6	CD785958	EST657319
cl111	311.5	13.2	900	9	AG377938	AG377938 Mus muscu	cl184	309	13.1	821	9	AG528123	Mus muscu
cl112	311.5	13.2	919	5	BU947182	rf23all.y	cl185	309	13.1	852	9	AG572355	Mus muscu
cl113	311.5	13.2	926	9	CL506892	SAIL 775	cl186	309	13.1	857	9	AG044313	Pan trogl
cl114	311.5	13.2	949	9	AG449791	Mus muscu	1187	309	13.1	859	9	AG120272	Pan trogl
cl115	311.5	13.2	978	9	AG384397	Mus muscu	cl188	309	13.1	884	9	AG494104	Mus muscu
cl116	311.5	13.2	1037	9	AG136804	Pan trogl	1189	309	13.1	990	9	AG395520	Mus muscu
cl117	311.5	13.2	1045	5	BU251753	603403810	1190	309	13.1	1039	9	CL058627	CH216-88H
cl118	311.5	13.2	1405	5	BO798843	EST 1012	1191	309	13.1	1067	4	BI952138	HVSMEM000
cl119	311.5	13.2	1409	4	BM800727	AGENCOURT	cl192	309	13.1	1133	8	CC253516	CH261-115
cl120	311.5	13.2	1497	9	AG381917	Mus muscu	1193	309	13.1	1486	9	AG393289	Mus muscu
cl121	311.5	13.2	1552	9	CL646265	CH213-111	1194	308.5	13.1	1543	9	AG395168	Mus muscu
cl122	311.5	13.2	1970	9	CG748837	P042-4-E0	1195	308.5	13.1	1763	6	CB905486	tr1c074xm
cl123	311	13.2	546	9	CR273299	Forward s	1196	308.5	13.1	1763	7	CF876992	tr1c074xm
cl124	311	13.2	605	7	CF398896	RTPD3_11	1197	308.5	13.1	1861	9	AG131093	Pan trogl
cl125	311	13.2	619	9	CG898398	pastbac07	1198	308.5	13.1	1867	4	BI958202	HVSMEM001
cl126	311	13.2	723	9	CNS001HT	AL074798 Drosophi	1199	308.5	13.1	1877	9	AG367290	Mus muscu
cl127	311	13.2	840	9	AG369179	Mus muscu	1200	308.5	13.1	1884	6	CD790234	EST661595
cl128	311	13.2	843	9	AG598500	Mus muscu	1201	308.5	13.1	1890	7	CN048619	V2_p1_G14
cl129	311	13.2	864	9	AG543704	Mus muscu	1202	308.5	13.1	1894	9	AG392360	Mus muscu
cl130	311	13.2	890	9	AG515316	Mus muscu	1203	308.5	13.1	1894	9	AG136784	Pan trogl
cl131	311	13.2	890	9	AG515316	Mus muscu	1204	308.5	13.1	1894	9	AG423948	Mus muscu
cl132	311	13.2	1049	5	BO928368	AGENCOURT	cl205	308.5	13.1	1894	9	CL497282	SAIL 639
cl133	311	13.2	1333	9	CL493190	SAIL 575	1206	308.5	13.1	1894	9	CL474970	SAIL 22_D
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## ORIGIN

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US-10-063-699-52 (1-440) x AK081753 (1-2065)

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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

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Db 301 ACATGGCCCTGGGAGAGCCCTGAGCGAAGGGGGTGGGAACAGGCCATTTGGCAAGAGGCCG 360

QY 60 lYgLYAlaAlaGlySerLYeValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValG 80

Db 361 GAGGGCAGCTGGCTCTTAAGTCAGTGAGGCCCTTGGCCAGGGGACCAAGAGAGCAGTTG 420

QY 80 lYThrGlyValArgGlnValProGlyPheGly-AlaAlaAspAlaLeuGlyAsnArgVal 99

Db 421 GCACCTGGAGTCAGGCAGGTTCCAGGGCTTGGCTGCAGCAGATGCTTTGGGCAACAGGGTC 480

QY 100 GlyGluAlaAlaHisAlaLeuGlyAsnThrGlyHisGluLeuGlyArgGlnAlaGluAsp 119

Db 481 GGGGAAGACGCCCATGCTCTGGGAACACCTGGGCACGAGATTGGCAGACAGGCAAGAT 540

QY 120 ValIleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSer 139

Db 541 GTCAATTCGACACGAGCAGATGCTGTCCGGGGCTCTGGCAGGGGGTGGCTGGCCCAAT 600

QY 140 GlyAlaTrp-GluThrSerGlyGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyG 159

Db 601 GGTGCTTGGGAAACTCTCGAGGCCATGGCATCTTTGGCTCTCAAGGTGGCCCTGGAGG 660

QY 159 yGlnGlyGlnGlyAsnProGlyGlyLeuGly-ThrProTrp-ValHisGlyTrpProGly 178

Db 661 CCAGGGCCAGGACAATCTCGAGGCTCTGGGAGACTCCGTGGGGTCCACGGATACCCCGGA 720

QY 179 AsnSerAlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGly-GlyAs 198

Db 721 AACTCAGCAGGAGCTTTGGAAATGATCTTCAGGGAGCTTCTGGGGTCAAGGAGGGCAA 780

QY 198 nGlyGlyPro 201

Db 781 TGGAGGGCCA 790

RESULT 5

LOCUS BG675558

DEFINITION 602622157F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4746926 5', mRNA sequence.

ACCESSION BG675558

VERSION BG675558.1 GI:13906954

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 969)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [csapbs-x@mail.nih.gov](mailto:csapbs-x@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLNL0596 row: b column: 15  
High quality sequence stop: 613.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4746926"  
/tissue\_type="squamous cell carcinoma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI CGAP Skn4"  
/notes="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life

FEATURES

source

Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Alignment Scores:

Pred. No.: 4,26e-44 Length: 969  
Score: 829.50 Matches: 203  
Percent Similarity: 76.81% Conservatives: 9  
Best Local Similarity: 73.55% Mismatches: 51  
Query Match: 35.10% Indels: 18  
DB: 4 Gaps: 3

US-10-063-699-52 (1-440) x BG675558 (1-969)

QY 1 MetLYePheGlnGlyProLeuAlaCysLeuLeuLeuAlaLeuCysLeuGlySerGlyGlu 20

Db 160 ATGAAGTTCAGGGCCCTG-GCCTGCTCTGCTGCGCCCTCTGCTGGCAGTGGGAG 218

QY 21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyGluAlaLeuGly 40

Db 219 GCTGGCCCTG-CAGAGCGAGAGGAAGCACTGGGACAAATATTGGGAGGCCCTTGA 277

QY 41 HisGlyLeuGlyAspAlaLeuSerGluGlyValGlyLYeAlaIle-GlyLYeGluAlaG 60

Db 278 CATGGCTGGAGAGCCCTGAGCGAGGGGTGGGAAGGCCATTTGGCAAGAGGCCCG 337

QY 60 yGlyAlaAlaGlySerLYeValSerGluAlaLeuGlyGlnGlyThrArgGluAlaVal-- 79

Db 338 AGGGGCAGCTGGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGACCAGAGAAGCAGTTG 397

QY 80 -GlyThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgVa 99

Db 398 GCACCTGGGAAGTCAGGCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGG 457

QY 99 lGlyGluAlaAlaHisAlaLeuGlyAsnThrGlyHisGluIleGlyArgGlnAla-GluA 119

Db 458 CGGGAGAGCAGCCCATGCTCTGGGAACACTGGGCACGAGATTGGCAGACAGCAGAGAG 517

QY 119 spValIleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHis 139

Db 518 ATGTCAATTCGACACGAGCAGATGCTGTCGGGGCTCTGGCAGGGGTGCTGGCCACA 577

QY 139 erGlyAlaTrpGlu-ThrSerGlyGlyHisGlyIlePhe-GlySerGlnGlyGlyLeuG 158

Db 578 ATGTGCTTTGGGAAACCTTCTGGAGGATGGCATCTTCTGGGCTCTCAAGGTGGCTGTG 637

QY 158 yGlyGlnGlyGlnGlyAsnProGlyGlyLeuGlyThr-ProTrpValHisGlyTrpProG 178

Db 638 GAGGCCAGCCAGGCCATCTTGGAGTCTGGGACTTCCGTGGTCCACGGATACCCCG 697

QY 178 lYAsnSerAlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGln-GlyGly 197

Db 698 A-AACTCAGCAAG-CAGTTGGGATGAATCCTCA-GGAGCTCCTGGGTTCACAGGAGGC 754

QY 198 AsnGly-GlyProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnPro---- 215

Db 755 CATGGAGGGCCACCAAGCTTTGGGAACCAAGAACCTCCAGGACGCTGCGAGAGCCACCT 814

QY 216 -GlyTrpGlySerValArg---AlaSerAsnGlnAsnGluGlyCys-ThrAsnProPro- 233

Db 815 GGGCTATGCTACTGTAGACAGCCACCAACCGGATGGAGGGTGGAGAAATCCCCCAG 874

QY 234 ProSerGlySerGlyGlySerSerAsnSerGlyGlyGlySerGlnSerGlnSerGly 253

Db 875 CCTCTGGGTCAAGAGGGCGAGCCCGAATACTCGGGGAGCGAGGGGGCACACCGCGGG 934

QY 254 SerSerGlySerGlySerAsnGlyAspAsn 263

Db 935 CACAAGGGAAGGGCGACATCGCTACAAAC 964

RESULT 6

CA446785/c

LOCUS CA446785

DEFINITION UI-H-EDI-axx-j-11-0-UI.B1 NCI\_CGAP\_ED1 Homo sapiens cDNA clone

EST 08-NOV-2002

linear

634 bp mRNA

NCI\_CGAP





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Db      120 AAACCCGGGTGTGAAGACCCAGGGAATGAAGCCCGCGGAGCGGGGAATCTGGGATTCAG 179
Qy      351 GlyPheArgGlyGlnGlyValSerSerAsnMetArgGluIleSerIysGluGlyAsnArg 370
Db      180 GGCTTTCAGAGACAGGAGATTTCAGCAATGAGGGAATAAGCAAGAGGGCAATCGC 239
Qy      371 LeuLeuGlyGlySerGlyAspAsnTyrArgGlyGlnGlySerSerTrpGlySerGlyGly 390
Db      240 CTCTTGGAGGCTCTGGAGACATTATTCGGGGCAAGGGTCGAGCTGGGGCACTGGAGGA 299
Qy      391 GlyAspAlaValGlyGlyValAsnThrValAsnSerGluThrSerProGlyMetPheAsn 410
Db      300 GGTGACGCTGTGGTGAGTCAATCTGTAACCTCTGAGACGCTCTCTGGGATGTTTAAAC 359
Qy      411 PheAspThrPheTrpIysAsnPheIysSerIysLeuGlyPheIleAsnTrpAspAlaIle 430
Db      360 TTTGACACTTCTCGGAAGAATTTTAAATCCAAAGCTGGGTTTCATCAACTGGGATGCCATA 419
Qy      431 AsnIysAspGln 434
Db      420 AACAAAGAACCCAG 431

RESULT 9
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LOCUS      532 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION MR2-HN0035-221200-019-h09 HN0035 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF829704
VERSION     BF829704.1 GI:12175544
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 532)
            Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
PUBMED     10737800
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HN0035-
            221200-019-h09&t3=2000-12-2&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 462.
            Location/Qualifiers
                1..532
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="HN0035"
                /notes="Organ: head normal; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORFESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the puc 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
FEATURES
source

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ORIGIN
Alignment Scores:      1.13e-33      Length:      532
Pred. No.:      684.00      Matches:      145
Score:      83.52%      Conservative:      7
Percent Similarity:      79.67%      Mismatches:      20
Best Local Similarity:      28.10%      Indels:      10
Query Match:      2      Gaps:      0
DB:

US-10-063-699-52 (1-440) x BF829704 (1-532)
Qy      105 AlaLeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGly 124
Db      530 GCTCTGGGAACCCCTGGCCACGAGATTGCCAGACAGCCAGAGATGTCATTTCACACGGA 471
Qy      125 Ala-AspAlaValArgGlySerTrpGln-GlyValProGlyHisSerGlyAlaTrpGluT 144
Db      470 GCACGATGCTGTCGCGGCTCCTGCACACGCGGGTGCTGCCCAACAATGGTGTGGGAA 411
Qy      144 hr-SerGlyGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGlnGlyGlnGly 163
Db      410 CATTCGGAGTCCCTGGCATCTTTGGCTCTCAAGATGNCCTTGGAGGCCAGGGCCAGGCC 351
Qy      164 Asn-ProGlyGlyLeuGly-ThrProTrpValHisGlyTyrProGlyAsnSerAlaGlys 183
Db      350 AACTCTCGAGGTCCTGGCGGACTCCGTCGGTCCACGATACCCCGGAAACTCAGCAGGCA 291
Qy      183 erPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsn-GlyGlyProPro 202
Db      290 GCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCCACTGGAGGGCCACCA 231
Qy      203 AsnPheGlyThrAsnThrGlnGly-AlaValAlaGlnProGlyTyrGlySerValArgAl 222
Db      230 AACTTTGGGACCAACAACTCAGGAGCCGCTGTGGCCAGCTGGCTATGCTTCAGTGAGGC 171
Qy      222 aSerAsnGlnAsnGluGlyCyeThrAsnProProProSerGlySer-GlyGlyGlySers 242
Db      170 CAGCAACCAAGATGAAGGGTGTCTCGAATCCCCACCACCATCTGGCTCATGTGGAGGCTCCA 111
Qy      242 er-AsnSerGlyGlySerGlySerGlnSerGlySerGlnSerGlySerGlySerGlySer 261
Db      110 CGCAACTCTGGGGAGACCAACCGCTCACCGTCGGGCCGCGCAGTGCGCAGTGCGCAGCAATGGT 51
Qy      262 AspAsnAsnAsnGlySerSer-SerGlyGlySerSerSerGlySer 276
Db      50 GACAACCCCTATGCAGCAGCGTGGTGGCAGTAGTAGTAGAGGGCAGC 5

RESULT 10
LOCUS      BI822399      843 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION 603037966F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178952 5',
            mRNA sequence.
ACCESSION  BI822399
VERSION    BI822399.1 GI:15933949
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 843)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA library Preparation: Life Technologies, Inc.
            cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov

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Plate: L1AM1446 row: c column: 17  
 High quality sequence stop: 825.  
 Location/Qualifiers  
 1. .843  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5178952"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /notes="Organ: pooled brain, lung, testis; Vector: pCMV-SPT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

FEATURES  
 source  
 1. .761  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30790221"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_203"  
 /notes="Organ: placenta; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from three placentas from female C57/BL6 mice at 16 days pregnancy. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:  
 5'-pGACTAGTTCTAGATCGGAGCGGCCCC(CT)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.3 kb. This primary, microquantity library is normalized to Cot5 (non-normalized primary library is NIH\_MGC\_222) and was constructed by Express Genomics (Frederick, MD)."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,98e-33 Length: 761  
 Score: 663.00 Matches: 145  
 Percent Similarity: 63.18% Conservatives: 30  
 Best Local Similarity: 52.35% Mismatches: 50  
 Query Match: 28.06% Indels: 53  
 DB: 7 Gaps: 10  
 US-10-063-699-52 (1-440) x CK128355 (1-761)  
 QY 93 AspAlaLeuGlyAenArgValGlyGluAlaAlaHieAlaLeuGlyAenThrGlyHisGlu 112  
 DB 23 GATGTTTTTGAGCACCCTGTTGGGAAGCAGCAAGATCTCTGGGAACGCTGGGAATGAG 82  
 QY 113 IleGlyArgGlnAlaGluAspValIleArgHisGlyAlaAspAlaValArgGlySerTrp 132  
 DB 83 ATTGGCAGACAGCTGAGGATATCATTCGCAAGGGTAGATCTGTCCAC----- 133  
 QY 133 GlnGlyValProGlyHisSerGlyAlaTrpGluThrSerGlyGlyHisGlyIlePheGly 152  
 DB 134 -----AACGCTGGGTCTCTGGGGACATCTGGAGGTCTATGGCGCATATGGC 178  
 QY 153 SerGlnGlyLeuGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGly 172  
 DB 179 TCTCAAGGTGGTCTGGA-----GTCCAGGGCAATCTGTCTCTCAAGGGACACCTGG 232  
 QY 173 ValHisGlyTyProGlyAenSerAlaGlySerPheGlyMetAenProGlnGlyAlaPro 192  
 DB 233 GCCTCAGGA-----GGCACTATGGGACTAACTCTCTGGGTGGCTCT 274  
 QY 193 TrpGlyGlnGlyAenGlyGlyProProAenPheGlyThrAenThrGlnGlyAlaVal 212  
 DB 275 GTGGGTGAGGTGGCAATGCGGACCACCTCACTATATGAACCAATGCCAGGAGCTGTG 334

FEATURES  
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 /mol\_type="mRNA"  
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 /clone="IMAGE:5178952"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /notes="Organ: pooled brain, lung, testis; Vector: pCMV-SPT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,91e-33 Length: 843  
 Score: 664.00 Matches: 122  
 Percent Similarity: 99.19% Conservatives: 1  
 Best Local Similarity: 98.39% Mismatches: 1  
 Query Match: 28.10% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-063-699-52 (1-440) x BI822399 (1-843)  
 QY 311 GlySerThrGlySerSerSerGlyAenHisGlyGlySerGlyGlyAenGlyHis 330  
 DB 70 GGATCCAGCACCCTCTCTCTCGGCAACACACGCTGGAGCGCGGAGAAATGGACAT 129  
 QY 331 LysProGlyCysGluLysProGlyAenGluAlaArgGlySerGlyGlySerGlyIleGln 350  
 DB 130 AAACCCGGGTGTGAAGAGCAGTGAATGAAGCCCGCGGAGCGGGAAATCTGGGATTCAG 189  
 QY 351 GlyPheArgGlyGlnGlyValSerAenMetArgGluIleSerLysGluGlyAenArg 370  
 DB 190 GGCTTCAGAGCAGGAGGTTTCGCAACATGAGGAAATAGCAAGAGGGCAATCGC 249  
 QY 371 LeuLeuGlyGlySerGlyAspAenTyArgGlyGlnGlySerSerTrpGlySerGlyGly 390  
 DB 250 CTCTTGAGGCTCTCGAGACAATATATCGGGGCAAGCGTCTGGGCGAGTGGAGGA 309  
 QY 391 GlyAspAlaValGlyGlyValAenThrValAenSerGluThrSerProGlyMetPheAen 410  
 DB 310 GGTGACGCTGTGGTGAGTCAATACCTCTGAACTCTGAGACGCTCTCTGGGATGTTTAA 369  
 QY 411 PheAspThrPheTrpLysAenPheLysSerLysLeuGlyPheIleAenTrpAspAlaIle 430  
 DB 370 TTGACACTTCTGGAAGAATTTTAAATCAAGCTGGGTTCATCAACTGGGATGCCATA 429  
 QY 431 AsnLysAspGln 434  
 DB 430 AACAGAACCCAG 441

RESULT 11  
 CK128355  
 LOCUS  
 DEFINITION AGENCOURT 16686398 NIH\_MGC\_203 Mus musculus cDNA clone  
 IMAGE:30790221 5', mRNA sequence.  
 CK128355  
 ACCESSION CK128355.1 GI:38618791  
 VERSION  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 761)

```

Qy 213 AlaGlnProGlyTyrGlySerValArgAlaSerAsnGlnAsnGluGlyCysThrAsnPro 232
Db 335 GCTCAGCTGGCTAGGAGCAGTGGAGGCAACACAGAACTCAGGCTGTACCAACCCC 394
Qy 233 ProProSerGlySer-----GlyGlyGlySerSerAsnSerGlyGly 246
Db 395 CCACCTTCTGGCTCCCATGAAGCTTCAGTAACCTCTGGGGAAGCAGCAATGATGGCAGT 454
Qy 247 ---GlySerGlySerGlnSerGlySerSerGlySerGlySerAsnGly----- 261
Db 455 CGTGGTACCAAGCAGCAGTCATGGCAGTAATGGTCAGGGCAGCAGCAGTGGCGTGGC 514
Qy 262 -----AspAsnAsnAsnGlySerSerGlyGlySerSerGlySerSerSer 278
Db 515 CAAGGCAACGCGCAACATGGCAGCAGTAC-----AGTAGCAGCGGAGCAGACAGT 568
Qy 279 GlySerSerSerGlyGlySerSerGlyGlySerSerGlyGlySerSerGly 298
Db 569 GGCAACAGCAACAGTGGCAACAGCGGCAACAGCAGTGGCAACAGCGGCAACAGCGGT 628
Qy 299 ---GlySerArgGlyAspSerGlySerGlySerTrpGlySerSerThrGlySerSer 317
Db 629 TCTGGGTCCTGGGGA----- 643
Qy 318 SerGlyAsnHisGlyGlySerGlyGlyGlyAsnGly-----HisLysProGly 333
Db 644 ACCGGCAGCAGCGGTGGAGTGGTGGAGTGGTGGAGTGGTGGAGTGGTGGAGTGGTGG 703
Qy 334 CysGluLysProGlyAsnGluAlaArgGlySerGlyGluSerGlyIleGln 350
Db 704 TGTAACACCCAGCGGAT-GATGTGCGCATGCGCGGAGGATTGGGAGTCAGG 753

RESULT 12
CO384272 752 bp mRNA linear EST 30-JUN-2004
LOCUS AGENCOURT 26626332 NIH MGC 253 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7301888 5', mRNA sequence.
ACCESSION CO384272
VERSION CO384272.1 GI:49490095
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 752)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloned by: Agencourt Bioscience Corporation
Cloned distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLN15334 row: g column: 06
High quality sequence stop: 664.
Location/Qualifiers
1. 752
/orxanisms="Rattus norvegicus"
/mol type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7301888"
/tissue type="Ovary - Brown Norway Line 3 Age 8 weeks.
Tissues were snap-frozen and transferred in -70C. RNase
free the entire procedure."

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/lab host="DH10B Tona"
/clone lib="NIH_MGC_253"
/note="Organ: ovary; Vector: pExpress-1; Site: 1: EcorV;
Site_2: NotI; RNA obtained from female animals at 8 wk
old. Tissues were snap-frozen and kept at -80C for two
days before RNA extraction and purification (TRI-reagent
method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTTACATCGCAGCGCGCC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >1.25Kb
resulted in an average insert size of 1.5 Kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 252) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 1,27e-31 Length: 752
Score: 635.00 Matches: 144
Percent Similarity: 58.72% Conservative: 21
Best Local Similarity: 51.25% Mismatches: 73
Query Match: 26.87% Indels: 43
DB: 7 Gaps: 10

US-10-063-699-52 (1-440) x CO384272 (1-752)
Qy 121 IleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGly 140
Db 3 ATTCGAGAGGGGTAGACGCTGCCAC-----AACTCTGGG 38
Qy 141 AlaTrpGluThrSerGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGln 160
Db 39 TCCTGGGGACATCTGGAGGTCATGGCTGTATGGCTCTCAAGGTGGTGGTGGTGGTGG 92
Qy 161 GlyGlnGlyAsnProGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSer 180
Db 93 AGCCAGGCGCAATCCTGGTGTGAAGGGACACCCCTGGGCTTCAGGA----- 137
Qy 181 AlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlnGlyGlyAsnGlyGly 200
Db 138 ---GGCAACTATGGAACCTAACTCTCTGGGGTGGCTCTGTGGGTGAGGTGGGAGG 194
Qy 201 ProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerVal 220
Db 195 CCGCTCAACTATGAAACCAATGCCAGGGGGCTGTGGCTCAGCTGGCTATGGAGCAGTG 254
Qy 221 ArgAlaSerAsnGlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyGly 240
Db 255 AGAGGCAACCAACAGAAATTCAGGGTGTACCAACCCCTCTTCTGACTCCCAAGAACG 314
Qy 241 SerSerAsnSerGlyGlySer-----GlySerGlnSerGlySerSerGlySerGly 258
Db 315 TTGAGGAGCTCTGGGGAAGCAGCAATGGCGGAGTCATGGTGGCCNAGGCAACCAAGGC 374
Qy 259 SerAsnGlyAspAsnAsnAsnGlySerSerSerGlyGlySerSerSerSerSerSer 278
Db 375 AGCAATGGTCAGGGCAACAGCGCGGTAAACAGCGGCGCAAGGAGCAGTGGCAGTGGC 434
Qy 279 GlySerSerSerGlyGlySerSerGlyGlySerSerGlyGlySerSerGlyAsnSerGly 298
Db 435 AACAGTGGCAACCAACAGCGGCGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 494
Qy 299 ---GlySerArgGly-----AspSerGlySerGluSerSerTrpGly 311
Db 495 TCTGGGTCCCGGACCTGGAAACGCTCTAATTTGATGATGGCTATTTCAGTTTCCAGGGGA 554
Qy 312 SerSerThrGlySerSerSerGlyAsnHisGlyGlySer-GlyGlyGlyAsnGlyHis 331
Db 555 -----ACTAGCTCATCTCCGCGCAGCAGAGGTGGTAGTGGTGGTGGTGGTGGTGGT 605
Qy 331 sProGlyCysGluLysProGlyAsnGluAlaArgGlySerGlyGlySerGlyIleGln 351
Db 606 ACCCGAGTGTAAACCAACCCAGGGGAATGACGTGGCGCATGGCTGGTGGAGGATCTGGG 657

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FEATURES  
source

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Qy 351 yPheArgGlyGlnGlyValSerSerAsnMetArgGluIleSerLysGluGlyAsnArgLe 371
Db 658 -----AGTCANGAAAGTAAAGAAAGCAGCCATCT 686
Qy 371 uLeuGlyGlySerGlyAspAntyArGgGlyGlnGlySerSerTrpGlySerGlyGlyG1 391
Db 687 CTTTGGAGGCTCCCATGAC---TACCAGGGGACAGGGGTCCGGGCACGCGTCCAATGGTGG 743
Qy 391 Y 391
Db 744 G 744

RESULT 13
BG676132
LOCUS
DEFINITION BG676132 415 bp mRNA linear EST 01-MAY-2001
602622528F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:474746 5',
mRNA sequence.
ACCESSION BG676132
VERSION BG676132.1 GI:13907528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cga@b-re@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10597 row: h column: 07
High quality sequence stop: 342.

FEATURES
source
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/db_xref="taxon:9606"
/clone="IMAGE:474746"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn4"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI,
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 9,47e-30 Length: 415
Score: 601.50 Matches: 114
Percent Similarity: 86.96% Conservative: 6
Best Local Similarity: 82.61% Mismatches: 12
Query Match: 25.45% Indels: 6
DB: 4 Gaps: 1

US-10-063-699-52 (1-440) x BG676132 (1-415)

Qy 107 GlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGlyAlaAsp 126
Db 2 GGAACACCTGGCAGCAGATTTGGCAGACAGCAGAGATGTCAATCGACGCGGACGAT 61
Qy 127 AlaValArgGlySerTrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSerGly 146
Db 62 GCTGTCCGGCGCTCTCTGGCAGGGGGTCCCTGGCCACCAATGGTGTCTGGGAACCTTCGGA 121
Qy 147 GlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGlnGlyGlnGlyAsnProGly 166

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Db 122 GGCCATGGCATCTTTGGCTCTCAAGGTGGCTTTGGAGGCCAGGCCCAATCTCTGGA 181
Qy 167 GlyLeuGlyThrProTrpValHisGlyTrpProGlyAsnSerAlaGlySerPheGlyMet 186
Db 182 GGTCTGGGGACTCGTGGGTCCACGGATACCCCGGAACCTCAGCAGCAGCTTTGGAAATG 241
Qy 187 AsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsnGlyGlyProPro-AenPheGlyTh 206
Db 242 AATCCTCAGGGAGCTCCTCGGGGTCAAGGAGGAATGGAGGGCCACCAAGCTTTGGGAC 301
Qy 206 rAsnThrGlnGly-AlaValAlaGln-ProGlyTyrgly-----SerValArgAla 222
Db 302 CAACACTCAGGGACGCTGTGGCCAGTCCTGGCGTATGTTTCAGGTGACGAGCGCAGAG 361
Qy 223 SerAsnGlnAsnGluGlyCysThrAsnProProSerGlySerGly 238
Db 362 ACCAGGACTGCAAGGGGTGCACGTAAGTTCCCGGACCAAGTCGTGGG 409

RESULT 14
CN369384
LOCUS
DEFINITION 17000600007808 GRN_PRENU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN369384
VERSION CN369384.1 GI:47369318
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 515 Std Error: 0.00.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENU"
/notes="Oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

ORIGIN
Alignment Scores:
Pred. No.: 3,72e-29 Length: 515
Score: 594.00 Matches: 112
Percent Similarity: 86.15% Conservative: 0
Best Local Similarity: 86.15% Mismatches: 0
Query Match: 25.14% Indels: 18
DB: 7 Gaps: 1

US-10-063-699-52 (1-440) x CN369384 (1-515)

Qy 311 GlySerThrGlySerSerGlyAsnHisGlySerGlyGlyAsnGlyHis 330
Db 71 GGATCCAGCACCCGGCTCTCTCCGGCAACACCGTGGAGCGCGGAGGAATGGACAT 130

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Qy 331 LysProGlyCysGluLysProGlyAsnGluAlaArgLysSerGlyGluSerGlyGlyGln 350  
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 Qy 351 GlyPheArgGlyGlnGlyValSerSerAsnMetArgGluLysSerLysGluGlyAsnArg 370  
 Db 191 GGCTTTCAGACAGGAGATTTCAGCAACATG----- 223  
 Qy 371 LeuLeuGlyGlySerGlyAspAsnTyrArgGlyGlnGlySerSerTrpGlySerGlyGly 390  
 Db 224 -----AGGGGGCAAGGGTCGAGCTCGGGCAGTGGAGGA 256  
 Qy 391 GlyAspAlaValGlyGlyValAsnThrValAsnSerGluThrSerProGlyMetPheAsn 410  
 Db 257 GGTGACGCTGTGTGGTGAATCAATACCTGTGAACTCTGAGAGCTCTCTGGGATGTTAAC 316  
 Qy 411 PheAspThrPheTrpLysAsnPhelLysSerLysLeuGlyPheIleAsnTrpAspAlaIle 430  
 Db 317 TTTGACACTTCTCGAAGAATTTTAAATCCAAAGCTGGGTTTCATCAACTGGGATGCCATA 376  
 Qy 431 AsnLysAspGlnArgSerSerArgIlePro 440  
 Db 377 AACAAAGGACCAGAGAAGCTCTCGCATCCG 406

## RESULT 15

CV113267 712 bp mRNA linear EST 30-AUG-2004  
 LOCUS AGNCCOURT 31543348 NIH MGC 269 Rattus norvegicus cDNA clone  
 DEFINITION IMAGE:7462729 5', mRNA sequence.  
 CV113267

ACCESSION CV113267.1 GI:51628955

VERSION EST.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 712)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Daniela S. Gerhard, Ph.D.

COMMENT Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical College of Wisconsin

CDNA Library Preparation: Open Biosystems  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: L1AM15736 row: h column: 23

High quality sequence stop: 678.

## FEATURES

source

1. 712

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

/clone="IMAGE:7462729"

/tissue\_type="whole placenta, 2 pooled"

/lab\_host="DH10B Tona"

/note="Organ: placenta; Vector: pExpress-1; Site:1: EcoRV;

Site 2: NotI; Tissue was collected from two pooled

placentas from the 21st day of pregnancy. 1st strand cDNA

was primed with a Not I - oligo(dT) primer,

double-stranded cDNA was cloned into the Not I and EcoRV

sites of pExpress-1. Library was size-selected for >1.25

kb fragments for an average insert size of 2.05 kb. A

normalized version of this library is also available

(NIH MGC 270). Library was constructed by Open Biosystems (Huntsville, AL). Note: this is a Mammalian Gene Collection library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.13e-26 Length: 712  
 Score: 549.50 Matches: 117  
 Percent Similarity: 63.84% Conservative: 26  
 Best Local Similarity: 52.23% Mismatches: 56  
 Query Match: 23.25% Indels: 25  
 DB: 7 Gaps: 6

US-10-063-699-52 (1-440) x CV113267 (1-712)

Qy 1 MetLysPheGlnGlyProLeuAlaCysLeuLeuAlaLeuCysLeuGlySerGlyGlu 20  
 Db 116 ATGAAGCCACAAAGGTCCTCGGCTGTCTCTGTCGCCCTATGTCTGGGCAGCGGGTA 175  
 Qy 21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyGluAlaLeuGly 40  
 Db 176 GCTAATCCGCTGCACGCGGAGGGGAGGCACAGGGGCAATGCTGCCCC- 226  
 Qy 41 HisGlyLeuGlyAspAlaLeuSerGluGlyValGlyLysAlaIleGlyLysGluAlaGly 60  
 Db 227 ---GGAATGGAGGTACCATTCATGGAATTGGAGAGTCTGTGGGCCAAGGGCTAAA 283  
 Qy 61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80  
 Db 284 GAAGCAGCCAGCTCTGGAATCCAGGATCGCCCTGGGTGAGGCAC- 331  
 Qy 81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100  
 Db 332 GAAGTGGTGTACGACTGATGGG---GGCAGAGGCGATGTTTTCGACCACCGCTTGGG 388  
 Qy 101 GluAlaAlaHisAlaLeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspVal 120  
 Db 389 GAGCAGCTCGATCTCTGGAGAACGCTGGGAATGAGATTGGCAGCGGCTGAGGATGT 448  
 Qy 121 IleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGly 140  
 Db 449 ATTCGACAGGGGTAGACGCTGCCAC- 484  
 Qy 141 AlaTrpGluThrSerGlyGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGln 160  
 Db 485 TCCTGGGGGACATCTGGAGTCTATGGCTGTATGGCTCTCAGGTTGTTTGA- 538  
 Qy 161 GlyGlnGlyAsnProGlyGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSer 180  
 Db 539 AGCAGGCGCAATCTGTGTGTTGAAGGACACCCCTGGGCTCAGGA- 583  
 Qy 181 AlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsnGlyGly 200  
 Db 584 ---GGCAACTATGGAACATACTCTCTGGGGTGGCTCTGTGGGTTCAGGGTGCAGTGGCAGG 640  
 Qy 201 ProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerVal 220  
 Db 641 CCGTCAACTATGAACCAATGCCAGGGGCTGTGGCTCAGCTTGGCTATGAGGACAGT 700  
 Qy 221 ArgAlaSerAsn 224  
 Db 701 AGAGGCAACAAC 712

Search completed: May 15, 2005, 07:13:38  
 Job time : 3598 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 15, 2005, 06:10:03 ; Search time 225 Seconds  
(without alignments)  
3199.830 Million cell updates/sec

Title: US-10-063-699-52  
Perfect score: 2363  
Sequence: 1 MKFQGLACLLALCLSGE.....KLGFINDAINKQRRSRIP 440

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_P/US10063699/runat\_12052005\_103529\_15817/app\_query.fasta\_1.583  
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-LIST=1500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFTN=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:  
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4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
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	1	669	28.3	914	4	US-09-673-395A-39
	2	450.5	19.1	4403765	3	US-09-103-840A-2
	3	450.5	19.1	4411529	3	US-09-103-840A-1
C	4	442	18.7	4411529	3	US-09-103-840A-1
C	5	441	18.7	4403765	3	US-09-103-840A-2
	6	383	16.2	1926	3	US-09-249-585A-2
	7	383	16.2	1926	4	US-09-410-399-3
	8	383	16.2	2580	3	US-09-050-863-2
	9	383	16.2	2580	3	US-09-359-081-2
C	10	383	16.2	2452	2	US-09-130-114-1
C	11	383	16.2	8705	4	US-09-647-344A-14
	12	383	16.2	9600	3	US-08-910-647-1
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						Sequence 39, Appl
						Sequence 2, Appl
						Sequence 1, Appl
						Sequence 1, Appl
						Sequence 2, Appl
						Sequence 3, Appl
						Sequence 2, Appl
						Sequence 2, Appl
						Sequence 1, Appl
						Sequence 14, Appl
						Sequence 1, Appl

13	383	16.2	9600	3	US-09-620-925-1	Sequence 1, Appl	
14	383	16.2	10596	1	US-07-884-811-15	Sequence 15, Appl	
15	383	16.2	10596	1	US-07-885-971-15	Sequence 15, Appl	
16	383	16.2	10596	1	US-08-087-783A-15	Sequence 15, Appl	
17	383	16.2	10596	1	US-08-194-088B-15	Sequence 15, Appl	
18	383	16.2	10596	2	US-08-194-087-15	Sequence 15, Appl	
19	383	16.2	10596	5	PCT-US93-04648-15	Sequence 15, Appl	
C	20	383	16.2	16080	4	US-09-724-566A-48	Sequence 48, Appl
C	21	383	16.2	16080	4	US-09-471-669A-48	Sequence 48, Appl
C	22	373	15.8	686	3	US-09-328-111-364	Sequence 364, App
C	23	373	15.8	2338	1	US-08-425-069-1	Sequence 1, Appl
C	24	373	15.8	2338	2	US-08-317-844B-1	Sequence 1, Appl
C	25	373	15.8	2830	2	US-09-010-928B-1	Sequence 1, Appl
C	26	364.5	15.4	2824	2	US-09-010-928B-3	Sequence 3, Appl
C	27	363	15.4	6530	2	US-08-146-930-1	Sequence 1, Appl
C	28	363	15.4	6530	3	US-08-458-240-1	Sequence 1, Appl
C	29	363	15.4	6530	5	PCT-US93-03993-1	Sequence 1, Appl
C	30	361	15.3	2367	3	US-09-056-556-201	Sequence 201, App
C	31	361	15.3	2367	3	US-09-072-596-196	Sequence 196, App
C	32	361	15.3	2367	4	US-09-072-967-201	Sequence 201, App
C	33	358	15.2	2457	4	US-09-863-859-21	Sequence 21, Appl
C	34	358	15.2	4881	4	US-09-863-859-23	Sequence 23, Appl
C	35	355	15.0	1505	1	US-07-915-246-1	Sequence 1, Appl
C	36	349	14.8	1854	4	US-09-894-844-103	Sequence 103, App
C	37	347.5	14.7	1588	4	US-09-490-291-7	Sequence 7, Appl
C	38	345	14.6	590	4	US-09-513-999C-1487	Sequence 1487, Ap
C	39	343	14.5	2046	4	US-09-490-291-3	Sequence 3, Appl
C	40	343	14.5	2076	4	US-09-490-291-5	Sequence 5, Appl
C	41	335.5	14.2	2793	1	US-08-209-747-1	Sequence 1, Appl
C	42	335.5	14.2	2793	1	US-08-458-298-1	Sequence 1, Appl
C	43	334	14.1	1926	3	US-09-249-589A-4	Sequence 4, Appl
C	44	334	14.1	1931	2	US-09-130-114-2	Sequence 2, Appl
C	45	331	14.0	1280	3	US-09-060-756-4	Sequence 4, Appl
C	46	331	14.0	1280	4	US-09-670-314-4	Sequence 4, Appl
C	47	312.5	13.2	8229	4	US-09-949-016-11983	Sequence 11983, A
C	48	312.5	13.2	8276	4	US-09-949-016-15561	Sequence 15561, A
C	49	310.5	13.1	984	4	US-09-248-796A-8121	Sequence 8121, Ap
C	50	304	12.9	142783	4	US-09-949-016-15127	Sequence 15127, A
C	51	302	12.8	12001	1	US-08-458-568A-11	Sequence 11, Appl
C	52	301	12.7	767677	4	US-09-949-016-12147	Sequence 12147, A
C	53	301	12.7	767677	4	US-09-949-016-17361	Sequence 17361, A
C	54	300.5	12.7	39154	4	US-09-949-016-12384	Sequence 12384, A
C	55	300.5	12.7	39154	4	US-09-949-016-12801	Sequence 12801, A
C	56	304.3	12.7	39443	4	US-09-949-016-14326	Sequence 14326, A
C	57	300.5	12.7	39443	4	US-09-949-016-14327	Sequence 14327, A
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C	59	300	12.7	3331	3	US-08-864-038A-2	Sequence 2, Appl
C	60	300	12.7	3331	3	US-08-864-038A-4	Sequence 4, Appl
C	61	298.5	12.6	767677	4	US-09-949-016-12147	Sequence 12147, A
C	62	298.5	12.6	767677	4	US-09-949-016-17361	Sequence 17361, A
C	63	296	12.5	1995	1	US-08-425-069-3	Sequence 3, Appl
C	64	296	12.5	1995	2	US-08-317-844B-3	Sequence 3, Appl
C	65	295	12.5	26659	4	US-09-902-540-1237	Sequence 1237, Ap
C	66	290.5	12.3	2524	1	US-08-317-522A-1	Sequence 1, Appl
C	67	290.5	12.3	2524	1	US-08-439-818A-1	Sequence 1, Appl
C	68	290.5	12.3	2524	2	US-08-751-965-1	Sequence 1, Appl
C	69	290.5	12.3	2524	2	US-08-738-975-1	Sequence 1, Appl
C	70	290.5	12.3	2524	2	US-08-728-626-1	Sequence 1, Appl
C	71	290.5	12.3	2524	3	US-08-808-599A-1	Sequence 1, Appl
C	72	290	12.3	985	3	US-09-056-556-182	Sequence 182, App
C	73	290	12.3	985	3	US-09-072-596-177	Sequence 177, App
C	74	290	12.3	985	4	US-09-072-967-182	Sequence 182, App
C	75	285	12.1	1449	4	US-09-902-540-7506	Sequence 7506, Ap
C	76	285	12.1	5618	4	US-09-902-540-728	Sequence 728, App
C	77	283.5	12.0	1071	4	US-09-902-540-4828	Sequence 4828, Ap
C	78	283.5	12.0	2130	4	US-09-909-862A-6	Sequence 6, Appl
C	79	283	12.0	3483	3	US-08-808-599A-23	Sequence 23, Appl
C	80	282	11.9	12695	4	US-09-949-016-16775	Sequence 16775, A
C	81	281.5	11.9	1935	4	US-09-902-540-7710	Sequence 7710, Ap
C	82	281.5	11.9	6611	4	US-09-902-540-762	Sequence 762, App
C	83	280.5	11.9	1740	4	US-09-902-540-2679	Sequence 2679, App
C	84	280.5	11.9	2130	4	US-09-909-962A-7	Sequence 7, Appl
C	85	280.5	11.9	17622	4	US-09-902-540-1125	Sequence 1125, Ap

86	280	11.8	1439	3	US-09-056-556-167	Sequence 167, App	159	257.5	10.9	13234	4	US-09-902-540-386	Sequence 986, App
87	280	11.8	1439	3	US-09-072-596-162	Sequence 162, App	c 160	257	10.9	4793	4	US-09-902-540-790	Sequence 790, App
88	280	11.8	1439	3	US-09-072-596-167	Sequence 167, App	161	257	10.9	8438	1	US-07-945-283-1	Sequence 1, Appli
c 89	279	11.8	15840	4	US-09-902-540-1134	Sequence 1134, App	162	256	10.8	11766	4	US-09-949-016-12531	Sequence 12531, A
c 90	279	11.8	18955	4	US-09-949-016-13343	Sequence 13343, A	163	256	10.8	11770	4	US-09-949-016-12720	Sequence 12720, A
c 91	279	11.8	30678	4	US-09-949-016-12818	Sequence 12818, A	164	256	10.8	11770	4	US-09-949-016-13487	Sequence 13487, A
c 92	278	11.8	53526	3	US-08-658-136-2	Sequence 2, Appli	165	256	10.8	11770	4	US-09-949-016-13488	Sequence 13488, A
c 93	278	11.8	53577	3	US-08-658-136-1	Sequence 1, Appli	c 166	255.5	10.8	1505	4	US-09-270-767-11623	Sequence 11623, A
c 94	276	11.7	696	4	US-09-248-796A-178	Sequence 178, App	167	255.5	10.8	154745	4	US-09-827-688-8	Sequence 8, Appli
c 95	276	11.7	3120	4	US-09-169-768-29	Sequence 29, Appli	c 168	255.5	10.8	154746	4	US-09-827-688-8	Sequence 8, Appli
c 96	276	11.7	3120	4	US-09-169-768-31	Sequence 31, Appli	169	254	10.7	2574	4	US-09-902-540-5041	Sequence 5041, App
c 97	276	11.7	3344	4	US-09-902-540-552	Sequence 552, App	170	254	10.7	2699	4	US-09-902-540-6501	Sequence 6501, App
c 98	276	11.7	5086	4	US-09-949-016-11	Sequence 11, Appli	171	254	10.7	2700	4	US-09-902-540-467	Sequence 467, App
c 99	275.5	11.7	1113	4	US-09-902-540-6765	Sequence 6765, App	172	254	10.7	6200	4	US-09-795-061-3	Sequence 3, Appli
c 100	275.5	11.7	14230	4	US-09-949-016-12052	Sequence 12052, A	173	252.5	10.7	2026	4	US-09-902-540-6163	Sequence 6163, App
c 101	275.5	11.7	128470	4	US-09-949-016-13765	Sequence 13765, A	174	252.5	10.7	2027	4	US-09-902-540-303	Sequence 303, App
c 102	275	11.6	1860	4	US-09-252-991A-9781	Sequence 9781, App	175	252	10.7	6201	4	US-09-902-540-740	Sequence 740, App
c 103	275	11.6	109690	4	US-09-949-016-13525	Sequence 13525, A	176	251.5	10.6	1684	4	US-09-919-039-323	Sequence 323, App
c 104	274.5	11.6	3211	2	US-08-574-959A-8	Sequence 8, Appli	177	251.5	10.6	4826	4	US-09-772-304A-1	Sequence 1, Appli
c 105	274.5	11.6	3211	3	US-09-357-014-8	Sequence 8, Appli	178	250.5	10.6	10717	4	US-09-902-540-991	Sequence 991, App
c 106	274.5	11.6	3901	2	US-08-574-959A-6	Sequence 6, Appli	c 179	250	10.6	53500	4	US-09-266-965-76	Sequence 76, Appli
c 107	274.5	11.6	3901	3	US-09-357-014-6	Sequence 6, Appli	180	249	10.5	1980	4	US-09-902-540-9228	Sequence 9228, App
c 108	273	11.6	2467	4	US-09-799-451-628	Sequence 628, App	181	248.5	10.5	9321	4	US-09-902-540-898	Sequence 898, App
c 109	272.5	11.5	412	4	US-09-513-999C-1486	Sequence 1486, App	182	247.5	10.5	1391	4	US-09-270-767-10171	Sequence 10171, A
c 110	272	11.5	876	4	US-09-490-291-1	Sequence 1, Appli	183	247.5	10.5	2831	4	US-09-477-135A-117	Sequence 117, App
c 111	272	11.5	1848	4	US-09-252-991A-10124	Sequence 10124, A	184	247.5	10.5	6109	4	US-09-795-061-1	Sequence 1, Appli
c 112	272	11.5	3763	4	US-09-919-039-243	Sequence 243, App	185	247	10.5	2928	4	US-09-328-352-638	Sequence 638, App
c 113	272	11.5	5185	4	US-09-976-594-640	Sequence 640, App	186	246.5	10.4	538	3	US-09-056-556-180	Sequence 180, App
c 114	272	11.5	28438	4	US-09-820-790B-3	Sequence 3, Appli	187	246.5	10.4	538	3	US-09-072-596-175	Sequence 175, App
c 115	272	11.5	30135	4	US-09-902-540-1249	Sequence 1249, App	188	246.5	10.4	538	3	US-09-072-596-180	Sequence 180, App
c 116	271.5	11.5	152132	4	US-09-949-016-13845	Sequence 13845, A	189	246.5	10.4	1344	4	US-09-248-796A-5032	Sequence 5032, App
c 117	271.5	11.5	152145	4	US-09-949-016-12371	Sequence 12371, A	190	246.5	10.4	1671	4	US-09-248-796A-8235	Sequence 8235, App
c 118	269.5	11.4	19455	4	US-09-902-540-1147	Sequence 1147, App	191	246	10.4	3168	4	US-09-902-540-8270	Sequence 8270, App
c 119	269	11.4	8917	4	US-09-902-540-887	Sequence 887, App	192	246	10.4	3171	4	US-09-169-768-19	Sequence 19, App
c 120	267.5	11.3	14462	4	US-09-902-540-1090	Sequence 1090, App	c 193	246	10.4	8090	4	US-09-902-540-855	Sequence 855, App
c 121	267.5	11.3	14462	4	US-09-902-540-9597	Sequence 9597, App	194	246	10.4	30656	4	US-09-949-016-14613	Sequence 14613, A
c 122	267	11.3	114793	4	US-10-148-806-3	Sequence 3, Appli	195	245.5	10.4	1062	4	US-09-894-844-61	Sequence 61, Appli
c 123	266.5	11.3	792	4	US-09-902-540-8438	Sequence 8438, App	196	245	10.4	4266	4	US-09-949-016-3879	Sequence 3879, App
c 124	266.5	11.3	2703	4	US-09-902-540-2939	Sequence 2939, App	197	245	10.4	4266	4	US-09-949-016-3880	Sequence 3880, App
c 125	266.5	11.3	23417	4	US-09-902-540-1207	Sequence 1207, App	198	244.5	10.3	4409	4	US-09-331-347C-22	Sequence 22, Appli
c 126	266	11.3	77536	4	US-09-410-551B-1	Sequence 1, Appli	c 199	244.5	10.3	87562	4	US-09-949-016-13685	Sequence 13685, A
c 127	266	11.3	77536	4	US-09-940-316B-1	Sequence 1, Appli	c 200	244	10.3	29559	4	US-09-902-540-1254	Sequence 1254, App
c 128	265.5	11.2	1938	4	US-09-902-540-3216	Sequence 3216, App	201	243.5	10.3	43267	4	US-09-949-016-17117	Sequence 17117, A
c 129	265.5	11.2	15566	4	US-09-949-016-17104	Sequence 17104, A	c 202	243	10.3	4466	4	US-09-410-551B-20	Sequence 20, Appli
c 130	264.5	11.2	2888	3	US-08-763-907A-1	Sequence 1, Appli	c 203	243	10.3	4466	4	US-09-940-316B-20	Sequence 20, Appli
c 131	264.5	11.2	2888	4	US-09-987-614A-1	Sequence 1, Appli	c 204	243	10.3	4478	4	US-09-940-316B-16	Sequence 16, Appli
c 132	263.5	11.2	57280	4	US-09-949-016-11796	Sequence 11796, A	c 205	243	10.3	4478	4	US-09-940-316B-16	Sequence 16, Appli
c 133	263.5	11.2	57280	4	US-09-949-016-12843	Sequence 12843, A	c 206	243	10.3	4547	4	US-09-940-316B-22	Sequence 22, Appli
c 134	263.5	11.2	57280	4	US-09-949-016-12844	Sequence 12844, A	c 207	243	10.3	4547	4	US-09-940-316B-22	Sequence 22, Appli
c 135	263.5	11.2	57280	4	US-09-949-016-12846	Sequence 12846, A	c 208	243	10.3	4571	4	US-09-410-551B-18	Sequence 18, Appli
c 136	263.5	11.2	57280	4	US-09-949-016-13542	Sequence 13542, A	c 209	243	10.3	4571	4	US-09-940-316B-18	Sequence 18, Appli
c 137	263.5	11.2	57280	4	US-09-949-016-13543	Sequence 13543, A	c 210	243	10.3	7463	4	US-09-902-540-928	Sequence 928, App
c 138	263.5	11.2	57280	4	US-09-949-016-13544	Sequence 13544, A	c 211	242.5	10.3	1275	4	US-09-902-540-3545	Sequence 3545, App
c 139	263.5	11.2	57280	4	US-09-949-016-13545	Sequence 13545, A	c 212	242.5	10.3	1512	4	US-09-902-540-4044	Sequence 4044, App
c 140	263.5	11.2	57280	4	US-09-949-016-13546	Sequence 13546, A	c 213	242.5	10.3	3084	4	US-09-902-540-4461	Sequence 4461, App
c 141	263.5	11.2	57280	4	US-09-949-016-14634	Sequence 14634, A	c 214	242.5	10.3	4568	4	US-09-949-016-2498	Sequence 2498, App
c 142	263.5	11.2	57280	4	US-09-949-016-14635	Sequence 14635, A	c 215	242.5	10.3	17228	4	US-09-902-540-1170	Sequence 1170, App
c 143	263.5	11.2	57280	4	US-09-949-016-14636	Sequence 14636, A	c 216	242.5	10.3	19394	4	US-09-902-540-1172	Sequence 1172, App
c 144	263.5	11.2	57280	4	US-09-949-016-14637	Sequence 14637, A	c 217	242.5	10.3	24986	4	US-09-902-540-1200	Sequence 1200, App
c 145	263.5	11.2	57280	4	US-09-949-016-14638	Sequence 14638, A	c 218	242.5	10.3	28172	4	US-09-902-540-1221	Sequence 1221, App
c 146	263.5	11.2	57280	4	US-09-949-016-14639	Sequence 14639, A	c 219	242.5	10.3	44377	2	US-08-804-227C-7	Sequence 7, Appli
c 147	263.5	11.2	57280	4	US-09-949-016-14640	Sequence 14640, A	c 220	242.5	10.3	44377	2	US-08-804-198-1	Sequence 1, Appli
c 148	262.5	11.1	13706	4	US-09-902-540-1124	Sequence 1124, App	c 221	242.5	10.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
c 149	262	11.1	5418	4	US-09-949-016-2477	Sequence 2477, App	c 222	242.5	10.3	77536	4	US-09-940-316B-1	Sequence 1, Appli
c 150	262	11.1	18662	4	US-09-949-016-14655	Sequence 14655, A	c 223	241.5	10.2	1758	4	US-09-949-016-16803	Sequence 16803, A
c 151	260	11.0	1548	2	US-08-762-106-5	Sequence 5, Appli	c 224	241.5	10.2	67002	4	US-09-949-016-16803	Sequence 16803, A
c 152	260	11.0	1548	3	US-09-320-774-5	Sequence 5, Appli	c 225	241	10.2	753	4	US-09-248-796A-8384	Sequence 8384, App
c 153	260	11.0	1581	2	US-08-762-106-6	Sequence 6, Appli	c 226	241	10.2	1351	4	US-09-902-540-5939	Sequence 5939, App
c 154	260	11.0	1581	3	US-09-320-774-6	Sequence 6, Appli	c 227	241	10.2	1351	4	US-09-902-540-192	Sequence 192, App
c 155	259	11.0	1939	4	US-09-919-039-322	Sequence 322, App	c 228	240.5	10.2	1755	4	US-09-949-016-2716	Sequence 2716, App
c 156	258.5	10.9	1682	4	US-09-220-132-82	Sequence 82, Appli	c 229	240.5	10.2	2852	3	US-09-056-556-203	Sequence 203, App
c 157	258.5	10.9	17188	4	US-09-902-540-1166	Sequence 1166, App	c 230	240.5	10.2	2852	3	US-09-072-596-198	Sequence 198, App
c 158	258	10.9	47981	4	US-09-679-279-1	Sequence 1, Appli	c 231	240.5	10.2	2852	4	US-09-072-596-203	Sequence 203, App

232	240.5	10.2	4167	4	US-09-169-768-12	Sequence 12, Appl	305	232.5	9.8	15644	4	US-09-902-540-1133	Sequence 1133, Ap
233	240.5	10.2	5788	4	US-09-949-016-12498	Sequence 12498, A	306	231.5	9.8	2433	4	US-09-902-540-5148	Sequence 5148, Ap
234	240.5	10.2	5788	4	US-09-949-016-14458	Sequence 14458, A	C 307	231.5	9.8	2514	4	US-09-902-540-2072	Sequence 2072, Ap
235	240.5	10.2	5870	4	US-09-949-016-15247	Sequence 15247, A	C 308	231.5	9.8	152331	3	US-09-128-155-16	Sequence 16, Appl
236	240	10.2	2862	4	US-09-902-540-7479	Sequence 7479, Ap	C 309	231	9.8	12001	1	US-08-458-568A-11	Sequence 11, Appl
237	240	10.2	3505	4	US-09-266-225D-15	Sequence 15, Appl	C 310	231	9.8	17125	4	US-09-902-540-1158	Sequence 1158, Ap
238	240	10.2	5482	4	US-09-902-540-723	Sequence 723, Ap	C 311	231	9.8	17503	4	US-09-902-540-1114	Sequence 1114, Ap
239	240	10.2	5883	4	US-09-949-016-5001	Sequence 5001, Ap	C 312	230.5	9.8	1560	2	US-08-794-795-5	Sequence 5, Appl
240	239.5	10.1	3170	4	US-09-169-768-1	Sequence 1, Appl	C 313	230.5	9.8	1560	3	US-09-249-200-5	Sequence 5, Appl
241	239.5	10.1	3171	4	US-09-169-768-15	Sequence 15, Appl	C 314	230.5	9.8	1560	3	US-09-902-540-2966	Sequence 2966, Ap
242	239.5	10.1	3181	1	US-08-655-086-1	Sequence 1, Appl	C 315	230.5	9.8	10178	4	US-09-902-540-977	Sequence 977, App
243	239.5	10.1	3349	4	US-09-169-768-13	Sequence 13, Appl	C 316	230.5	9.8	22218	4	US-09-949-016-14240	Sequence 14240, A
244	239.5	10.1	3531	4	US-09-169-768-7	Sequence 7, Appl	C 317	230.5	9.8	83617	4	US-09-949-016-12254	Sequence 12254, A
245	239.5	10.1	3541	4	US-09-169-768-9	Sequence 9, Appl	C 318	230.5	9.8	97195	4	US-09-949-016-12212	Sequence 12212, A
246	239.5	10.1	6158	4	US-09-919-497-6	Sequence 6, Appl	C 319	230.5	9.8	97196	4	US-09-949-016-16971	Sequence 16971, A
247	239.5	10.1	68750	3	US-09-335-409-1	Sequence 1, Appl	C 320	230	9.7	8552	4	US-09-949-016-14227	Sequence 14227, A
248	239.5	10.1	68750	3	US-09-568-102-1	Sequence 1, Appl	C 321	230	9.7	33529	3	US-09-144-085-3	Sequence 3, Appl
249	239.5	10.1	68750	3	US-09-567-969-1	Sequence 1, Appl	C 322	229.5	9.7	774	3	US-08-956-3078-12	Sequence 12, Appl
250	239.5	10.1	68750	3	US-09-568-480-1	Sequence 1, Appl	C 323	229.5	9.7	778	3	US-08-956-3078-11	Sequence 11, Appl
251	239.5	10.1	68750	3	US-09-568-486-1	Sequence 1, Appl	C 324	229.5	9.7	1610	1	US-08-056-051-5	Sequence 5, Appl
252	239.5	10.1	68750	3	US-09-568-472-1	Sequence 1, Appl	C 325	229.5	9.7	1610	1	US-07-928-611-21	Sequence 21, Appl
253	239.5	10.1	68750	3	US-09-567-899-1	Sequence 1, Appl	C 326	229.5	9.7	1610	2	US-08-487-811A-21	Sequence 21, Appl
254	239	10.1	3225	4	US-09-902-540-3099	Sequence 3099, Ap	C 327	229.5	9.7	1610	3	US-09-060-694-21	Sequence 21, Appl
255	239	10.1	15499	4	US-09-902-540-1140	Sequence 1140, Ap	C 328	229.5	9.7	1610	3	US-09-378-074-21	Sequence 21, Appl
256	238.5	10.1	2409	4	US-09-902-540-6842	Sequence 6842, Ap	C 329	229.5	9.7	1610	5	PCT-US93-07370-21	Sequence 21, Appl
257	238.5	10.1	3899	4	US-09-902-540-573	Sequence 573, App	C 330	229.5	9.7	1632	4	US-09-902-540-5283	Sequence 5283, Ap
258	238.5	10.1	25686	4	US-09-902-540-1246	Sequence 1246, Ap	C 331	229.5	9.7	11706	4	US-09-902-540-1038	Sequence 1038, Ap
259	238	10.1	6625	4	US-09-949-016-13534	Sequence 13534, A	C 332	229.5	9.7	17726	4	US-09-902-540-1148	Sequence 1148, Ap
260	238	10.1	9127	4	US-09-949-016-13535	Sequence 13535, A	C 333	229	9.7	1965	4	US-09-902-540-1894	Sequence 1894, Ap
261	238	10.1	16562	4	US-09-949-016-13852	Sequence 13852, A	C 334	229	9.7	2184	4	US-09-902-540-5116	Sequence 5116, Ap
262	237	10.0	2070	4	US-09-270-767-14667	Sequence 14667, A	C 335	229	9.7	2413	4	US-09-949-016-5163	Sequence 5163, Ap
263	237	10.0	3053	4	US-09-902-540-643	Sequence 643, App	C 336	229	9.7	28058	4	US-09-902-540-1252	Sequence 1252, Ap
264	236.5	10.0	9369	4	US-10-237-551-190	Sequence 190, App	C 337	229	9.7	197336	4	US-09-949-016-12881	Sequence 12881, A
265	236.5	10.0	9369	4	US-10-237-551-247	Sequence 247, App	C 338	229	9.7	197337	4	US-09-949-016-14376	Sequence 14376, A
266	236.5	10.0	13987	2	US-08-804-227C-13	Sequence 13, Appl	C 339	229	9.7	234288	4	US-09-949-016-17272	Sequence 17272, A
267	236	10.0	1771	2	US-08-533-669A-7	Sequence 7, Appl	C 340	227.5	9.6	1394	4	US-09-949-016-1793	Sequence 1793, Ap
268	236	10.0	1771	2	US-08-511-872-1	Sequence 1, Appl	C 341	227.5	9.6	2058	2	US-08-749-391-1	Sequence 1, Appl
269	236	10.0	1771	3	US-09-183-861-7	Sequence 7, Appl	C 342	227.5	9.6	2058	3	US-09-390-200-1	Sequence 1, Appl
270	236	10.0	1771	3	US-09-022-765-7	Sequence 7, Appl	C 343	227.5	9.6	2631	4	US-09-902-540-4168	Sequence 4168, Ap
271	236	10.0	1771	4	US-09-551-974A-7	Sequence 7, Appl	C 344	227.5	9.6	2889	1	US-08-537-002A-4	Sequence 4, Appl
272	236	10.0	1771	4	US-09-555-501A-7	Sequence 7, Appl	C 345	227.5	9.6	2889	3	US-08-863-010-4	Sequence 4, Appl
273	236	10.0	1771	4	US-09-639-206A-7	Sequence 7, Appl	C 346	227.5	9.6	2889	3	US-09-024-429-4	Sequence 4, Appl
274	236	10.0	1771	4	US-09-874-923-7	Sequence 7, Appl	C 347	227.5	9.6	3600	1	US-08-537-002A-5	Sequence 5, Appl
275	236	10.0	1771	4	US-08-798-841-7	Sequence 7, Appl	C 348	227.5	9.6	3600	3	US-08-863-010-5	Sequence 5, Appl
276	236	10.0	6583	4	US-09-902-540-841	Sequence 841, App	C 349	227.5	9.6	3600	3	US-09-024-429-5	Sequence 5, Appl
277	236	10.0	14077	4	US-09-902-540-1109	Sequence 1109, App	C 350	227.5	9.6	5121	4	US-09-902-540-704	Sequence 704, App
278	235.5	10.0	1491	4	US-09-902-540-7572	Sequence 7572, Ap	C 351	227.5	9.6	18686	4	US-09-902-540-1206	Sequence 1206, Ap
279	235.5	10.0	1536	4	US-09-902-540-3580	Sequence 3580, Ap	C 352	227.5	9.6	20975	4	US-09-949-016-15927	Sequence 15927, A
280	235.5	10.0	2196	4	US-09-902-540-4673	Sequence 4673, Ap	C 353	227.5	9.6	72704	4	US-09-902-540-1273	Sequence 1273, Ap
281	235.5	10.0	6674	4	US-09-620-312D-110	Sequence 110, App	C 354	227	9.6	1398	4	US-09-902-540-1258	Sequence 1258, Ap
282	235.5	10.0	8144	4	US-09-902-540-820	Sequence 820, App	C 355	227	9.6	4380	3	US-08-955-565A-3	Sequence 3, Appl
283	235.5	10.0	24754	4	US-09-902-540-1105	Sequence 1105, Ap	C 361	226	9.6	1292	3	US-08-483-533-37	Sequence 37, Appl
284	235	9.9	30678	4	US-09-949-016-12343	Sequence 12343, A	C 362	226	9.6	1292	3	US-09-283-471A-37	Sequence 37, Appl
285	235	9.9	2350	4	US-09-949-016-12818	Sequence 12818, A	C 363	226	9.6	1703	2	US-08-794-795-1	Sequence 1, Appl
286	235	9.9	9293	4	US-09-949-016-16801	Sequence 16, Appl	C 364	227	9.6	5036	4	US-09-918-951-2	Sequence 2, Appl
287	234.5	9.9	2811	4	US-09-902-540-2406	Sequence 2406, Ap	C 358	227	9.6	5046	4	US-09-948-938A-5	Sequence 5, Appl
288	234.5	9.9	9164	4	US-09-814-915A-80	Sequence 80, Appl	C 359	227	9.6	16541	4	US-09-902-540-1165	Sequence 1165, Ap
289	234.5	9.9	16782	4	US-09-902-540-1105	Sequence 1105, Ap	C 360	226.5	9.6	30783	4	US-09-902-540-1019	Sequence 1019, Ap
290	233.5	9.9	18955	4	US-09-949-016-13343	Sequence 13343, A	C 361	226	9.6	11563	4	US-09-949-016-16376	Sequence 16376, A
291	233	9.9	30678	4	US-09-949-016-12818	Sequence 12818, A	C 362	226	9.6	13634	4	US-09-902-540-1175	Sequence 1175, Ap
292	233	9.9	913	3	US-08-818-112-16	Sequence 16, Appl	C 363	226	9.6	19269	4	US-09-902-540-1276	Sequence 1276, Ap
293	233	9.9	913	3	US-08-818-111-16	Sequence 16, Appl	C 364	226	9.6	1504	4	US-09-016-434-1276	Sequence 320, Ap
294	233	9.9	913	3	US-09-056-556-16	Sequence 16, Appl	C 365	226	9.6	1848	4	US-09-902-540-3320	Sequence 3320, Ap
295	233	9.9	913	3	US-09-072-596-16	Sequence 16, Appl	C 366	226	9.6	3342	4	US-09-902-540-1165	Sequence 1165, Ap
296	233	9.9	913	3	US-09-072-596-16	Sequence 16, Appl	C 367	226	9.6	6645	4	US-09-902-540-8819	Sequence 8819, Ap
297	233	9.9	4897	6	519516-7	Patent No. 519516	C 368	225	9.6	10210	4	US-09-902-540-938	Sequence 938, App
298	233	9.9	4897	6	519516-7	Patent No. 519516	C 369	225.5	9.5	19302	4	US-09-902-540-1155	Sequence 1155, Ap
299	233	9.9	7552	4	US-09-949-016-4770	Sequence 4770, Ap	C 370	225.5	9.5	9818	4	US-09-902-540-987	Sequence 987, App
300	232.5	9.8	57218	4	US-09-949-016-16512	Sequence 16512, A	C 371	225.5	9.5	34094	4	US-09-902-540-1266	Sequence 1266, Ap
301	232.5	9.8	535	3	US-09-056-556-171	Sequence 171, App	C 372	225.5	9.5	41768	4		
302	232.5	9.8	535	3	US-09-072-596-166	Sequence 166, App	C 373	225.5	9.5				
303	232.5	9.8	535	4	US-09-072-596-171	Sequence 171, App	C 374	225	9.5				
304	232.5	9.8	1608	4	US-09-270-767-12185	Sequence 12185, A	C 375	225	9.5				
					Sequence 40, Appl		C 376	225	9.5				
							C 377	225	9.5				

378	225	9.5	71989	3	US-09-443-501A-2	Sequence 2, Appl1	c 451	219.5	9.3	6803	3	US-08-665-259-19	Sequence 19, Appl1
c 379	224.5	9.5	7628	4	US-09-902-540-875	Sequence 875, App	c 452	219.5	9.3	6803	3	US-08-762-500-19	Sequence 19, Appl1
380	224	9.5	2109	3	US-09-370-838-153	Sequence 153, App	c 453	219	9.3	9933	4	US-09-902-540-942	Sequence 942, App
381	224	9.5	2109	4	US-09-854-133-153	Sequence 153, App	c 454	219	9.3	17315	4	US-09-902-540-1103	Sequence 1103, App
c 382	224	9.5	2109	4	US-09-902-540-8825	Sequence 8825, App	c 455	219	9.3	19598	4	US-09-902-540-1143	Sequence 1143, App
c 383	224	9.5	4674	4	US-09-410-551B-26	Sequence 26, Appl1	c 456	218.5	9.2	10580	4	US-09-902-540-5147	Sequence 5147, App
c 384	224	9.5	4674	4	US-09-940-316B-26	Sequence 26, Appl1	c 457	218.5	9.2	10486	4	US-09-902-540-997	Sequence 997, App
c 385	224	9.5	4725	4	US-09-410-551B-24	Sequence 24, Appl1	c 458	218.5	9.2	29899	4	US-09-902-540-1265	Sequence 1265, App
c 386	224	9.5	4725	4	US-09-940-316B-24	Sequence 24, Appl1	c 459	218	9.2	2934	4	US-09-010-147B-17	Sequence 17, Appl1
c 387	224	9.5	4737	4	US-09-410-551B-30	Sequence 30, Appl1	c 460	217.5	9.2	2061	4	US-09-949-016-165983	Sequence 165983, App
c 388	224	9.5	4737	4	US-09-940-316B-30	Sequence 30, Appl1	c 461	217.5	9.2	601	1	US-08-343-428-1	Sequence 1, Appl1
c 389	224	9.5	4767	4	US-09-410-551B-28	Sequence 28, Appl1	c 462	217.5	9.2	3725	4	US-09-949-016-2724	Sequence 2724, App
c 390	224	9.5	4767	4	US-09-940-316B-28	Sequence 28, Appl1	c 463	217.5	9.2	4847	4	US-10-164-595-57	Sequence 57, Appl1
c 391	224	9.5	4818	4	US-09-410-551B-32	Sequence 32, Appl1	c 464	217.5	9.2	5017	4	US-09-949-016-4956	Sequence 4956, App
c 392	224	9.5	4818	4	US-09-940-316B-32	Sequence 32, Appl1	c 465	217.5	9.2	6644	4	US-08-875-435B-5	Sequence 5, Appl1
c 393	224	9.5	8765	4	US-09-902-540-939	Sequence 939, App	c 466	217.5	9.2	21707	4	US-09-949-016-16698	Sequence 16698, A
c 394	224	9.5	9571	4	US-09-949-016-14023	Sequence 14023, A	c 467	217.5	9.2	43280	2	US-08-804-227C-1	Sequence 1, Appl1
c 395	223.5	9.5	1779	4	US-09-902-540-3312	Sequence 3312, A	c 468	217.5	9.2	61461	4	US-09-949-016-16419	Sequence 16419, A
c 396	223.5	9.5	1854	4	US-09-902-540-8051	Sequence 8051, App	c 469	217	9.2	320	3	US-09-165-264-14	Sequence 14, Appl1
c 397	223.5	9.5	2730	4	US-09-902-540-489	Sequence 489, App	c 470	217	9.2	762	4	US-09-216-393B-125	Sequence 125, App
c 398	223.5	9.5	3603	4	US-09-902-540-3266	Sequence 3266, App	c 471	217	9.2	885	4	US-09-248-796A-11612	Sequence 11612, A
c 399	223.5	9.5	3773	3	US-09-130-242-1	Sequence 1, Appl1	c 472	217	9.2	1722	4	US-09-902-540-9668	Sequence 9668, App
c 400	223.5	9.5	3773	4	US-09-583-610D-1	Sequence 1, Appl1	c 473	217	9.2	2436	4	US-09-902-540-8185	Sequence 8185, App
c 401	223.5	9.5	8563	4	US-09-902-540-3318	Sequence 3318, App	c 474	217	9.2	3117	4	US-09-902-540-4620	Sequence 4620, App
c 402	223.5	9.5	15351	4	US-09-902-540-1154	Sequence 1154, App	c 475	217	9.2	3684	4	US-09-902-540-683	Sequence 683, App
c 403	223.5	9.5	18159	4	US-09-949-016-12401	Sequence 12401, A	c 476	217	9.2	8352	4	US-09-902-540-832	Sequence 832, App
c 404	223.5	9.5	18160	4	US-09-949-016-13677	Sequence 13677, A	c 477	217	9.2	12239	4	US-09-902-540-1056	Sequence 1056, App
c 405	223.5	9.5	19954	4	US-09-902-540-1150	Sequence 1150, App	c 478	217	9.2	27490	4	US-09-902-540-1227	Sequence 1227, App
c 406	223	9.4	1231	4	US-09-248-796A-12242	Sequence 12242, A	c 479	217	9.2	31467	4	US-09-949-016-13134	Sequence 13134, A
c 407	223	9.4	1259	4	US-09-902-540-2800	Sequence 2800, App	c 480	217	9.2	31868	4	US-09-949-016-11907	Sequence 11907, A
c 408	223	9.4	201529	4	US-09-949-016-12740	Sequence 12740, A	c 481	217	9.2	119032	4	US-09-949-016-12160	Sequence 12160, A
c 409	222.5	9.4	2424	4	US-09-902-540-4231	Sequence 4231, App	c 482	217	9.2	119032	4	US-09-949-016-17268	Sequence 17268, A
c 410	222.5	9.4	10644	4	US-09-902-540-1028	Sequence 1028, App	c 483	216.5	9.2	1581	4	US-09-902-540-8127	Sequence 8127, App
c 411	222.5	9.4	14555	4	US-09-902-540-1096	Sequence 1096, App	c 484	216.5	9.2	1902	4	US-09-902-540-8758	Sequence 8758, App
c 412	222	9.4	5102	1	US-08-494-168-1	Sequence 1, Appl1	c 485	216.5	9.2	2214	4	US-09-902-540-9189	Sequence 9189, App
c 413	222	9.4	10747	2	US-08-147-777-1	Sequence 1, Appl1	c 486	216.5	9.2	5173	4	US-09-949-016-1194	Sequence 1194, App
c 414	222	9.4	10747	3	US-08-452-872-1	Sequence 1, Appl1	c 487	216.5	9.2	5281	4	US-09-949-016-13	Sequence 13, Appl1
c 415	222	9.4	10747	5	PCT-US93-03985-1	Sequence 1, Appl1	c 488	216.5	9.2	6586	4	US-09-949-016-3897	Sequence 3897, App
c 416	222	9.4	24979	2	US-08-147-777-3	Sequence 3, Appl1	c 489	216.5	9.2	9039	4	US-09-902-540-983	Sequence 983, App
c 417	222	9.4	24979	3	US-08-452-872-3	Sequence 3, Appl1	c 490	216.5	9.2	9556	4	US-09-902-540-929	Sequence 929, App
c 418	222	9.4	24979	5	PCT-US93-03985-3	Sequence 3, Appl1	c 491	216.5	9.2	21375	2	US-09-902-540-1193	Sequence 1193, App
c 419	221.5	9.4	1225	4	US-09-976-594-416	Sequence 416, App	c 492	216	9.1	3147	2	US-08-781-802-7	Sequence 7, Appl1
c 420	221.5	9.4	2167	4	US-09-216-393B-326	Sequence 326, App	c 493	216	9.1	3147	3	US-09-058-260-7	Sequence 7, Appl1
c 421	221.5	9.4	2167	4	US-09-216-393B-326	Sequence 326, App	c 494	216	9.1	3147	3	US-09-058-260-7	Sequence 7, Appl1
c 422	221.5	9.4	3130	4	US-09-949-016-5779	Sequence 5779, App	c 495	216	9.1	3457	4	US-09-949-016-5747	Sequence 5747, App
c 423	221.5	9.4	3744	4	US-09-949-016-1064	Sequence 1064, App	c 496	216	9.1	4272	4	US-09-949-016-5747	Sequence 5747, App
c 424	221.5	9.4	74804	4	US-09-902-540-981	Sequence 981, App	c 497	216	9.1	4530	4	US-09-949-016-5747	Sequence 5747, App
c 425	221.5	9.4	11612	4	US-09-902-540-981	Sequence 981, App	c 498	216	9.1	4851	4	US-09-902-540-647	Sequence 647, App
c 426	221	9.4	815	3	US-08-818-112-139	Sequence 139, App	c 499	216	9.1	10301	4	US-09-902-540-985	Sequence 985, App
c 427	221	9.4	815	3	US-08-818-111-134	Sequence 134, App	c 500	216	9.1	10391	4	US-09-902-540-958	Sequence 958, App
c 428	221	9.4	815	3	US-09-056-556-139	Sequence 134, App	c 501	216	9.1	13631	4	US-09-902-540-1092	Sequence 1092, App
c 429	221	9.4	815	3	US-09-072-967-139	Sequence 134, App	c 502	216	9.1	60990	4	US-09-949-016-14080	Sequence 14080, A
c 430	221	9.4	815	4	US-09-072-967-139	Sequence 139, App	c 503	215.5	9.1	1332	4	US-09-902-540-9176	Sequence 9176, App
c 431	221	9.4	1505	4	US-09-620-312D-544	Sequence 544, App	c 504	215.5	9.1	1344	4	US-09-902-540-2519	Sequence 2519, App
c 432	221	9.4	5682	4	US-10-164-595-1	Sequence 1, Appl1	c 505	215.5	9.1	1521	4	US-09-902-540-7920	Sequence 7920, App
c 433	221	9.4	198942	4	US-09-949-016-13209	Sequence 13209, A	c 506	215.5	9.1	1710	4	US-09-902-540-2988	Sequence 2988, App
c 434	220.5	9.3	1691	4	US-09-902-540-5564	Sequence 5564, App	c 507	215.5	9.1	3597	4	US-09-902-540-5402	Sequence 5402, App
c 435	220.5	9.3	1953	4	US-09-902-540-1924	Sequence 1924, App	c 508	215.5	9.1	6488	4	US-09-902-540-799	Sequence 799, App
c 436	220.5	9.3	8559	4	US-09-949-016-13412	Sequence 13412, App	c 509	215.5	9.1	34552	4	US-09-902-540-1262	Sequence 1262, App
c 437	220.5	9.3	11613	4	US-09-949-016-16905	Sequence 16905, A	c 510	215	9.1	318	3	US-09-165-264-12	Sequence 12, Appl1
c 438	220.5	9.3	18632	4	US-09-949-016-16574	Sequence 16574, A	c 511	215	9.1	319	3	US-09-165-264-8	Sequence 8, Appl1
c 439	220.5	9.3	27219	4	US-09-902-540-1244	Sequence 1244, App	c 512	215	9.1	320	3	US-09-165-264-13	Sequence 13, Appl1
c 440	220.5	9.3	34094	4	US-09-902-540-1	Sequence 1, Appl1	c 513	215	9.1	1927	4	US-09-949-016-3372	Sequence 3372, App
c 441	220	9.3	2196	4	US-09-902-540-359	Sequence 359, App	c 514	215	9.1	2632	4	US-09-902-540-440	Sequence 440, App
c 442	220	9.3	2543	1	US-08-555-669-11	Sequence 11, Appl1	c 515	215	9.1	6285	4	US-09-949-016-12815	Sequence 12815, A
c 443	220	9.3	2543	3	US-09-073-663-11	Sequence 11, Appl1	c 516	215	9.1	6286	4	US-09-949-016-17179	Sequence 17179, A
c 444	220	9.3	4084	4	US-09-902-540-697	Sequence 697, App	c 517	215	9.1	8604	4	US-09-902-540-5331	Sequence 5331, App
c 445	220	9.3	8280	4	US-09-949-016-12806	Sequence 12806, A	c 518	215	9.1	35399	4	US-09-902-540-1260	Sequence 1260, App
c 446	220	9.3	8283	4	US-09-949-016-14466	Sequence 14466, A	c 519	214.5	9.1	2073	3	US-09-902-540-308	Sequence 308, App
c 447	220	9.3	9574	4	US-09-902-540-1043	Sequence 1043, App	c 520	214.5	9.1	2455	4	US-09-103-429A-1	Sequence 1, Appl1
c 448	219.5	9.3	4355	4	US-09-799-451-941	Sequence 941, App	c 521	214.5	9.1	2455	4	US-09-894-599A-35	Sequence 35, Appl1
c 449	219.5	9.3	4529	4	US-09-799-451-940	Sequence 940, App	c 522	214.5	9.1	2481	4	US-09-894-599A-35	Sequence 35, Appl1
c 450	219.5	9.3	4646	4	US-09-799-451-939	Sequence 939, App	c 523	214.5	9.1	2481	4	US-10-237-551-35	Sequence 35, Appl1



c 524	214.5	9.1	2821	3	US-09-103-429A-2	Sequence 2, Appli	c 597	211	8.9	17654	4	US-09-902-540-1161	Sequence 1161, Ap
c 525	214.5	9.1	2821	4	US-09-294-663-2	Sequence 2, Appli	c 598	211	8.9	54711	4	US-09-949-016-17489	Sequence 17489, A
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c 527	214.5	9.1	3213	4	US-09-902-540-8187	Sequence 8187, Ap	c 600	211	8.9	137000	4	US-10-172-911-11	Sequence 11, Appl
c 528	214.5	9.1	4027	2	US-08-551-356-5	Sequence 5, Appli	c 601	210.5	8.9	1572	4	US-09-297-269-39	Sequence 39, Appl
c 529	214.5	9.1	4027	5	PCT-US93-12887-5	Sequence 5, Appli	c 602	210.5	8.9	1806	4	US-09-252-991A-1534	Sequence 1534, Ap
c 530	214.5	9.1	5467	4	US-09-902-540-703	Sequence 703, App	c 603	210.5	8.9	2051	1	US-08-343-785-7	Sequence 7, Appli
c 531	214.5	9.1	6301	4	US-09-902-540-842	Sequence 842, App	c 604	210.5	8.9	2051	2	US-08-462-221-7	Sequence 7, Appli
c 532	214.5	9.1	13178	4	US-09-949-016-17116	Sequence 17116, A	c 605	210.5	8.9	2051	3	US-08-946-458-7	Sequence 7, Appli
c 533	214	9.1	2703	4	US-09-902-540-8634	Sequence 8634, Ap	c 606	210.5	8.9	2111	1	US-08-343-785-1	Sequence 1, Appli
c 534	214	9.1	8320	4	US-09-902-540-913	Sequence 913, App	c 607	210.5	8.9	2111	2	US-08-462-221-1	Sequence 1, Appli
c 535	214	9.1	8983	4	US-09-949-016-15437	Sequence 15437, A	c 608	210.5	8.9	2111	3	US-08-946-458-1	Sequence 1, Appli
c 536	213.5	9.0	2211	4	US-09-902-540-5403	Sequence 5403, App	c 609	210.5	8.9	8944	4	US-09-902-540-915	Sequence 915, App
c 537	213.5	9.0	2880	4	US-09-614-221A-485	Sequence 485, App	c 610	210	8.9	320	3	US-09-165-264-7	Sequence 7, Appli
c 538	213.5	9.0	3536	4	US-09-949-016-1083	Sequence 1083, Ap	c 611	210	8.9	320	3	US-09-165-264-11	Sequence 11, Appl
c 539	213.5	9.0	3957	4	US-10-237-551-193	Sequence 193, App	c 612	210	8.9	522	4	US-09-949-016-103758	Sequence 103758,
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c 541	213.5	9.0	11282	4	US-09-902-540-1039	Sequence 1039, Ap	c 614	210	8.9	2103	4	US-09-902-540-4585	Sequence 4585, Ap
c 542	213.5	9.0	28374	4	US-09-949-016-17508	Sequence 17508, A	c 615	210	8.9	2319	4	US-09-902-540-2035	Sequence 2035, Ap
c 543	213	9.0	1590	4	US-09-381-656-2	Sequence 2, Appli	c 616	210	8.9	3969	1	US-08-026-138B-16	Sequence 16, Appl
c 544	213	9.0	1737	4	US-09-902-540-7262	Sequence 7262, Ap	c 617	210	8.9	4689	3	US-09-105-537-34	Sequence 34, Appl
c 545	213	9.0	11958	3	US-09-134-246-8	Sequence 8, Appli	c 618	210	8.9	5372	4	US-09-949-016-5039	Sequence 5039, Ap
c 546	213	9.0	11958	4	US-09-664-186-8	Sequence 8, Appli	c 619	210	8.9	19068	4	US-09-902-540-1123	Sequence 1123, Ap
c 547	213	9.0	15209	4	US-09-902-540-1110	Sequence 1110, Ap	c 620	210	8.9	16778	3	US-09-105-537-5	Sequence 5, Appli
c 548	213	9.0	61663	3	US-09-453-702B-62	Sequence 62, Appl	c 621	210	8.9	38506	3	US-09-320-878-19	Sequence 19, Appl
c 549	212.5	9.0	1756	1	US-08-642-255-50	Sequence 50, Appl	c 622	210	8.9	38506	4	US-09-141-908-1	Sequence 1, Appli
c 550	212.5	9.0	1326	4	US-09-902-540-3917	Sequence 3917, Ap	c 623	210	8.9	38506	4	US-09-657-440-19	Sequence 19, Appl
c 551	212.5	9.0	1781	4	US-09-534-101D-19	Sequence 19, Appl	c 624	209.5	8.9	1404	4	US-09-902-540-7362	Sequence 7362, Ap
c 552	212.5	9.0	15252	4	US-09-949-016-13584	Sequence 13584, A	c 625	209.5	8.9	1608	4	US-09-949-016-5737	Sequence 5737, Ap
c 553	212.5	9.0	19112	4	US-09-902-540-1181	Sequence 1181, Ap	c 626	209.5	8.9	1692	4	US-09-902-540-4219	Sequence 4219, Ap
c 554	212	9.0	1335	5	PCT-US91-06532-1	Sequence 1, Appli	c 627	209.5	8.9	2236	4	US-09-902-540-6853	Sequence 6853, Ap
c 555	212	9.0	1522	1	US-08-106-981-3	Sequence 3, Appli	c 628	209.5	8.9	2363	4	US-09-818-780-22	Sequence 22, Appl
c 556	212	9.0	4683	4	US-09-902-540-9346	Sequence 9346, Ap	c 629	209.5	8.9	2493	1	US-07-977-434-5	Sequence 5, Appli
c 557	212	9.0	8829	4	US-09-902-540-2387	Sequence 2387, Ap	c 630	209.5	8.9	2493	5	US-08-458-819-5	Sequence 5, Appli
c 558	212	9.0	9905	4	US-09-902-540-998	Sequence 998, App	c 631	209.5	8.9	2493	5	PCT-US91-07035-5	Sequence 5, Appli
c 559	212	9.0	13862	4	US-09-902-540-1198	Sequence 1198, Ap	c 632	209.5	8.9	2990	4	US-09-854-133-731	Sequence 731, App
c 560	212	9.0	27707	4	US-09-902-540-1226	Sequence 1226, Ap	c 633	209.5	8.9	3105	4	US-09-252-991A-10087	Sequence 10087, A
c 561	212	9.0	47727	4	US-09-949-016-12904	Sequence 12904, A	c 634	209.5	8.9	3435	4	US-09-252-991A-10017	Sequence 10017, A
c 562	212	9.0	62728	4	US-09-949-016-12539	Sequence 12539, A	c 635	209.5	8.9	4302	4	US-09-902-540-576	Sequence 576, App
c 563	212	9.0	97989	4	US-09-949-016-13208	Sequence 13208, A	c 636	209.5	8.9	8798	4	US-09-949-016-14609	Sequence 14609, A
c 564	211.5	9.0	1702	4	US-09-902-540-8057	Sequence 8057, Ap	c 637	209.5	8.9	26289	4	US-09-902-540-1210	Sequence 1210, Ap
c 565	211.5	9.0	2392	4	US-08-216-393B-331	Sequence 331, App	c 638	209.5	8.9	131978	4	US-09-949-016-13117	Sequence 13117, A
c 566	211.5	9.0	2724	4	US-09-216-393B-329	Sequence 329, App	c 639	209	8.8	298	4	US-09-902-540-3929	Sequence 3929, Ap
c 567	211.5	9.0	2923	4	US-09-902-540-3470	Sequence 3470, Ap	c 640	209	8.8	4526	4	US-09-902-540-772	Sequence 772, App
c 568	211.5	9.0	2824	3	US-07-757-022B-13	Sequence 13, Appl	c 641	209	8.8	16423	4	US-09-902-540-1017	Sequence 1017, Ap
c 569	211.5	9.0	3066	3	US-07-757-022B-83	Sequence 83, Appl	c 642	209	8.8	21295	4	US-09-902-540-1120	Sequence 1120, Ap
c 570	211.5	9.0	3117	3	US-07-757-022B-73	Sequence 73, Appl	c 643	208.5	8.8	1164	3	US-09-902-540-1194	Sequence 1194, Ap
c 571	211.5	9.0	3148	3	US-07-757-022B-57	Sequence 57, Appl	c 644	208.5	8.8	2387	4	US-09-295-593-35	Sequence 35, Appl
c 572	211.5	9.0	3420	3	US-07-757-022B-103	Sequence 103, App	c 645	208.5	8.8	2387	4	US-09-949-016-4474	Sequence 4474, Ap
c 573	211.5	9.0	3813	3	US-07-757-022B-43	Sequence 43, Appl	c 646	208.5	8.8	3867	4	US-09-902-540-572	Sequence 572, App
c 574	211.5	9.0	3936	3	US-07-757-022B-41	Sequence 41, Appl	c 647	208.5	8.8	11199	4	US-09-902-540-5017	Sequence 5017, Ap
c 575	211.5	9.0	3942	3	US-07-757-022B-141	Sequence 141, App	c 648	208.5	8.8	16365	4	US-09-949-016-16970	Sequence 16970, A
c 576	211.5	9.0	3945	3	US-07-757-022B-49	Sequence 49, Appl	c 649	208.5	8.8	30922	4	US-09-949-016-16700	Sequence 16700, A
c 577	211.5	9.0	3963	3	US-07-757-022B-45	Sequence 45, Appl	c 650	208.5	8.8	36223	4	US-09-949-016-14417	Sequence 14417, A
c 578	211.5	9.0	4063	3	US-07-757-022B-59	Sequence 59, Appl	c 651	208	8.8	1327	3	US-08-483-533-36	Sequence 36, Appl
c 579	211.5	9.0	4093	3	US-07-757-022B-47	Sequence 47, Appl	c 652	208	8.8	1327	3	US-09-283-471A-36	Sequence 36, Appl
c 580	211.5	9.0	4086	3	US-07-757-022B-39	Sequence 39, Appl	c 653	208	8.8	1575	4	US-09-902-540-6429	Sequence 6429, Ap
c 581	211.5	9.0	4092	3	US-07-757-022B-51	Sequence 51, Appl	c 654	208	8.8	1575	4	US-09-902-540-442	Sequence 442, App
c 582	211.5	9.0	4215	3	US-07-757-022B-61	Sequence 61, Appl	c 655	208	8.8	1868	1	US-08-392-367B-1	Sequence 1, Appli
c 583	211.5	9.0	4937	4	US-09-949-016-4121	Sequence 4121, Ap	c 656	208	8.8	1868	1	US-08-893-467A-1	Sequence 1, Appli
c 584	211.5	9.0	5008	3	US-07-757-022B-1	Sequence 1, Appli	c 657	208	8.8	2070	4	US-09-949-016-5405	Sequence 5405, Ap
c 585	211.5	9.0	5041	4	US-09-023-655-981	Sequence 981, App	c 658	208	8.8	3389	4	US-09-620-312D-1061	Sequence 1061, Ap
c 586	211.5	9.0	5041	4	US-09-298-970A-2	Sequence 2, Appli	c 659	208	8.8	12695	4	US-09-949-016-16775	Sequence 16775, A
c 587	211.5	9.0	6269	4	US-09-902-540-726	Sequence 726, App	c 660	208	8.8	22071	4	US-09-949-016-15458	Sequence 15458, A
c 588	211.5	9.0	7160	4	US-09-902-540-821	Sequence 821, App	c 661	207.5	8.8	4992	4	US-09-902-540-635	Sequence 635, App
c 589	211.5	9.0	16541	4	US-09-902-540-1165	Sequence 1165, Ap	c 662	207.5	8.8	29103	4	US-09-902-540-1236	Sequence 1236, Ap
c 590	211.5	9.0	25231	4	US-09-949-016-12041	Sequence 12041, A	c 663	207	8.8	30780	4	US-09-902-540-1243	Sequence 1243, Ap
c 591	211.5	9.0	40586	4	US-09-949-016-16965	Sequence 16965, A	c 664	207	8.8	1799	4	US-09-976-594-46	Sequence 46, Appl
c 592	211	8.9	1403	4	US-09-902-540-163	Sequence 163, App	c 665	207	8.8	2100	4	US-10-237-551-179	Sequence 179, App
c 593	211	8.9	1422	4	US-09-902-540-5473	Sequence 5473, Ap	c 666	207	8.8	2100	4	US-10-237-551-252	Sequence 252, App
c 594	211	8.9	2064	4	US-09-902-540-3408	Sequence 3408, Ap	c 667	207	8.8	2547	4	US-09-902-540-7505	Sequence 7505, Ap
c 595	211	8.9	6456	4	US-09-949-016-15557	Sequence 15557, A	c 668	207	8.8	2790	2	US-08-718-661-1	Sequence 1, Appli
c 596	211	8.9	12955	4	US-09-902-540-1068	Sequence 1068, Ap	c 669	207	8.8	3167	4	US-09-949-001-7	Sequence 7, Appli

670	207	8.8	3198	4	US-09-949-001-2	Sequence 2, Appli	c 743	205	8.7	120217	4	US-09-949-016-12260	Sequence 12260, A
c 671	207	8.8	4408	4	US-09-902-540-744	Sequence 744, App	744	204.5	8.7	2034	4	US-09-902-540-8514	Sequence 8514, Ap
672	207	8.8	10544	4	US-09-949-001-28	Sequence 28, Appl	745	204.5	8.7	2124	4	US-09-266-965-44	Sequence 44, Appl
673	207	8.8	10544	4	US-09-949-001-33	Sequence 33, Appl	746	204.5	8.7	2150	2	US-08-318-837-1	Sequence 1, Appli
c 674	207	8.8	14467	4	US-09-902-540-1058	Sequence 1058, Ap	747	204.5	8.7	2218	4	US-09-919-039-120	Sequence 5, Appli
c 675	207	8.8	28762	4	US-09-902-540-1232	Sequence 1232, Ap	748	204.5	8.7	2648	3	US-09-373-157-5	Sequence 120, App
676	206.5	8.7	1035	1	US-08-891-254-8	Sequence 8, Appli	749	204.5	8.7	2746	4	US-09-902-540-1968	Sequence 1968, Ap
677	206.5	8.7	1035	2	US-08-819-539-8	Sequence 8, Appli	750	204.5	8.7	2946	4	US-09-902-540-2504	Sequence 2504, Ap
678	206.5	8.7	1035	2	US-08-030-270A-8	Sequence 8, Appli	751	204.5	8.7	3626	4	US-09-949-016-2711	Sequence 2711, Ap
679	206.5	8.7	1035	3	US-08-984-207-8	Sequence 8, Appli	c 752	204.5	8.7	4286	4	US-09-976-594-632	Sequence 632, App
680	206.5	8.7	1035	3	US-09-013-587-8	Sequence 8, Appli	753	204.5	8.7	6855	4	US-09-902-540-897	Sequence 897, App
681	206.5	8.7	1035	4	US-09-086-118-28	Sequence 8, Appli	754	204.5	8.7	11585	4	US-09-949-016-14453	Sequence 14453, A
682	206.5	8.7	1035	4	US-09-431-614-16	Sequence 16, Appl	755	204.5	8.7	16833	4	US-09-902-540-1112	Sequence 1112, Ap
683	206.5	8.7	1035	5	PCT-US96-08819-8	Sequence 8, Appli	756	204.5	8.7	18537	4	US-09-902-540-1157	Sequence 1157, Ap
684	206.5	8.7	1362	4	US-09-902-540-8360	Sequence 860, Ap	757	204	8.6	1280	3	US-08-483-533-38	Sequence 38, Appl
685	206.5	8.7	1458	4	US-09-902-540-3711	Sequence 3711, Ap	c 758	204	8.6	1280	3	US-09-283-471A-38	Sequence 38, Appl
686	206.5	8.7	3909	4	US-09-902-540-7652	Sequence 7652, Ap	759	204	8.6	1967	4	US-09-902-540-2665	Sequence 2665, Ap
687	206.5	8.7	4761	4	US-09-902-540-739	Sequence 739, App	760	204	8.6	1995	4	US-09-902-540-9209	Sequence 9209, Ap
688	206.5	8.7	6161	4	US-09-902-540-753	Sequence 753, App	761	204	8.6	1998	4	US-09-894-844-6	Sequence 6, Appli
c 689	206.5	8.7	6330	4	US-09-902-540-718	Sequence 718, App	c 762	204	8.6	2050	4	US-09-050-739-69	Sequence 69, Appl
690	206.5	8.7	7353	4	US-09-949-016-14895	Sequence 14895, A	c 763	204	8.6	4257	2	US-08-690-473-1	Sequence 1, Appli
691	206.5	8.7	18031	4	US-09-902-540-1180	Sequence 1180, Ap	c 764	204	8.6	4257	3	US-09-259-821A-1	Sequence 1, Appli
692	206.5	8.7	21010	4	US-09-902-540-1188	Sequence 1188, Ap	c 765	204	8.6	4257	3	US-08-843-659-1	Sequence 1, Appli
c 693	206.5	8.7	28493	4	US-09-902-540-1241	Sequence 1241, Ap	c 766	204	8.6	4359	4	US-09-825-288A-1	Sequence 4, Appli
694	206	8.7	772	3	US-09-575-602-1	Sequence 1, Appli	767	204	8.6	4359	3	US-09-484-970B-4	Sequence 14464, A
695	206	8.7	772	4	US-09-032-086-1	Sequence 1, Appli	c 768	204	8.6	14205	4	US-09-949-016-14464	Sequence 14464, A
c 696	206	8.7	1300	3	US-08-483-533-39	Sequence 39, Appl	c 769	203.5	8.6	601	4	US-09-949-016-94075	Sequence 94075, A
c 697	206	8.7	1300	3	US-09-283-471A-39	Sequence 39, Appl	c 770	203.5	8.6	21295	4	US-09-902-540-1194	Sequence 1194, Ap
698	206	8.7	1776	4	US-09-902-540-4682	Sequence 4682, Ap	771	203.5	8.6	74550	4	US-09-949-016-12310	Sequence 12310, A
699	206	8.7	4551	4	US-09-949-016-2338	Sequence 2338, Ap	772	203.5	8.6	74550	4	US-09-949-016-12764	Sequence 12764, A
700	206	8.7	14207	4	US-09-949-016-12187	Sequence 12187, A	773	203.5	8.6	74550	4	US-09-949-016-13649	Sequence 13649, A
701	206	8.7	14207	4	US-09-949-016-17460	Sequence 17460, A	774	203.5	8.6	74550	4	US-09-949-016-13650	Sequence 13650, A
c 702	206	8.7	14367	4	US-09-902-540-1113	Sequence 1113, Ap	775	203	8.6	1104	4	US-09-902-540-7332	Sequence 7332, Ap
c 703	206	8.7	23847	4	US-09-902-540-1177	Sequence 1177, Ap	776	203	8.6	2022	4	US-09-902-540-5510	Sequence 5510, Ap
c 704	206	8.7	24754	4	US-09-902-540-1230	Sequence 1230, Ap	777	203	8.6	4184	4	US-09-949-016-4495	Sequence 4495, Ap
c 705	206	8.7	26533	4	US-09-902-540-1199	Sequence 1199, Ap	c 778	203	8.6	7994	4	US-09-902-540-797	Sequence 797, App
c 706	206	8.7	42053	4	US-09-949-016-15924	Sequence 15924, A	c 779	203	8.6	11566	4	US-09-902-540-1088	Sequence 1088, Ap
707	205.5	8.7	293	4	US-09-621-976-13359	Sequence 13359, A	c 780	203	8.6	15148	4	US-09-949-016-15058	Sequence 15058, A
708	205.5	8.7	337	4	US-09-621-976-13384	Sequence 13384, A	c 781	203	8.6	15268	4	US-09-902-540-1142	Sequence 1142, A
709	205.5	8.7	342	4	US-09-621-976-13367	Sequence 13367, A	c 782	203	8.6	15778	4	US-09-949-016-13538	Sequence 13538, A
c 710	205.5	8.7	1368	4	US-09-902-540-9337	Sequence 9337, Ap	c 783	203	8.6	41768	4	US-09-902-540-1266	Sequence 1266, Ap
c 711	205.5	8.7	1597	2	US-08-724-974A-1	Sequence 1, Appli	784	202.5	8.6	1395	4	US-09-902-540-3185	Sequence 3185, Ap
c 712	205.5	8.7	1697	4	US-09-364-425B-26	Sequence 26, Appl	785	202.5	8.6	3211	4	US-09-902-540-6633	Sequence 6633, Ap
713	205.5	8.7	1860	4	US-09-902-540-6841	Sequence 6841, Ap	786	202.5	8.6	3212	4	US-09-902-540-510	Sequence 510, App
714	205.5	8.7	1998	4	US-09-902-540-8696	Sequence 8696, Ap	787	202.5	8.6	4743	4	US-09-902-540-7191	Sequence 7191, Ap
c 715	205.5	8.7	2179	2	US-08-551-356-3	Sequence 3, Appli	c 788	202.5	8.6	5822	4	US-09-902-540-668	Sequence 668, App
716	205.5	8.7	2179	5	PCT-US93-12687-3	Sequence 3, Appli	c 789	202.5	8.6	5943	1	US-08-206-176-1	Sequence 1, Appli
c 717	205.5	8.7	2916	4	US-09-902-540-3680	Sequence 3680, Ap	790	202.5	8.6	8310	4	US-09-902-540-1001	Sequence 1001, Ap
c 718	205.5	8.7	5117	4	US-09-774-528-438	Sequence 438, App	791	202.5	8.6	9165	4	US-09-902-540-1050	Sequence 1050, Ap
c 719	205.5	8.7	5147	4	US-09-902-540-780	Sequence 780, App	792	202.5	8.6	14861	4	US-09-902-540-1127	Sequence 1127, Ap
720	205.5	8.7	6100	4	US-09-949-016-11939	Sequence 11939, A	793	202.5	8.6	34316	4	US-09-902-540-1257	Sequence 1257, Ap
721	205.5	8.7	6100	4	US-09-949-016-16584	Sequence 16584, A	794	202	8.5	1458	4	US-09-902-540-3540	Sequence 3540, Ap
722	205.5	8.7	7325	4	US-09-949-016-13839	Sequence 13839, A	795	202	8.5	1671	4	US-09-902-540-5803	Sequence 5803, Ap
723	205.5	8.7	7530	4	US-09-902-540-921	Sequence 921, App	796	202	8.5	2031	4	US-09-395-017B-3	Sequence 3, Appli
c 724	205.5	8.7	16885	1	US-08-390-878-16	Sequence 16, Appl	c 797	202	8.5	2205	1	US-08-081-610-1	Sequence 1, Appli
c 725	205.5	8.7	16924	4	US-09-902-540-1178	Sequence 1178, Ap	798	202	8.5	2235	4	US-09-949-016-3736	Sequence 3736, Ap
c 726	205.5	8.7	149543	4	US-09-949-016-15947	Sequence 15947, A	c 799	202	8.5	2712	3	US-09-025-691-4	Sequence 4, Appli
727	205	8.7	564	4	US-09-680-175-3	Sequence 3, Appli	c 800	202	8.5	12173	4	US-09-902-540-1022	Sequence 1022, Ap
728	205	8.7	1206	4	US-09-902-540-7709	Sequence 7709, Ap	801	202	8.5	15689	4	US-09-902-540-1129	Sequence 1129, Ap
729	205	8.7	1356	4	US-09-902-540-8249	Sequence 8249, Ap	802	202	8.5	18538	4	US-09-902-540-1169	Sequence 1169, Ap
730	205	8.7	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	803	202	8.5	29927	4	US-09-949-016-11814	Sequence 11814, A
c 731	205	8.7	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	804	202	8.5	29927	4	US-09-949-016-17474	Sequence 17474, A
c 732	205	8.7	3077	4	US-09-680-175-1	Sequence 1, Appli	805	202	8.5	29927	4	US-09-949-016-17475	Sequence 17475, A
c 733	205	8.7	3432	4	US-09-254-594-4	Sequence 4, Appli	806	202	8.5	37802	4	US-09-949-016-12639	Sequence 12639, A
734	205	8.7	4248	4	US-09-252-991A-9867	Sequence 9867, Ap	807	202	8.5	43280	2	US-08-804-227C-1	Sequence 1, Appli
c 735	205	8.7	4483	4	US-09-799-451-390	Sequence 390, App	c 808	202	8.5	72704	4	US-09-902-540-1273	Sequence 1273, Ap
736	205	8.7	5387	4	US-09-949-016-265	Sequence 265, App	809	202	8.5	114793	4	US-10-148-806-3	Sequence 3, Appli
737	205	8.7	6698	4	US-09-902-540-852	Sequence 852, App	810	201.5	8.5	371	3	US-09-072-596-237	Sequence 237, App
c 738	205	8.7	8916	3	US-09-579-181-10	Sequence 11, Appl	811	201.5	8.5	371	4	US-09-252-991A-8312	Sequence 242, App
c 739	205	8.7	9354	3	US-09-579-181-10	Sequence 10, Appl	812	201.5	8.5	1395	4	US-09-902-540-3148	Sequence 8312, Ap
740	205	8.7	16004	4	US-09-949-016-15510	Sequence 15510, A	813	201.5	8.5	1437	4	US-09-902-540-6006	Sequence 6006, Ap
741	205	8.7	50725	4	US-09-902-540-1271	Sequence 1271, A	814	201.5	8.5	2271	4	US-09-902-540-6006	Sequence 10, Appl
c 742	205	8.7	120213	4	US-09-949-016-13304	Sequence 13304, A	815	201.5	8.5	4992	4	US-09-015-399-10	Sequence 10, Appl

816	201.5	8.5	5337	4	US-09-902-540-810	Sequence 810, App	889	198.5	8.4	4638	4	US-09-023-655-1215	Sequence 1215, Ap
c 817	201.5	8.5	10505	4	US-09-902-540-1044	Sequence 32, Appl	890	198.5	8.4	6651	4	US-09-902-540-4944	Sequence 4944, Ap
c 818	201.5	8.5	11220	3	US-09-105-537-32	Sequence 1048, Ap	c 891	198.5	8.4	7713	4	US-09-902-540-900	Sequence 900, App
c 819	201.5	8.5	12865	4	US-09-902-540-1048	Sequence 13690, A	892	198.5	8.4	9649	4	US-09-949-016-15672	Sequence 15672, A
c 820	201.5	8.5	13821	4	US-09-949-016-13690	Sequence 12309, A	893	198.5	8.4	20103	4	US-09-949-016-17223	Sequence 17223, A
c 821	201.5	8.5	19973	4	US-09-949-016-12309	Sequence 13533, A	c 894	198.5	8.4	27579	4	US-09-949-016-13465	Sequence 13465, A
c 822	201.5	8.5	19980	4	US-09-949-016-13533	Sequence 1245, Ap	c 895	198.5	8.4	61158	4	US-09-949-016-15041	Sequence 15041, A
c 823	201.5	8.5	23951	4	US-09-902-540-1245	Sequence 17150, A	c 896	198.5	8.4	70770	4	US-09-949-016-16938	Sequence 16938, A
c 824	201.5	8.5	88950	4	US-09-949-016-17150	Sequence 4958, A	c 897	198.5	8.4	75431	4	US-09-949-016-15122	Sequence 15122, A
c 825	201	8.5	11555	4	US-09-902-540-4958	Sequence 6127, Ap	898	198	8.4	12666	4	US-09-902-540-3662	Sequence 3662, Ap
c 826	201	8.5	1419	4	US-09-902-540-6127	Sequence 1336, Ap	c 899	198	8.4	2481	4	US-09-894-998A-35	Sequence 35, Appl
c 827	201	8.5	1987	4	US-09-949-016-1536	Sequence 286, App	c 900	198	8.4	2481	4	US-10-237-551-35	Sequence 35, Appl
c 828	201	8.5	2070	4	US-09-902-540-286	Sequence 9681, Ap	c 901	198	8.4	2721	6	5215881-2	Patent No. 5215881
c 829	201	8.5	2841	4	US-09-902-540-9681	Sequence 580, App	c 902	198	8.4	2721	6	5215881-2	Patent No. 5215881
c 830	201	8.5	3784	4	US-09-902-540-580	Sequence 819, App	c 903	198	8.4	3066	4	US-10-237-551-152	Sequence 152, App
c 831	201	8.5	6808	4	US-09-902-540-819	Sequence 844, App	c 904	198	8.4	7736	4	US-09-949-016-17579	Sequence 17579, A
c 832	201	8.5	7553	4	US-09-902-540-844	Sequence 8197, Ap	c 905	198	8.4	8614	4	US-09-902-540-787	Sequence 787, App
c 833	201	8.5	7553	4	US-09-902-540-8197	Sequence 1078, Ap	c 906	198	8.4	18551	4	US-09-902-540-1187	Sequence 1187, Ap
c 834	201	8.5	13534	4	US-09-902-540-1078	Sequence 5004, Ap	c 907	198	8.4	20757	4	US-09-902-540-1189	Sequence 1189, Ap
c 835	201	8.5	13637	4	US-09-902-540-1097	Sequence 1247, Ap	c 908	198	8.4	32010	4	US-09-949-016-13127	Sequence 13127, A
c 836	201	8.5	24459	4	US-09-902-540-5004	Sequence 1255, Ap	c 909	198	8.4	44377	2	US-08-804-227C-7	Sequence 7, Appl
c 837	201	8.5	24905	4	US-09-902-540-1225	Sequence 13867, A	c 910	198	8.4	44377	2	US-08-804-198-1	Sequence 1, Appl
c 838	201	8.5	32241	4	US-09-902-540-1247	Sequence 1272, Ap	c 911	197.5	8.4	1629	4	US-09-902-540-8462	Sequence 8462, Ap
c 839	201	8.5	34199	4	US-09-902-540-1255	Sequence 11752, A	c 912	197.5	8.4	4825	4	US-09-902-540-692	Sequence 692, App
c 840	200.5	8.5	1412	1	US-09-902-540-1412	Sequence 1, Appl	c 913	197.5	8.4	7012	4	US-09-902-540-890	Sequence 890, App
c 841	200.5	8.5	4456	3	US-09-902-540-4456	Sequence 1, Appl	c 914	197.5	8.4	10318	4	US-09-902-540-973	Sequence 973, App
c 842	200.5	8.5	4978	4	US-09-902-540-4978	Sequence 775, App	c 915	197.5	8.4	29899	4	US-09-902-540-1265	Sequence 1265, Ap
c 843	200.5	8.5	9408	4	US-09-949-016-13867	Sequence 13867, A	c 916	197	8.3	906	4	US-09-902-540-8544	Sequence 8544, Ap
c 844	200.5	8.5	14264	4	US-09-949-016-17479	Sequence 1272, Ap	c 917	197	8.3	3432	4	US-09-949-016-266	Sequence 266, App
c 845	200.5	8.5	27490	4	US-09-902-540-1227	Sequence 1272, Ap	c 918	197	8.3	3432	4	US-09-949-016-5314	Sequence 5314, Ap
c 846	200.5	8.5	36538	4	US-09-949-016-11752	Sequence 11752, A	c 919	197	8.3	5076	4	US-09-949-016-1616	Sequence 1616, Ap
c 847	200	8.5	1603	4	US-09-902-540-355	Sequence 355, App	c 920	197	8.3	7218	4	US-09-949-016-1775	Sequence 1775, Ap
c 848	200	8.5	1864	1	US-09-454-720A-38	Sequence 38, Appl	c 921	197	8.3	7218	4	US-09-949-016-1775	Sequence 1775, Ap
c 849	200	8.5	2109	3	US-09-370-838-153	Sequence 153, App	c 922	197	8.3	7598	4	US-09-902-540-863	Sequence 863, App
c 850	200	8.5	2109	4	US-09-854-133-153	Sequence 153, App	c 923	197	8.3	17862	4	US-09-902-540-1130	Sequence 1130, Ap
c 851	200	8.5	4217	4	US-09-902-540-9677	Sequence 9677, Ap	c 924	197	8.3	30001	1	US-08-125-468-1	Sequence 1, Appl
c 852	200	8.5	4238	4	US-09-949-016-5338	Sequence 5338, Ap	c 925	197	8.3	30001	2	US-08-474-933-1	Sequence 1, Appl
c 853	200	8.5	9793	4	US-09-949-016-2258	Sequence 2258, Ap	c 926	197	8.3	82125	4	US-09-949-016-13517	Sequence 13517, A
c 854	200	8.5	11854	4	US-09-902-540-1037	Sequence 1037, Ap	c 927	197	8.3	82125	4	US-09-949-016-13518	Sequence 13518, A
c 855	200	8.5	18079	4	US-09-949-016-13344	Sequence 13344, A	c 928	196.5	8.3	966	4	US-09-902-540-5891	Sequence 5891, Ap
c 856	200	8.5	21758	4	US-09-902-540-1238	Sequence 1238, Ap	c 929	196.5	8.3	1173	4	US-09-894-844-60	Sequence 60, Appl
c 857	200	8.5	49401	4	US-09-949-016-17080	Sequence 17080, A	c 930	196.5	8.3	2112	4	US-09-902-540-3277	Sequence 3277, Ap
c 858	200	8.5	154626	4	US-09-949-016-14000	Sequence 14000, A	c 931	196.5	8.3	2358	4	US-09-902-540-2632	Sequence 2632, Ap
c 859	199.5	8.4	999	4	US-09-902-540-2460	Sequence 2460, Ap	c 932	196.5	8.3	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
c 860	199.5	8.4	2211	4	US-09-799-451-181	Sequence 181, App	c 933	196.5	8.3	4296	4	US-09-902-540-3291	Sequence 3291, Ap
c 861	199.5	8.4	9097	4	US-09-902-540-947	Sequence 947, App	c 934	196.5	8.3	5973	4	US-09-902-540-3951	Sequence 3951, Ap
c 862	199.5	8.4	11958	3	US-09-134-246-8	Sequence 8, Appl	c 935	196.5	8.3	6596	3	US-09-575-602-11	Sequence 11, Appl
c 863	199.5	8.4	11958	4	US-09-684-186-8	Sequence 8, Appl	c 936	196.5	8.3	6596	4	US-09-032-086-11	Sequence 11, Appl
c 864	199.5	8.4	12730	4	US-09-902-540-1029	Sequence 1029, Ap	c 937	196.5	8.3	15338	4	US-09-902-540-1121	Sequence 1121, Ap
c 865	199.5	8.4	21964	4	US-09-902-540-1190	Sequence 1190, Ap	c 938	196.5	8.3	17173	4	US-09-902-540-1122	Sequence 1122, Ap
c 866	199.5	8.4	60785	4	US-09-949-016-12774	Sequence 12774, A	c 939	196.5	8.3	17480	4	US-09-902-540-1151	Sequence 1151, Ap
c 867	199.5	8.4	60785	4	US-09-949-016-15665	Sequence 15665, A	c 940	196.5	8.3	17727	4	US-09-902-540-1152	Sequence 1152, Ap
c 868	199	8.4	1626	4	US-09-248-796A-12016	Sequence 12016, A	c 941	196.5	8.3	22156	4	US-09-902-540-1195	Sequence 1195, Ap
c 869	199	8.4	2891	4	US-09-949-016-3019	Sequence 3019, Ap	c 942	196.5	8.3	23704	4	US-09-949-016-12104	Sequence 12104, A
c 870	199	8.4	9521	4	US-09-902-540-953	Sequence 953, App	c 943	196.5	8.3	23704	4	US-09-949-016-15312	Sequence 15312, A
c 871	199	8.4	11188	4	US-09-821-167-1	Sequence 1, Appl	c 944	196.5	8.3	31623	4	US-09-949-016-15945	Sequence 15945, A
c 872	199	8.4	15312	4	US-09-902-540-1115	Sequence 1115, Ap	c 945	196	8.3	2459	4	US-09-902-540-533	Sequence 533, App
c 873	199	8.4	21143	4	US-09-902-540-1191	Sequence 1191, Ap	c 946	196	8.3	4719	4	US-09-902-540-5392	Sequence 5392, Ap
c 874	199	8.4	31713	4	US-09-949-016-16960	Sequence 16960, A	c 947	196	8.3	6012	4	US-09-902-540-808	Sequence 808, App
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c 876	199	8.4	43950	4	US-10-060-332-3	Sequence 3, Appl	c 949	196	8.3	14340	4	US-09-949-016-16972	Sequence 16972, A
c 877	199	8.4	43950	4	US-10-339-657-3	Sequence 3, Appl	c 950	196	8.3	17938	4	US-09-902-540-1111	Sequence 1111, Ap
c 878	198.5	8.4	326	4	US-09-621-976-13398	Sequence 13398, A	c 951	196	8.3	49931	4	US-09-949-016-13727	Sequence 13727, A
c 879	198.5	8.4	494	3	US-09-056-556-176	Sequence 176, App	c 952	196	8.3	49931	4	US-09-949-016-13728	Sequence 13728, A
c 880	198.5	8.4	494	4	US-09-072-596-171	Sequence 171, App	c 953	196	8.3	49931	4	US-09-949-016-13729	Sequence 13729, A
c 881	198.5	8.4	494	4	US-09-072-596-171	Sequence 176, App	c 954	196	8.3	55195	4	US-09-949-016-15854	Sequence 15854, A
c 882	198.5	8.4	601	4	US-09-949-016-180704	Sequence 180704, A	c 955	196	8.3	100836	4	US-09-949-016-12871	Sequence 12871, A
c 883	198.5	8.4	1185	4	US-09-902-540-5940	Sequence 5940, Ap	c 956	196	8.3	100837	4	US-09-949-016-17063	Sequence 17063, A
c 884	198.5	8.4	1446	4	US-09-902-540-193	Sequence 193, App	c 957	196	8.3	125902	4	US-09-949-016-13715	Sequence 13715, A
c 885	198.5	8.4	1446	4	US-09-902-540-8541	Sequence 8541, App	c 958	195.5	8.3	1272	4	US-09-902-540-9234	Sequence 9234, Ap
c 886	198.5	8.4	1924	4	US-09-963-137-164	Sequence 164, App	c 959	195.5	8.3	3381	4	US-09-902-540-7493	Sequence 7493, Ap
c 887	198.5	8.4	1924	4	US-09-963-137-185	Sequence 185, App	c 960	195.5	8.3	5288	3	US-09-428-711A-15	Sequence 15, Appl
c 888	198.5	8.4	2561	4	US-09-616-289-48	Sequence 48, Appl	c 961	195.5	8.3	5494	4	US-09-437-568A-45	Sequence 45, Appl

c 962	195.5	8.3	9053	4	US-09-976-594-306	Sequence 306, App	c1035	193.5	8.2	4399	3	US-08-899-595-2	Sequence 2, Appli
c 963	195.5	8.3	17897	4	US-09-902-540-1182	Sequence 1182, Ap	1036	193.5	8.2	4632	4	US-09-902-540-8368	Sequence 8368, Ap
964	195.5	8.3	19726	4	US-09-902-540-1164	Sequence 1164, Ap	c1037	193.5	8.2	5972	4	US-09-902-540-690	Sequence 690, App
965	195.5	8.3	23694	4	US-09-902-540-1216	Sequence 1216, Ap	1038	193.5	8.2	6339	4	US-09-902-540-866	Sequence 866, App
966	195	8.3	407	3	US-09-056-556-173	Sequence 173, App	c1039	193.5	8.2	7463	4	US-09-902-540-928	Sequence 928, App
967	195	8.3	407	3	US-09-072-556-168	Sequence 168, App	c1040	193.5	8.2	9321	4	US-09-902-540-898	Sequence 898, App
968	195	8.3	407	3	US-09-072-967-173	Sequence 173, App	1041	193.5	8.2	15482	4	US-09-902-540-1067	Sequence 1067, Ap
969	195	8.3	1323	4	US-09-902-540-2671	Sequence 2671, Ap	1042	193.5	8.2	20113	4	US-09-902-540-1173	Sequence 1173, Ap
c 970	195	8.3	1500	5	PCT-US93-08386-3	Sequence 3, Appli	1043	193.5	8.2	80161	3	US-09-036-987A-1	Sequence 1, Appli
971	195	8.3	1707	1	US-08-790-309-1	Sequence 1, Appli	1044	193.5	8.2	80161	3	US-09-370-700-1	Sequence 1, Appli
972	195	8.3	1707	3	US-09-250-585A-1	Sequence 1, Appli	1045	193.5	8.2	80161	4	US-09-603-207-1	Sequence 1, Appli
973	195	8.3	2078	4	US-09-789-451-486	Sequence 486, App	1046	193	8.2	1080	4	US-09-270-767-12170	Sequence 12170, A
974	195	8.3	4047	4	US-09-081-385-1	Sequence 1, Appli	1047	193	8.2	1551	4	US-09-902-540-7329	Sequence 7329, A
c 975	195	8.3	4047	4	US-09-081-385-147	Sequence 147, App	1048	193	8.2	1553	4	US-09-902-540-4604	Sequence 4604, Ap
976	195	8.3	6306	1	US-08-466-390-3	Sequence 3, Appli	1049	193	8.2	1743	4	US-09-902-540-5822	Sequence 5822, Ap
977	195	8.3	6306	1	US-08-470-950-3	Sequence 3, Appli	1050	193	8.2	1995	4	US-09-902-540-4902	Sequence 4902, Ap
978	195	8.3	6306	1	US-08-467-481-3	Sequence 3, Appli	c1051	193	8.2	2220	3	US-08-765-907A-14	Sequence 14, Appli
979	195	8.3	6306	1	US-08-195-487-3	Sequence 3, Appli	c1052	193	8.2	2220	4	US-09-987-614A-14	Sequence 14, Appli
980	195	8.3	6306	1	US-08-483-924-3	Sequence 3, Appli	1053	193	8.2	2286	4	US-09-902-540-2486	Sequence 2486, Ap
981	195	8.3	6306	5	PCT-US93-06160-3	Sequence 3, Appli	1054	193	8.2	2487	4	US-09-620-312D-160	Sequence 160, App
982	195	8.3	15543	4	US-09-949-016-17225	Sequence 17225, A	c1055	193	8.2	4039	3	US-09-902-540-696	Sequence 696, Appli
983	195	8.3	15695	4	US-09-949-016-15644	Sequence 15644, A	c1056	193	8.2	4848	3	US-08-955-957A-1	Sequence 1, Appli
984	195	8.3	17622	4	US-09-902-540-1125	Sequence 1125, Ap	c1057	193	8.2	4848	3	US-08-955-957A-4	Sequence 4, Appli
985	195	8.3	17727	4	US-09-902-540-1152	Sequence 1152, Ap	c1058	193	8.2	4848	3	US-08-955-957A-6	Sequence 6, Appli
c 986	195	8.3	41310	4	US-09-902-540-1264	Sequence 1264, Ap	c1059	193	8.2	12521	4	US-09-949-016-15988	Sequence 15988, A
c 987	194.5	8.2	601	4	US-09-949-016-186116	Sequence 186116,	1060	193	8.2	27270	4	US-09-949-016-13822	Sequence 13822, A
988	194.5	8.2	729	4	US-09-902-540-8977	Sequence 8977, Ap	1061	193	8.2	67620	4	US-09-949-016-16939	Sequence 16939, A
989	194.5	8.2	1329	4	US-09-248-796A-7297	Sequence 7297, Ap	1062	192.5	8.1	1140	4	US-09-902-540-2965	Sequence 2965, Ap
990	194.5	8.2	1641	4	US-09-902-540-3948	Sequence 3948, Ap	1063	192.5	8.1	1167	4	US-09-902-540-4736	Sequence 4736, Ap
c 991	194.5	8.2	4698	1	US-07-807-043B-5	Sequence 5, Appli	1064	192.5	8.1	1446	4	US-09-902-540-3664	Sequence 3664, Ap
c 992	194.5	8.2	4698	1	US-08-299-849B-5	Sequence 5, Appli	1065	192.5	8.1	1770	4	US-09-902-540-7790	Sequence 7790, Ap
c 993	194.5	8.2	4698	2	US-08-142-368A-5	Sequence 5, Appli	1066	192.5	8.1	1905	4	US-09-902-540-3879	Sequence 3879, Ap
c 994	194.5	8.2	4698	3	US-08-967-727-5	Sequence 5, Appli	1067	192.5	8.1	2586	4	US-09-902-540-5619	Sequence 5619, Ap
c 995	194.5	8.2	4698	3	US-08-037-230D-5	Sequence 5, Appli	c1068	192.5	8.1	5246	4	US-09-799-451-474	Sequence 474, App
c 996	194.5	8.2	4698	4	US-09-583-850-5	Sequence 5, Appli	1069	192.5	8.1	9391	4	US-09-949-016-14299	Sequence 14299, A
c 997	194.5	8.2	4698	4	US-09-579-197-5	Sequence 5, Appli	c1070	192.5	8.1	13377	4	US-09-949-016-16358	Sequence 16358, A
c 998	194.5	8.2	4698	4	US-09-404-026-5	Sequence 5, Appli	1071	192.5	8.1	49225	4	US-09-902-540-1269	Sequence 1269, Ap
c 999	194.5	8.2	4698	4	US-09-312-464-5	Sequence 5, Appli	c1072	192.5	8.1	136058	4	US-09-949-016-12565	Sequence 12565, A
c1000	194.5	8.2	6935	4	US-09-902-540-865	Sequence 865, App	c1073	192.5	8.1	136480	4	US-09-949-016-17064	Sequence 17064, A
1001	194.5	8.2	7419	4	US-09-252-991A-481	Sequence 481, App	c1074	192.5	8.1	304533	4	US-09-949-016-15371	Sequence 15371, A
c1002	194.5	8.2	7449	4	US-09-252-991A-396	Sequence 396, App	c1075	192.5	8.1	304533	4	US-09-949-016-15372	Sequence 15372, A
c1003	194.5	8.2	7811	4	US-09-902-540-824	Sequence 824, App	c1076	192.5	8.1	389504	4	US-09-949-016-15372	Sequence 15372, A
c1004	194.5	8.2	14823	4	US-09-902-540-1087	Sequence 1087, Ap	1077	192	8.1	400	3	US-09-056-556-179	Sequence 1774, A
c1005	194.5	8.2	17879	4	US-09-949-016-12992	Sequence 12992, A	1078	192	8.1	400	3	US-09-072-596-174	Sequence 179, App
1006	194.5	8.2	11282	3	US-09-754-250-3	Sequence 3, Appli	1079	192	8.1	400	3	US-09-072-596-179	Sequence 179, App
1007	194	8.2	1428	4	US-09-902-540-2630	Sequence 2630, Ap	1080	192	8.1	810	1	US-08-642-255-60	Sequence 60, Appli
1008	194	8.2	1473	4	US-09-902-540-5372	Sequence 5372, Ap	1081	192	8.1	1791	1	US-09-902-540-6583	Sequence 6583, Ap
1009	194	8.2	1674	4	US-09-894-844-14	Sequence 14, Appli	1082	192	8.1	2032	4	US-09-902-540-8077	Sequence 8077, Ap
1010	194	8.2	1674	4	US-09-894-844-15	Sequence 15, Appli	1083	192	8.1	2453	4	US-09-270-767-9964	Sequence 9964, Ap
1011	194	8.2	2481	4	US-09-902-540-5228	Sequence 5228, Ap	1084	192	8.1	3595	4	US-09-902-540-3658	Sequence 3658, Ap
c1012	194	8.2	2565	4	US-09-949-016-4203	Sequence 4203, Ap	1085	192	8.1	3860	4	US-09-902-540-494	Sequence 494, App
c1013	194	8.2	2973	4	US-09-902-540-4476	Sequence 4476, Ap	c1086	192	8.1	5822	3	US-08-899-595-4	Sequence 4, Appli
c1014	194	8.2	3372	4	US-09-949-016-165	Sequence 165, App	1087	192	8.1	5822	3	US-08-899-595-5	Sequence 5, Appli
c1015	194	8.2	4219	4	US-09-902-540-519	Sequence 519, App	c1088	192	8.1	18192	4	US-09-902-540-1162	Sequence 1162, Ap
c1016	194	8.2	5972	4	US-09-949-016-14669	Sequence 14669, A	1089	192	8.1	21296	4	US-09-949-016-14504	Sequence 14504, A
1017	194	8.2	6817	4	US-09-949-016-12039	Sequence 12039, A	1090	192	8.1	21296	4	US-09-949-016-14505	Sequence 14505, A
c1018	194	8.2	6817	4	US-09-949-016-13340	Sequence 13340, A	1091	192	8.1	21296	4	US-09-949-016-15701	Sequence 15701, A
c1019	194	8.2	9521	4	US-09-902-540-953	Sequence 953, App	1092	192	8.1	21296	4	US-09-949-016-15702	Sequence 15702, A
c1020	194	8.2	11358	4	US-09-902-540-1075	Sequence 1075, Ap	1093	192	8.1	23847	4	US-09-902-540-1177	Sequence 1177, Ap
1021	194	8.2	14367	4	US-09-902-540-1113	Sequence 1113, Ap	c1094	192	8.1	44960	4	US-09-949-016-12197	Sequence 12197, A
1022	194	8.2	15593	4	US-09-949-016-17177	Sequence 17177, A	c1095	192	8.1	44960	4	US-09-949-016-17583	Sequence 17583, A
1023	194	8.2	18848	4	US-09-902-540-1174	Sequence 1174, Ap	c1096	192	8.1	51552	4	US-09-733-294A-30	Sequence 30, Appli
c1024	194	8.2	34662	4	US-09-902-540-1261	Sequence 1261, Ap	c1097	192	8.1	106256	4	US-09-949-016-16858	Sequence 16858, A
c1025	194	8.2	98701	4	US-09-949-016-15898	Sequence 15898, Ap	c1098	191.5	8.1	1098	4	US-09-170-496D-117	Sequence 117, App
c1026	194	8.2	98701	4	US-09-949-016-15899	Sequence 15899, A	1099	191.5	8.1	1839	4	US-09-902-540-6305	Sequence 6305, Ap
c1027	194	8.2	123380	4	US-09-949-016-12544	Sequence 12544, A	c1100	191.5	8.1	1841	4	US-09-902-540-383	Sequence 383, App
1028	193.5	8.2	1365	4	US-09-902-540-5489	Sequence 5489, Ap	1101	191.5	8.1	1968	4	US-09-902-540-9206	Sequence 9206, Ap
1029	193.5	8.2	2253	4	US-09-902-540-8302	Sequence 8302, Ap	1102	191.5	8.1	2082	4	US-09-818-780-67	Sequence 67, Appli
c1030	193.5	8.2	2316	4	US-09-902-540-3869	Sequence 3869, Ap	1103	191.5	8.1	2217	4	US-09-949-016-495	Sequence 495, Appli
1031	193.5	8.2	2670	4	US-09-902-540-8525	Sequence 8525, Ap	1104	191.5	8.1	4031	1	US-08-159-784-1	Sequence 1, Appli
1032	193.5	8.2	3846	4	US-09-902-540-2520	Sequence 2520, Ap	c1105	191.5	8.1	5392	2	US-08-403-852D-1	Sequence 1, Appli
c1033	193.5	8.2	4378	2	US-09-080-897-3	Sequence 3, Appli	c1106	191.5	8.1	5392	3	US-08-510-646B-1	Sequence 1, Appli
c1034	193.5	8.2	4378	3	US-09-323-735-3	Sequence 3, Appli	c1107	191.5	8.1	5392	3	US-09-231-818-1	Sequence 1, Appli

c1108	191.5	8.1	5392	4	US-09-635-359B-1	Sequence 1, Appli	c1181	190	8.0	3468	3	US-08-459-444-2	Sequence 2, Appli
c1109	191.5	8.1	8820	4	US-09-902-540-974	Sequence 974, App	c1182	190	8.0	3468	3	US-09-053-549-3	Sequence 3, Appli
c1110	191.5	8.1	12955	4	US-09-902-540-1068	Sequence 1068, Ap	c1183	190	8.0	3468	3	US-09-547-422-2	Sequence 2, Appli
c1111	191.5	8.1	16063	3	US-09-801-052-3	Sequence 3, Appli	c1184	190	8.0	3468	4	US-09-988-462-2	Sequence 2, Appli
c1112	191.5	8.1	16063	4	US-10-020-121-3	Sequence 3, Appli	c1185	190	8.0	3606	4	US-09-252-991A-15688	Sequence 15688, A
c1113	191.5	8.1	17245	4	US-09-902-540-1073	Sequence 1073, Ap	c1186	190	8.0	7661	4	US-09-902-540-912	Sequence 912, App
c1114	191.5	8.1	18471	4	US-09-902-540-1167	Sequence 1167, Ap	c1187	190	8.0	9805	4	US-09-949-016-13109	Sequence 13109, A
c1115	191.5	8.1	21511	4	US-09-902-540-1201	Sequence 1201, Ap	c1188	190	8.0	11620	4	US-09-902-540-1010	Sequence 1010, Ap
c1116	191.5	8.1	31713	4	US-09-949-016-16960	Sequence 16960, A	c1189	190	8.0	11922	4	US-09-902-540-1063	Sequence 1063, Ap
c1117	191	8.1	979	3	US-09-461-697-462	Sequence 462, App	c1190	190	8.0	12685	4	US-09-479-467A-3	Sequence 3, Appli
c1118	191	8.1	1059	4	US-09-902-540-3528	Sequence 3528, Ap	c1191	190	8.0	12907	4	US-09-949-016-16565	Sequence 16565, A
c1119	191	8.1	1307	4	US-09-023-655-293	Sequence 293, App	c1192	190	8.0	14101	4	US-09-902-540-1080	Sequence 1080, Ap
c1120	191	8.1	1323	4	US-09-902-540-3669	Sequence 3669, App	c1193	190	8.0	16265	4	US-09-902-540-1126	Sequence 1126, Ap
c1121	191	8.1	1470	4	US-09-902-540-2975	Sequence 2975, Ap	c1194	190	8.0	17977	4	US-09-949-016-12403	Sequence 12403, A
c1122	191	8.1	1773	4	US-09-902-540-7504	Sequence 7504, Ap	c1195	190	8.0	38239	4	US-09-949-016-12348	Sequence 12348, A
c1123	191	8.1	2415	4	US-09-902-540-354	Sequence 354, App	c1196	190	8.0	38252	4	US-09-949-016-13570	Sequence 13570, A
c1124	191	8.1	2709	4	US-09-949-016-3299	Sequence 3299, Ap	c1197	190	8.0	132871	4	US-09-949-016-13863	Sequence 13863, A
c1125	191	8.1	2787	4	US-09-902-540-5793	Sequence 5793, Ap	c1198	190	8.0	161607	4	US-09-949-016-12210	Sequence 12210, A
c1126	191	8.1	3489	2	US-08-728-323A-1	Sequence 1, Appli	c1199	189.5	8.0	1710	2	US-08-912-794-1	Sequence 1, Appli
c1127	191	8.1	3489	3	US-09-298-568-1	Sequence 1, Appli	c1200	189.5	8.0	1757	4	US-09-799-451-933	Sequence 933, App
c1128	191	8.1	3489	4	US-09-410-399-1	Sequence 1, Appli	c1201	189.5	8.0	2232	4	US-09-902-540-2830	Sequence 2830, Ap
c1129	191	8.1	3489	4	US-09-894-273-1	Sequence 1, Appli	c1202	189.5	8.0	2379	4	US-09-902-540-5434	Sequence 5434, Ap
c1130	191	8.1	4321	4	US-09-402-181B-6	Sequence 6, Appli	c1203	189.5	8.0	3036	4	US-09-902-540-4040	Sequence 4040, Ap
c1131	191	8.1	4695	2	US-08-231-193A-57	Sequence 57, Appl	c1204	189.5	8.0	5872	4	US-09-902-540-859	Sequence 859, App
c1132	191	8.1	4695	2	US-08-486-273A-57	Sequence 57, Appl	c1205	189.5	8.0	9455	4	US-09-949-016-15478	Sequence 15478, A
c1133	191	8.1	4695	3	US-08-940-086A-57	Sequence 57, Appl	c1206	189.5	8.0	9472	4	US-09-902-540-851	Sequence 851, App
c1134	191	8.1	4695	3	US-08-940-035A-57	Sequence 57, Appl	c1207	189.5	8.0	10216	4	US-09-902-540-976	Sequence 976, App
c1135	191	8.1	4695	3	US-08-935-105A-57	Sequence 57, Appl	c1208	189.5	8.0	13842	3	US-09-105-537-30	Sequence 30, Appl
c1136	191	8.1	4695	3	US-08-648-797-57	Sequence 57, Appl	c1209	189.5	8.0	14570	4	US-09-902-540-1012	Sequence 1012, Ap
c1137	191	8.1	4695	4	US-08-386-123-57	Sequence 57, Appl	c1210	189.5	8.0	22431	4	US-09-949-016-14099	Sequence 14099, A
c1138	191	8.1	4695	4	US-10-038-937-57	Sequence 57, Appl	c1211	189.5	8.0	34953	4	US-09-902-540-1263	Sequence 1263, Ap
c1139	191	8.1	5673	4	US-09-902-540-8259	Sequence 8259, Ap	c1212	189.5	8.0	124480	4	US-09-949-016-15921	Sequence 15921, A
c1140	191	8.1	8704	4	US-09-902-540-854	Sequence 854, App	c1213	189.5	8.0	134008	4	US-09-949-016-13841	Sequence 13841, A
c1141	191	8.1	12194	4	US-09-902-540-1091	Sequence 1091, Ap	c1214	189	8.0	1383	4	US-09-902-540-101	Sequence 101, App
c1142	191	8.1	13226	4	US-09-902-540-1132	Sequence 1132, Ap	c1215	189	8.0	1506	4	US-09-902-540-9624	Sequence 9624, Ap
c1143	191	8.1	15418	4	US-08-783-203-1	Sequence 1, Appli	c1216	189	8.0	3772	4	US-09-962-665-5	Sequence 5, Appli
c1144	191	8.1	15418	4	US-09-994-427A-1	Sequence 1, Appli	c1217	189	8.0	3772	4	US-09-963-333-5	Sequence 5, Appli
c1145	191	8.1	15418	4	US-09-244-438-1	Sequence 1, Appli	c1218	189	8.0	3772	4	US-09-962-677-5	Sequence 5, Appli
c1146	191	8.1	15782	4	US-09-902-540-1094	Sequence 1094, Ap	c1219	189	8.0	9278	1	US-08-243-542-9	Sequence 9, Appli
c1147	191	8.1	32207	2	US-08-770-379-20	Sequence 20, Appl	c1220	189	8.0	9278	1	US-08-477-407-9	Sequence 9, Appli
c1148	191	8.1	32207	3	US-08-757-669A-20	Sequence 20, Appl	c1221	189	8.0	9278	1	US-08-484-355-9	Sequence 9, Appli
c1149	191	8.1	32207	3	US-08-230-371A-20	Sequence 20, Appl	c1222	189	8.0	13299	4	US-09-902-540-968	Sequence 968, App
c1150	191	8.1	50937	3	US-09-428-517-1	Sequence 1, Appli	c1223	189	8.0	13624	4	US-09-902-540-1053	Sequence 1053, Ap
c1151	190.5	8.1	1437	4	US-09-902-540-5173	Sequence 5173, Ap	c1224	189	8.0	13855	4	US-09-902-540-1117	Sequence 1117, Ap
c1152	190.5	8.1	1596	4	US-09-949-016-4501	Sequence 4501, Ap	c1225	189	8.0	15095	4	US-09-902-540-1077	Sequence 1077, Ap
c1153	190.5	8.1	1914	4	US-09-248-796A-5031	Sequence 5031, Ap	c1226	189	8.0	17228	4	US-09-902-540-1170	Sequence 1170, Ap
c1154	190.5	8.1	2657	4	US-09-270-767-13823	Sequence 13823, A	c1227	189	8.0	23802	4	US-09-949-016-12107	Sequence 12107, A
c1155	190.5	8.1	2681	3	US-08-928-213B-7	Sequence 7, Appli	c1228	189	8.0	23803	4	US-09-949-016-15878	Sequence 15878, A
c1156	190.5	8.1	4524	2	US-08-845-998-7	Sequence 7, Appli	c1229	189	8.0	25497	4	US-09-902-540-1224	Sequence 1224, Ap
c1157	190.5	8.1	4524	3	US-09-206-537-7	Sequence 7, Appli	c1230	189	8.0	27825	4	US-09-949-016-17483	Sequence 17483, A
c1158	190.5	8.1	4524	3	US-09-430-854-7	Sequence 7, Appli	c1231	189	8.0	32207	2	US-08-770-379-20	Sequence 20, Appl
c1159	190.5	8.1	4955	4	US-09-902-540-553	Sequence 553, App	c1232	189	8.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
c1160	190.5	8.1	5764	4	US-09-902-540-693	Sequence 693, App	c1233	189	8.0	32207	3	US-09-230-371A-20	Sequence 20, Appl
c1161	190.5	8.1	7007	4	US-09-949-016-13645	Sequence 13645, Ap	c1234	188.5	8.0	1260	4	US-09-902-540-9533	Sequence 9533, Ap
c1162	190.5	8.1	7130	4	US-09-949-016-16128	Sequence 16128, A	c1235	188.5	8.0	1323	4	US-09-023-655-813	Sequence 813, App
c1163	190.5	8.1	9551	1	US-08-056-200-93	Sequence 93, Appl	c1236	188.5	8.0	1566	4	US-09-902-540-4578	Sequence 4578, Ap
c1164	190.5	8.1	9551	2	US-08-800-644-93	Sequence 93, Appl	c1237	188.5	8.0	1717	4	US-09-634-137-3	Sequence 3, Appli
c1165	190.5	8.1	12191	4	US-09-949-016-16237	Sequence 16237, A	c1238	188.5	8.0	1899	4	US-09-902-540-4564	Sequence 4564, Ap
c1166	190.5	8.1	17654	4	US-09-902-540-1161	Sequence 1161, Ap	c1239	188.5	8.0	2210	3	US-08-464-700-1	Sequence 1, Appli
c1167	190.5	8.1	31467	4	US-09-949-016-13134	Sequence 13134, A	c1240	188.5	8.0	2341	4	US-09-902-540-395	Sequence 395, App
c1168	190.5	8.1	31868	4	US-09-949-016-11907	Sequence 11907, A	c1241	188.5	8.0	2555	4	US-09-866-028-68	Sequence 68, Appl
c1169	190.5	8.1	37474	4	US-09-952-060-26	Sequence 26, Appl	c1242	188.5	8.0	2555	4	US-09-944-457-68	Sequence 68, Appl
c1170	190.5	8.1	72455	4	US-09-949-016-13793	Sequence 13793, A	c1243	188.5	8.0	4263	4	US-09-902-540-4659	Sequence 4659, Ap
c1171	190.5	8.1	104745	1	US-09-949-016-12115	Sequence 12115, A	c1244	188.5	8.0	7316	4	US-09-949-016-13935	Sequence 13935, A
c1172	190	8.0	702	1	US-08-458-568A-3	Sequence 3, Appli	c1245	188.5	8.0	8540	4	US-09-902-540-944	Sequence 944, App
c1173	190	8.0	831	3	US-08-506-553C-24	Sequence 24, Appl	c1246	188.5	8.0	9035	4	US-09-902-540-1084	Sequence 1084, Ap
c1174	190	8.0	1587	4	US-09-023-655-1192	Sequence 1192, Ap	c1247	188.5	8.0	10835	4	US-09-902-540-1031	Sequence 1031, Ap
c1175	190	8.0	1751	4	US-09-902-540-2529	Sequence 2529, Ap	c1248	188.5	8.0	15378	3	US-08-785-420-1	Sequence 1, Appli
c1176	190	8.0	1881	3	US-09-029-348-20	Sequence 20, Appl	c1249	188.5	8.0	18031	4	US-09-902-540-1180	Sequence 1180, Ap
c1177	190	8.0	3468	1	US-07-951-715A-2	Sequence 2, Appli	c1250	188.5	8.0	25431	4	US-09-949-016-13234	Sequence 13234, A
c1178	190	8.0	3468	2	US-08-459-448A-2	Sequence 2, Appli	c1251	188.5	8.0	29384	4	US-09-902-540-1229	Sequence 1229, Ap
c1179	190	8.0	3468	3	US-08-459-595A-2	Sequence 2, Appli	c1252	188	8.0	1242	4	US-09-902-540-6329	Sequence 6329, Ap
c1180	190	8.0	3468	3	US-08-459-504B-2	Sequence 2, Appli	c1253	188	8.0	1362	4	US-09-902-540-5154	Sequence 5154, Ap

1254	188	8.0	1560	3	US-09-453-702B-264	Sequence 264, App	c1327	186.5	7.9	21511	4	US-09-902-540-1201	Sequence 1201, Ap
c1255	188	8.0	1767	4	US-09-016-434-1488	Sequence 1488, Ap	1328	186.5	7.9	25497	4	US-09-902-540-1224	Sequence 1224, Ap
1256	188	8.0	2127	4	US-09-818-780-75	Sequence 75, Appl	c1329	186.5	7.9	59252	4	US-09-949-016-12150	Sequence 12150, A
1257	188	8.0	2133	4	US-09-902-540-8854	Sequence 8854, Ap	c1330	186.5	7.9	59252	4	US-09-949-016-15374	Sequence 15374, A
1258	188	8.0	2448	4	US-09-902-540-4835	Sequence 4835, Ap	1331	186.5	7.9	198632	4	US-09-949-016-17393	Sequence 17393, A
1259	188	8.0	2755	3	US-08-406-030A-3	Sequence 3, Appli	1332	186.5	7.9	198632	4	US-09-949-016-17393	Sequence 17393, A
c1260	188	8.0	4496	3	US-08-765-907A-6	Sequence 6, Appli	c1333	186	7.9	865	4	US-09-270-767-11042	Sequence 11042, A
c1261	188	8.0	4496	3	US-08-987-614A-6	Sequence 6, Appli	1334	186	7.9	1010	4	US-09-270-767-12954	Sequence 12954, A
c1262	188	8.0	5006	4	US-09-620-312D-310	Sequence 310, App	1335	186	7.9	1095	4	US-09-902-540-5522	Sequence 5522, Ap
1263	188	8.0	5064	4	US-09-774-528-224	Sequence 224, App	c1336	186	7.9	1098	4	US-09-170-496D-225	Sequence 225, App
1264	188	8.0	5481	4	US-09-902-540-7351	Sequence 7351, Ap	1337	186	7.9	1296	4	US-09-902-540-7937	Sequence 7937, Ap
c1265	188	8.0	5781	4	US-09-902-540-711	Sequence 711, App	1338	186	7.9	1423	4	US-09-799-451-728	Sequence 728, App
c1266	188	8.0	5802	4	US-09-902-540-702	Sequence 702, App	1339	186	7.9	1431	4	US-09-902-540-3996	Sequence 3996, Ap
c1267	188	8.0	9757	1	US-08-093-453B-1	Sequence 1, Appli	1340	186	7.9	1464	4	US-09-902-540-7537	Sequence 7537, Ap
c1268	188	8.0	9759	1	US-08-459-041A-1	Sequence 1, Appli	1341	186	7.9	1497	4	US-09-902-540-9440	Sequence 9440, Ap
c1269	188	8.0	9759	3	US-08-999-733-1	Sequence 1, Appli	1342	186	7.9	2176	6	5320958-1	Patent No. 5320958
c1270	188	8.0	15872	3	US-09-105-537-1	Sequence 1, Appli	1343	186	7.9	2176	6	5320958-1	Patent No. 5320958
c1271	188	8.0	15872	4	US-09-091-609-1	Sequence 1, Appli	1344	186	7.9	2266	4	US-09-799-451-917	Sequence 917, App
c1272	188	8.0	15872	4	US-09-091-609-3	Sequence 3, Appli	c1345	186	7.9	3337	1	US-08-072-610-1	Sequence 1, Appli
c1273	188	8.0	18917	4	US-09-949-016-13129	Sequence 13129, A	c1346	186	7.9	3337	2	US-08-719-822B-1	Sequence 1, Appli
c1274	188	8.0	18917	4	US-09-949-016-13130	Sequence 13130, A	c1347	186	7.9	3337	3	US-09-092-458-1	Sequence 1, Appli
c1275	188	8.0	18917	4	US-09-949-016-13131	Sequence 13131, A	c1348	186	7.9	3337	4	US-08-719-821C-1	Sequence 1, Appli
1276	188	8.0	28493	4	US-09-902-540-1241	Sequence 1241, Ap	1349	186	7.9	5008	3	US-09-110-517-1	Sequence 1, Appli
c1277	188	8.0	119032	4	US-09-949-016-12160	Sequence 12160, A	1350	186	7.9	7518	4	US-09-902-540-870	Sequence 870, App
c1278	188	8.0	119032	4	US-09-949-016-17268	Sequence 17268, A	1351	186	7.9	7546	4	US-09-902-540-801	Sequence 801, App
1279	187.5	7.9	540	4	US-09-248-796A-8249	Sequence 8249, Ap	1352	186	7.9	8025	4	US-09-902-540-877	Sequence 877, App
1280	187.5	7.9	1479	4	US-09-902-540-7414	Sequence 7414, Ap	1353	186	7.9	13904	4	US-09-902-540-1076	Sequence 1076, Ap
1281	187.5	7.9	2455	4	US-09-902-540-8628	Sequence 8628, Ap	1354	186	7.9	14330	4	US-09-902-540-1009	Sequence 1009, Ap
1282	187.5	7.9	2542	4	US-09-902-540-6580	Sequence 6580, Ap	1355	186	7.9	28194	4	US-09-902-540-1250	Sequence 1250, Ap
c1283	187.5	7.9	2681	3	US-08-928-213B-7	Sequence 7, Appli	1356	186	7.9	40546	4	US-09-949-016-12847	Sequence 12847, A
1284	187.5	7.9	2754	4	US-09-902-540-5587	Sequence 5587, Ap	1357	186	7.9	40546	4	US-09-949-016-12915	Sequence 12915, A
1285	187.5	7.9	3312	4	US-09-902-540-493	Sequence 493, App	1358	186	7.9	120727	4	US-09-949-016-15787	Sequence 15787, A
1286	187.5	7.9	5245	4	US-09-902-540-714	Sequence 714, App	1359	186	7.9	120727	4	US-09-949-016-15788	Sequence 15788, A
c1287	187.5	7.9	5752	4	US-09-902-540-746	Sequence 746, App	1360	186	7.9	129658	4	US-09-949-016-17195	Sequence 17195, A
1288	187.5	7.9	7065	4	US-09-874-923-115	Sequence 115, App	1361	185.5	7.9	486	4	US-09-639-207-13	Sequence 13, Appl
c1289	187.5	7.9	7661	4	US-09-902-540-912	Sequence 912, App	1362	185.5	7.9	1245	4	US-09-902-540-4829	Sequence 4829, Ap
c1290	187.5	7.9	34316	4	US-09-902-540-1036	Sequence 1036, Ap	1363	185.5	7.9	1323	4	US-09-902-540-6143	Sequence 6143, Ap
c1291	187.5	7.9	38653	4	US-09-922-445-1	Sequence 1, Appli	c1364	185.5	7.9	1458	4	US-09-902-540-9498	Sequence 9498, Ap
1292	187.5	7.9	41927	4	US-09-902-540-1257	Sequence 1257, Ap	c1365	185.5	7.9	1506	4	US-09-902-540-294	Sequence 294, App
1293	187.5	7.9	77626	4	US-09-902-540-1268	Sequence 1268, Ap	c1366	185.5	7.9	1614	4	US-09-616-289-45	Sequence 45, Appl
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c1295	187	7.9	2526	4	US-09-758-282B-262	Sequence 262, App	1368	185.5	7.9	1893	4	US-09-902-540-3781	Sequence 3781, Ap
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1298	187	7.9	3279	4	US-09-902-540-366	Sequence 366, App	1371	185.5	7.9	2502	4	US-09-902-540-3862	Sequence 3862, Ap
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c1303	187	7.9	5165	4	US-09-949-016-12815	Sequence 12815, A	c1376	185.5	7.9	4335	3	US-08-974-549A-6	Sequence 6, Appli
c1304	187	7.9	6285	4	US-09-949-016-17179	Sequence 17179, A	c1377	185.5	7.9	4335	4	US-09-721-456-6	Sequence 6, Appli
c1305	187	7.9	6286	4	US-09-902-540-862	Sequence 862, App	1378	185.5	7.9	9191	4	US-09-902-540-918	Sequence 918, App
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1307	187	7.9	10182	4	US-09-902-540-1030	Sequence 1030, Ap	c1380	185.5	7.9	12567	4	US-09-949-016-16843	Sequence 16843, A
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1315	187	7.9	2145	4	US-09-902-540-8236	Sequence 8236, Ap	c1388	185.5	7.9	229354	4	US-09-705-400-64	Sequence 64, Appli
1316	186.5	7.9	2154	3	US-09-488-856A-3	Sequence 3, Appli	1389	185	7.8	888	3	US-08-765-907A-2	Sequence 2, Appli
1317	186.5	7.9	2352	4	US-09-902-540-4536	Sequence 4536, Ap	c1390	185	7.8	888	4	US-09-987-614A-2	Sequence 2, Appli
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## ALIGNMENTS

## RESULT 1

US-09-673-395A-39  
; Sequence 39, Application US/09673395A  
; Patent No. 6620923  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE  
; FILE REFERENCE: ALBRE-12  
; CURRENT APPLICATION NUMBER: US/09/673,395A  
; CURRENT FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 637  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 914  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-673-395A-39

Alignment Scores:  
Pred. No.: 1,23e+28  
Score: 669.00  
Percent Similarity: 100.00%  
Best Local Similarity: 98.39%  
Query Match: 28.31%  
DB: 4

US-10-063-699-52 (1-440) x US-09-673-395A-39 (1-914)

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RESULT 2
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
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US-10-063-699-52 (1-440) x US-09-103-840A-2 (1-4403765)
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Db 3936617 ACCGAGGCGCGCGCGCGCTCTCTAGCTACCAACGGCGGCGGCGCGCGCGCGCGCG 3936676
Qy 132 TrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSerGly----- 146
Db 3936677 ACCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3936736
Qy 147 -----GlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGly-----GlnGly 161
Db 3936737 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGT 3936796
Qy 162 GlnGlyAsnProGlyGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsn----- 179
Db 3936797 CAAGTGTGTCGCGCGGTGCGCGGACCGCGGCGCAACCGC-----GGCAATATCAC 3936850
Qy 180 -----SerAlaGlySerPheGlyMetAsnProGlnGlyAla 191
Db 3936851 GGCGGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGC 3936910
Qy 192 ProTrpGlnGlyGlyAsnGlyGlyProAsnPheGlyThrAsnThrGln---Gly 210
Db 3936911 GCCGCGCGCGCAAGCGCGCACCGGTGC-----GGGACCGGGGTGTCAGGGTGC 3936958
Qy 211 AlaValAlaGlnProGlyTyrGlySerValArgAlaSerAsnGlnAsnGluGlyCysThr 230
Db 3936959 GCCGCGCGCGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTGC 3937018
Qy 231 AsnProProSerGlySerGlyGlyGlySerSerAsnSerGly----- 245
Db 3937019 GTCCCGCGCGCTCCGCTGGACAAAGCGGTAAACGCTGGCGGTGTCGGCGCGCGCGCG 3937078
Qy 246 -----GlyGlySerGlnSerGlnSerGlySerSerGlySerGly 258
Db 3937079 GGTGAGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3937138
Qy 259 SerAsnGlyAspAsnAsnGlySerSerSerGlyGlySerSerSerGlySerSerSer 278
Db 3937139 GGTAAACGGCGGCAACCGTAATTCGGCAATGGCACCGCGCGCGCTGGCGCGCAACGGTGT 3937198
Qy 279 GlySerSerSerGlyGlySerSerGly---GlySerSerGlyGlySerSerGlyAsnSer 297
Db 3937199 GGTGCTTAACGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3937258
Qy 298 GlyGlySerArgGlyAspSerGlySerGluSerSerTrpGlySerSerThrGlySerSer 317
Db 3937259 GGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3937318
Qy 318 SerGlyAsnHisGlyGlySerGly-----GlyGlyAsnGlyHisLysPro 332
Db 3937319 AACGGCGCAACGGCGCGCAACGGCGCGCATCGCCGGCATGGCGCGCAAC----- 3937366
Qy 333 GlyCysGluLysProGlyAsnGluAlaArgGlySerGlyGluSerGlyIleGlnGlyPhe 352
Db 3937367 -----GGCGGTGCGCGGACCGCGCGCAACCGCGCGCAACCGCGCGCGCG 3937411
Qy 353 ArgGlyGlnGlyValSerSerAsnMetArgGluIleSerLysGluGlyAsnArgLeuLeu 372
Db 3937412 GGCGGCAACCGC-----GGCAACCGCGCGCATG 3937438
Qy 373 GlyGlySerGlyAspAsnTyrArgGlyGlnGlySerSerTrpGlySerGlyGlyGlyAsp 392
Db 3937439 GGCGGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3937498
Qy 393 AlaValGlyGlyValAsnThrValAsnSerGluThrSerProGly 407
```





```
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 1,08e-12 Length: 4411529
Score: 442.00 Matches: 148
Percent Similarity: 41.69% Conservative: 40
Best Local Similarity: 32.82% Mismatches: 176
Query Match: 18.71% Indels: 87
DB: 3 Gaps: 20

US-10-063-699-52 (1-440) x US-09-103-840A-1 (1-4411529)

Qy 17 GlySerGlyGluAlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGly 36
Dy 3739200 GGCACGCGCGCGCGCGCGC---AAGGGCGGCAACCGCGCGCGCGCGCGCGT 3739144
Qy 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGlyGlyValGly-----LysAla 54
Dy 3739143 -----TTGGGC-----GGTAGCCCGGCTCCGGCGCGCGCGCGCAATGGCGGT 3739099
Qy 55 IleGlyLysGluAlaGlyGlyAlaAlaGly-----64
Dy 3739098 ATCGGCACCGACGCGCGCGGTGCCGAGGGCGCGGTGGCGGTAAACGGCGGTAGC 3739039
Qy 65 SerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGlyThrGlyValArg 84
Dy 3739038 AGCAAAACGACGACCGCGCAACCGCGCGGTCCCGGTGGTCCCGCGGTAAATGGGGGCACT 3738979
Qy 85 GlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHis 104
Dy 3738978 GGCTTCAACGCGCGCGCGGTGTCTGGCGGCGCGCGCGCAACGGCGGTGTCTCGCGCGGTG 3738919
Qy 105 AlaLeuGlyAsn----ThrGlyHisGluLeuGlyArgGlnAlaGluAspValIleArgHis 123
Dy 3738918 TCCTTCGGCAACGCTGTGGCGGCGGACGGCGGCAACGGCGGCAACGGC-----GGCCAC 3738865
Qy 124 GlyAlaAspAlaValArgGly-----SerTrpGlnGlyValProGlyHisSerGlyAla 141
Dy 3738864 GGCGCGCACGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGC 3738805
Qy 142 TrpGluThrSerGly-----GlyHisGlyIlePheGlySerGlnGly 155
Dy 3738804 GCCAGCGCTCAGCGGTCTCAAGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738745
Qy 156 GlyLeuGlyGlyGlnGlyAsnProGlyGlyLeuGlyThrProTrpValHisGly 175
Dy 3738744 GGCAACGCGCGCAACGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738703
Qy 176 TyrProGlyAsnSerAlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGln 195
Dy 3738702 GGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738646
Qy 196 GlyGlyAsnGlyGlyProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnPro 215
Dy 3738645 GCGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738586
Qy 216 GlyTyrGlySerValArgAlaSerAsnGlnAsnGluGlyCysThrAsnProProSer 235
Dy 3738585 GGT---GGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738529
Qy 236 GlySerGlyGlyLysSerAsnSerGly-----GlyGlySerGlySerGlnSerGly 253
Dy 3738528 GCGCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738469
Qy 254 SerSerGlySerGlySerAsnGlyAspAsn---AsnAsnGlySerSerSerGly-Glyse 272
Dy 3738468 AACGGCGCGCGCGGTGTCTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738409
Qy 272 rSerSerGlySerSerGlySerSerSerGlyGlySerSerGly-----287
Dy 3738408 CGGACGCGGTGTCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738349
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Qy 288 -----GlySerSerGlyGlySerSerGlyAenSerGly-----298
Dy 3738348 TGGTGGCGGTGGCAACGGCGGTGCGCGCGCAACGGTGGCGGTGGCGATCGCGGCAACGC 3738289
Qy 299 -----GlySerArgGlyAs 303
Dy 3738288 CGGCTCAGGCGGCAATGGCGGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738229
Qy 303 pSerGlySerGluSerSerTrpGlySerSerThrGlySerSerThrGlySerSerGlyAsnHisGlyG1 323
Dy 3738228 CGCGGCGGCAAGGCGCGCGCGCTCGCGCAACGGCGGTTCAGCAACGGCAACGCTCGCGG 3738169
Qy 323 ySerGlyGlyGlyAsnGlyHisLysProGlyCysGluLysProGlyAsnGluAlaArgG1 343
Dy 3738168 TGGCAACCGCGGTAAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3738109
Qy 343 ySerGlyGluSerGlyIleGlnGlyPheArgGlyGlnGlyValSerSerAsnMetArgG1 363
Dy 3738108 CGCGGCGCAGGTGGCCAGGCGGTGGTTCGTGGCACCAGCGGCGCAGC-----3738063
Qy 363 uIleSerLysGluGlyAsnArgLeuLeuGlyGlySerGlyAspAsnTrpArgGlyGlnG1 383
Dy 3738062 -----GGCAGCGGCATTGGCGCGCGCGCGCGCGCGCGCAAC---GGCGGCAACGC 3738019
Qy 383 ySerSerTrpGlySerGly-----GlyGlyAspAlaValGlyGlyVa 397
Dy 3738018 CGCGCGCGCGCGCACCGCGCGTCTGTGGCGCGCGCGCGCGCGCGCGCGCGCGG---GGCAACGC 3737962
Qy 397 lAsnThrValAsnSerGluThrSerProGly 407
Dy 3737961 TGACCACGGTGGCGCTGCCACCAACCGCGGC 3737931
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## RESULT 5

```
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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## Alignment Scores:

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Pred. No.: 1,22e-12 Length: 4403765
Score: 441.00 Matches: 147
Percent Similarity: 40.04% Conservative: 36
Best Local Similarity: 32.17% Mismatches: 181
Query Match: 18.66% Indels: 93
DB: 3 Gaps: 19
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US-10-063-699-52 (1-440) x US-09-103-840A-2 (1-4403765)

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Qy 17 GlySerGlyGluAlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGly 36
Dy 3731493 GGCACGCGCGCGCGCGCGCGC---AAGGGCGGCAACCGCGCGCGCGCGCGTGGT 3731437
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Qy 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGluGlyValGly-----LysAla 54
Db 3731436 -----TTGGGC-----GGTACCGCCGCTCCCGCGCGCGGCAATGGCGGT 3731392
Qy 55 IleGlyLysGluAlaGlyGlyAlaAlaGly-----64
Db 3731391 ATCGGACCGGCGCGCGGTGCGCGAGGGCCGGTGGCGGTAAACGGCGGTAGC 3731332
Qy 65 SerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGlyThrGlyValArg 84
Db 3731331 AGCAAAAGCAGCACCCGCGCAACCGCGCTCCGGTGGTGGCGGTAAATGGGGCACT 3731272
Qy 85 GlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHis 104
Db 3731271 GGCCTCAACGCGCGCGGTGCTGGCGGGCGCGCGCAACGCGCGGTGTCGCGGGGTG 3731212
Qy 105 AlaLeuGlyAsn---ThrGlyHisGluLeuGlyArgGlnAlaGluAspValIleArgHis 123
Db 3731211 TCCTTCGCAACGCTGTGGCGCGCGACGCGCGCAACCGCGCGCAACCGG-----GGCCAC 3731158
Qy 124 GlyAlaAspAlaValArgGly-----SerTrpGlnGlyValProGlyHisSerGlyAla 141
Db 3731157 GCGCGCACGCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3731098
Qy 142 TrpGluThrSerGly-----GlyHisGlyIlePheGlySerGlnGly 155
Db 3731097 GCCAGCGGCTCAGCGCTCGTCAACGTCACCGCGCGCGCGCGCGCGCGCGCAATGGC 3731038
Qy 156 GlyLeuGlyGlyGlnGlyGlnGlyAsnProGlyGlyLeuGlyThrProTrpValHisGly 175
Db 3731037 GGCACCGCGCGCAACGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730996
Qy 176 TyrProGlyAsnSerAlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGln 195
Db 3730995 GGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730939
Qy 196 GlyGlyAsnGlyGlyProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnPro 215
Db 3730938 GCGCGCAACGCGCGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730879
Qy 216 GlyTyrGlySerValArgAlaSerAsnGlnAsnGlnGlyCysThrAsnProProSer 235
Db 3730878 GGT---GGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730822
Qy 236 GlySerGlyGlyGlySerAsnSerGlyGlyGlySerGlySer-----250
Db 3730821 GCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730762
Qy 250 -----250
Db 3730761 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730702
Qy 251 -----Gln-SerGlySerSerGlySerGlySerGlySerAsnGlyAspAs 263
Db 3730701 CAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730642
Qy 263 AsnAsnGlySerSerGlyGlySerSerGlySerSerGlySerSerGlySerSerGly 283
Db 3730641 CGGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730582
Qy 283 GlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGly 298
Db 3730581 TGGCGATCCGCGCAACCGCGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730522
Qy 299 ---GlySerArgGlyAspSerGlySerGlySerGlySerTrpGlySerSerThrGlySer 317
Db 3730521 CCCTGGCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730462
Qy 317 rSerGlyAsnHisGlyGlySerGlyGlyGlyAsnGlyHisLysProGlyCysGluLysPr 337
Db 3730461 CAACGGCAACGCTCGCGTGGCAACCGCGGTAAACGGCGCGCGCGCGCGCGCGCGCG 3730402
Qy 337 cGlyAsnGluAlaArgGlySerGlyGlySerGlyIleGlnGlyPheArgGlyGlnGly 357
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Db 3730401 CGCGCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730342
Qy 357 lSerSerAsnMetArgGluIleSerLysGluGlyAsnArgLeuLeuGlyGlySerGlyAs 377
Db 3730341 CAGC-----GGCAGCGCGCATTTGGCGCGCGCGCGCGCGCGCG 3730309
Qy 377 pAsnTyrArgGlyGlnGlySerSerTrpGlySerGly-----GlyGln 391
Db 3730308 CAAC---GGCGGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3730252
Qy 391 yAspAlaValGlyGlyValAsnThrValAsnSerGluThrSerProGly 407
Db 3730251 CGACGG---GGCAACGCTGACCAACGCGTGGCGCTGCCACCAACCGCGCG 3730206
RESULT 6
US-09-249-585A-2
; Sequence 2, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
Alignment Scores:
Pred. No.: 9,88e-13 Length: 1926
Score: 383.00 Matches: 119
Percent Similarity: 40.10% Conservative: 35
Best Local Similarity: 30.99% Mismatches: 186
Query Match: 16.21% Indels: 44
DB: 3 Gaps: 13
US-10-063-699-52 (1-440) x US-09-249-585A-2 (1-1926)
Qy 17 GlySerGlyGluAlaGlyProLeuGlnSerGlyGluSerThrGlyThrAsnIleGly 36
Db 73 GGCTCCGCGCGCGCATGTGGACCTCAAGAAGAGGG-----GGTGATAACCATGGA 120
Qy 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGly 56
Db 121 CGAGGACGGGAAGAGACCGAGGA-----CGAGGAGCGGAAGACCA---GGA 165
Qy 57 LysGluAlaGlyGlyAlaAlaGly-----SerLys 66
Db 166 GCCCGCGCGCGCTCAGGATCAGGCGCAAGACATAGAGATGGTGTCCGAGACCCCAAAA 225
Qy 67 ValSerGluAlaLeuGly-----GlnGlyThrArgGluAlaValGlyThrGlyValArgGln 85
Db 226 CGTCCAAGTTGCATTGGCTTCAAGGGACCCACCGTGGAAACAGGAGCAGGAGCA----- 279
Qy 86 ValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHisAla 105
Db 280 -----GGACCGGAGCGCGCGAGCAGGAGGCGCGAGGAGGAGGAGGAGGAGGAGCA 333
Qy 106 LeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGlyAla 125
Db 334 GGAGGAGGCGCGAGGAGGCGCGAGGAGG-----GCAGGAGGAGGCGCA 372
Qy 126 AspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSer 145
```







```
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/10903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 5452
; TYPE: DNA
; ORGANISM: VEBNA
US-09-130-114-1

Alignment Scores:
Pred. No.: 2,71e-12 Length: 5452
Score: 383.00 Matches: 119
Percent Similarity: 40.10% Conservative: 35
Best Local Similarity: 30.99% Mismatches: 186
Query Match: 16.21% Indels: 44
DB: 2 Gaps: 13

US-10-063-699-52 (1-440) x US-09-130-114-1 (1-5452)
QY 17 GlySerGlyGluAlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGly 36
DB 2349 GGCTCCGGGGGCGAGTGGACCTCAAGAGAGAGG-----GGTGATTAACCATGGA 2302
QY 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGly 56
DB 2301 CGAGGACGGGGAAGAGGACGAGCA-----CGAGGAGGCGGAAGACCA---GGA 2257
QY 57 LysGluAlaGlyClyAlaAlaGly-----SerLys 56
DB 2256 GCCCGGGCGGCTCAGGATCAGCGGCCAAGACATAGAGATGGTGTCCGAGAGACCCCAAAA 2197
QY 67 ValSerGluAlaLeuGly---GlnGlyThrArgGluAlaValGlyThrGlyValArgGln 85
DB 2196 CGTCCAGTTGCTTGGCTGCAAGGGACCCACGCTGGACAGGAGGAGCA-----2143
QY 86 ValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyClyAlaAlaHisAla 105
DB 2142 -----CGAGCGGAGGGGCGAGGACGAGGAGGCGGAGGAGGAGGAGGAGGAGCA 2089
QY 106 LeuGlyAsnThrGlyHisGlyLeuGlyArgGlnAlaGluAspValIleArgHisGlyAla 125
DB 2088 CGAGGAGGCGGAGGAGGCGGAGGAGG-----GCAGGAGGCGGCA 2050
QY 126 AspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSer 145
DB 2049 GGAGCA-----GGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCA 1996
QY 146 GlyGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGlyGlnGlyGln---GlyAsn 164
DB 1995 CGAGCAGGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1936
QY 165 ProGlyGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSerIleGlySerPhe 184
DB 1935 GCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1876
QY 185 GlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsnGlyClyProAsnPhe 204
DB 1875 GGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCA 1816
QY 205 GlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerValArgAlaSerAsn 224
DB 1815 CGAGCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1756
QY 225 GlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyCysSerSerAsnSer 244
DB 225 GlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyCysSerSerAsnSer 244
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DB 1755 GGGGCGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCA 1696
QY 245 GlyGlyGlySerGlySerGlnSerGlySerGlySerGlySerGlySerAsnGlyAspAsnAsn 264
DB 1695 CGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1636
QY 265 AsnGlySerSerSerGlySerSerSerGlySerSerSerGlySerSerSerGlySerSerGly 284
DB 1635 GCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1576
QY 285 SerSerGlyGlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySer 303
DB 1575 GGGGCGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1516
QY 304 SerGlySerGluSerSerTrpGlySerSerThrGlySerSerSerGlySerSerGlySer 323
DB 1515 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1456
QY 324 SerGlyGlyGlyAsnGlyHisIleProGlyCysGluLysProGlyAsnGluAlaArgGly 343
DB 1455 CGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1408
QY 344 SerGlyGluSerGlyIleGlnGlyPheArgGlyGlnGlyValSerSerAsnMetArgGlu 363
DB 1407 CGAGGAGGTAGT-----CGAGGCGGGGTCTGAGGAGGTAGTGGAGGCGCGCGGGGT 1357
QY 364 IleSerLysGluGlyAsnArgLeuLeuGlyGlySerGlyAspAsnTrpArgGlyGlnGly 383
DB 1356 AGAGGACCTGAA-----AGAGCCAGGCGGGGAGTCTGTAAAGAGCCAGGCGGAGAGGT 1303
QY 384 SerSerTrpGly 387
DB 1302 CGTGGACGTGGA 1291

RESULT 11
US-09-647-344A-14/C
; Sequence 14, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 14
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pShuttle
US-09-647-344A-14

Alignment Scores:
Pred. No.: 4,26e-12 Length: 8705
Score: 383.00 Matches: 119
Percent Similarity: 40.10% Conservative: 35
Best Local Similarity: 30.99% Mismatches: 186
Query Match: 16.21% Indels: 44
DB: 4 Gaps: 13

US-10-063-699-52 (1-440) x US-09-647-344A-14 (1-8705)
QY 17 GlySerGlyGluAlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGly 36
DB 8214 GGCTCCGGGGGCGAGTGGACCTCAAGAGAGAGG-----GGTGATTAACCATGGA 8167
QY 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGly 56
DB 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGly 56
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Db      8166  CGAGGACGGGGAAGAGCAGGACGGA-----CGAGGAGCGCGGAAGACCA---GGA 8122
Qy      57    LysGluAlaGlyGlyAlaAlaGly-----Sertlys 66
Db      8121  GCGCCGGCGGCTCAGGATCGGCGCAAGACATAGAGATGGTCTCCGAGACCCCAAAA 8062
Qy      67    ValSerGluAlaLeuGly---GlnGlyThrArgGluAlaValGlyThrGlyValArgGln 85
Db      8061  CGTCCAAGTTGATTGGCTGCAAGGGGACCCCGTGGACAGGACGAGCA----- 8008
Qy      86    ValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHisAla 105
Db      8007  -----GGAGCGGGGAGGGGCGAGGACGAGGAGGGGCGAGGAGGCGGCGAGGAGCA 7954
Qy      106   LeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGlyAla 125
Db      7953  GGAGGAGGGGCGAGGAGGGGCGAGGAG-----GCAGGAGGGGCGCA 7915
Qy      126   AspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSer 145
Db      7914  GGAGCA-----GGAGGAGGGGCGAGGACGAGGAGGGGCGAGGAGGGGCGCA 7861
Qy      146   GlyGlyHisGlyIlePheGlySerGlnGlyLeuGlyGlyGlnGlyGln---GlyAsn 164
Db      7860  CGAGCAGGAGGAGGGGCGAGGACGAGGAGGGGCGAGGAGGGGCGAGGAGGAGGGG 7801
Qy      165   ProGlyGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSerAlaGlySerPhe 184
Db      7800  GCAGGAGGGGCGAGGAGGGGCGAGGACGAGGAGGGGCGAGGAGGGGCGAGGAGGG 7741
Qy      185   GlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsnGlyGlyProProAsnPhe 204
Db      7740  GGGGCGAGGAGGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGCA 7681
Qy      205   GlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerValArgAlaSerAsn 224
Db      7680  CGAGCAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGAGGA 7621
Qy      225   GlnAsnGluGlyCysThrAsnProProProSerGlySerGlyGlySerSerAsnSer 244
Db      7620  GGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCA 7561
Qy      245   GlyGlyGlySerGlySerGlnSerGlySerGlySerGlySerAsnGlyAspAsnAsn 264
Db      7560  GGAGGGGCGAGGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGCA 7501
Qy      265   AsnGlySerSerSerGlyGlySerSerGlySerSerGlySerSerGlySerGlyGly 284
Db      7500  GCAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAG 7441
Qy      285   SerSerGlyGlySerSerGlyGlySerSerGlyAsnSerGly---GlySerArgGlyAsp 303
Db      7440  GGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCG 7381
Qy      304   SerGlySerGluSerSerTrpGlySerSerThrGlySerSerSerGlyAsnHisGlyGly 323
Db      7380  GCAGGAGCAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCGAGGAGGGGCA 7321
Qy      324   SerGlyGlyGlyAsnGlyHisLysProGlyCysGluLysProGlyAsnGluAlaArgGly 343
Db      7320  CGAGCAGGAGGTGAGGCGGGGCTCGAGCA-----GGCAGTGGAGGCGCGGGT 7273
Qy      344   SerGlyGluSerGlyIleGlnGlyPheArgGlyGlnGlyValSerSerAsnMetArgGlu 363
Db      7272  CGAGGAGGTAGT-----GGAGCCGGGGTTCGAGGAGGTAGTGGAGGCCCGCGGGGT 7222
Qy      364   IleSerLysGluGlyAsnArgLeuLeuGlyGlySerGlyGlySerGlyAsnTyrArgGlyGlnGly 383
Db      7221  AGAGGACGTGAA-----AGAGCCAGGGGGGGAGTCTCGTGAAGACCCAGGCGGAGAGGT 7168
Qy      384   SerSerTrpGly 387
Db      7167  COTGGACGTGGA 7156
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## RESULT 12

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US-08-910-647-1
; Sequence 1, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,647
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-1
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## Alignment Scores:

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Score:	383.00	Matches:	119
Percent Similarity:	40.10%	Conservative:	35
Best Local Similarity:	30.9%	Mismatches:	186
Query Match:	16.21%	Indels:	44
DB:	3	Gaps:	13

US-10-063-699-52 (1-440) x US-08-910-647-1 (1-9600)

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Qy      37    GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGluGlyValGlyLysAlaIleGly 56
Db      550  CGAGGACGGGGAAGAGGAGGAGCA-----CGAGGAGCGCGAAGACCA---GGA 594
Qy      57    LysGluAlaGlyGlyAlaAlaGly-----Sertlys 66
Db      595  GCGCCGGCGGCTCAGGATCAGGCGCAAGACATAGATGGTCTCCGAGACCCCAAAA 654
Qy      67    ValSerGluAlaLeuGly---GlnGlyThrArgGluAlaValGlyThrGlyValArgGln 85
Db      655  CGTCCAAGTTGATTGGCTGCAAGGGGACCCCGTGGAAACAGGAGGAGGAGCA----- 708
Qy      86    ValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHisAla 105
Db      709  -----GGAGCGGGGAGGGGCGAGGACGAGGAGGGGCGAGGAGGGGCGAGGAGCA 762
Qy      106   LeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGlyAla 125
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Qy 165 ProGlyGlyLeuGlyThrProTyrValHisGlyTyrProGlyAsnSerAlaGlySerPhe 184
Db 916 GCAGAGGGGCGAGGCGGCGAGGACGAGGAGGCGGCGAGGAGGAGGCGGCGAGGA 975
Qy 185 GlyMetAsnProGlnGlnAlaProTyrTrpGlyGlnGlyAsnGlyGlyProProAsnPhe 204
Db 976 GGGGCGAGGAGGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGAGGCGCA 1035
Qy 205 GlyThrAsnThrGlnGlnAlaValAlaGlnProGlyTyrGlySerValArgAlaSerAsn 224
Db 1036 GCAGCAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGAGGA 1095
Qy 225 GlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyGlySerSerAsnSer 244
Db 1096 GGGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCA 1155
Qy 245 GlyGlyGlySerGlySerGlnSerGlySerGlySerGlySerGlySerAsnGlyAspAsnAsn 264
Db 1156 GCAGGGGCGAGGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGA 1215
Qy 265 AsnGlySerSerSerGlySerGlySerSerGlySerSerGlySerSerGlySerGlyGly 284
Db 1216 GCAGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGA 1275
Qy 285 SerSerGlyGlySerSerGlySerGlySerSerGlySerSerGlySerGlySerArgGlyAsp 303
Db 1276 GGGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGAGGG 1335
Qy 304 SerGlySerGluSerSerTrpGlySerSerThrGlySerSerSerGlyAsnHisGlyGly 323
Db 1336 GCAGAGGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGGCGAGGAGGCGCA 1395
Qy 324 SerGlyGlyAsnGlyHisLysProGlyCysGluLysProGlyAsnGluAlaArgGly 343
Db 1396 GCAGCAGGAGTGGAGGCGGCGGCTCCAGCA-----GGCAGTGGAGGCGCGGGT 1443
Qy 344 SerGlyGluSerGlyIleGlnGlyPheArgGlyGlnGlyValSerSerAsnMetArgGlu 363
Db 1444 CGAGAGGAGTAGT-----GGAGGCGGCGGCTCGAGGAGGTAGTGGAGGCGCGCGGGT 1494
Qy 364 IleSerLysGluGlyAsnArgLeuLeuGlyGlySerGlyAspAsnTyrArgGlyGlnGly 383
Db 1495 AGAGACCGTGA-----AGACCAGGGGGGGAAGTCTGTGAAGACGCCGCGGCGAGAGGT 1548
Qy 384 SerSerTrpGly 387
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## RESULT 14

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US-07-884-811-15
; Sequence 15, Application US/07884811
; Patent No. 5316921
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/884,811
; FILING DATE: 19920518
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 755.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-884-811-15
Alignment Scores:
Pred. No.: 5,16e-12 Length: 10596
Score: 383.00 Matches: 119
Percent Similarity: 40.10% Conservative: 35
Best Local Similarity: 30.99% Mismatches: 186
Query Match: 16.21% Indels: 44
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US-10-063-699-52 (1-440) x US-07-884-811-15 (1-10596)
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Qy 37 GluAlaLeuGlyHisGlyLeuGlyAspAlaLeuSerGluGlyValGlyLysAlaIleGly 56
Db 2084 CGAGACCGGGGAAGACGAGCA-----CGAGGAGCGGAAGACCA---GGA 2128
Qy 57 LysGluAlaGlyGlyAlaAlaGly-----SerLys 66
Db 2129 GCGCGCGCGGCTCAGGATCAGGCGCAAGACATAGATGCTGTCGAGAGACCCCAAAA 2188
Qy 67 ValSerGluAlaLeuGly---GlnGlyThrArgGluAlaValGlyThrGlyValArgGln 85
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Qy 86 ValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGlyGluAlaAlaHisAla 105
Db 2243 -----GGAGCGGAGGCGGCGAGGAGGAGGCGGCGAGGAGGAGGAGGAGGAGCA 2296
Qy 106 LeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspValIleArgHisGlyAla 125
Db 2297 GGAGGAGGCGGCGAGGCGGCGAGGAGG-----GCAGGAGGCGCA 2335
Qy 126 AspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGlyAlaTrpGluThrSer 145
Db 2336 GGAGCA-----CGAGGAGGCGGCGAGGAGGAGGCGGCGAGGAGGAGGAGGAGGCA 2389
Qy 146 GlyGlyHisGlyIlePheGlySerGlnGlyLeuGlyGlyGlnGlyGln---GlyAsn 164
Db 2390 GGAGCAGGAGGCGGCGAGGAGGAGGAGGAGGCGGCGAGGAGGAGGAGGAGGAGGAGG 2449
Qy 165 ProGlyGlyLeuGlyThrProTyrValHisGlyTyrProGlyAsnSerAlaGlySerPhe 184
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Qy 185 GlyMetAsnProGlnGlnAlaProTyrGlyGlnGlyAsnGlyGlyProProAsnPhe 204
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Qy 205 GlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerValArgAlaSerAsn 224
Db 2570 GGAGCAGGAGGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCA 2629
Qy 225 GlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyGlySerSerAsnSer 244
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GenCore version 5.1.6  
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Total number of hits satisfying chosen parameters: 11324664

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Post-processing: Minimum Match 0%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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862	434	18.4	1199	18	US-10-479-638-8
C 863	430.5	18.2	1083	16	US-10-029-386-20723
864	427	18.1	1744	18	US-10-437-963-19774
865	415.5	17.6	4146	17	US-10-282-122A-28711
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C 867	408.5	17.3	1635	9	US-09-864-761-20241
C 868	408.5	17.3	1973	9	US-09-864-761-3471
C 869	406.5	17.2	2543	16	US-10-029-386-20536
870	405.5	17.2	1075	9	US-09-864-761-19241
871	405.5	17.2	1403	9	US-09-864-761-2513
872	404.5	17.1	1599	17	US-10-282-122A-28474
873	392.5	16.6	2732	17	US-10-282-122A-28290
874	392	16.6	69350	17	US-10-041-018-379
875	387.5	16.4	1304	18	US-10-437-963-19773
876	386	16.3	2337	17	US-10-282-122A-28567
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878	383	16.2	1926	15	US-10-194-046-3
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C 880	383	16.2	8705	15	US-10-291-249-14
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C 882	383	16.2	9482	17	US-10-888-961-4
C 883	383	16.2	9600	16	US-10-278-751-1
C 884	383	16.2	10233	16	US-10-050-898-283
C 885	383	16.2	10285	16	US-10-050-902-283
C 886	383	16.2	10330	18	US-10-856-269-22
C 887	383	16.2	10477	18	US-10-856-269-22
C 888	383	16.2	10516	18	US-10-856-269-20
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C 897	383	16.2	12242	18	US-10-678-816-6
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C 902	377	16.0	1731	17	US-10-282-122A-28363
C 903	375	15.9	2745	17	US-10-282-122A-28422
C 904	374.5	15.8	410	10	US-09-803-719-37
C 905	373.5	15.8	1682	18	US-10-479-638-10
C 906	373.5	15.8	1755	18	US-10-282-122A-28719
C 907	373.5	15.8	2004	17	US-10-282-122A-28310
C 908	373	15.8	686	9	US-09-879-536-364
C 909	373	15.8	1201	17	US-10-115-831-152
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913	372	15.7	2085	17	US-10-282-122A-28542	Sequence 28542, A	986	320.5	13.6	1077	17	US-10-425-114-307	Sequence 307, App
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916	368	15.6	1296	18	US-10-437-963-98895	Sequence 98895, A	c 990	319	13.5	1638	18	US-10-437-963-52487	Sequence 52487, A
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918	366	15.5	1776	17	US-10-488-056-20	Sequence 20, Appl	c 992	317.5	13.4	1262	18	US-10-739-930-5512	Sequence 5512, Ap
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920	364	15.4	1821	17	US-10-282-122A-28280	Sequence 28280, A	c 994	315.5	13.4	1667	18	US-10-437-963-35435	Sequence 35435, A
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922	363	15.4	1920	17	US-10-437-963-56998	Sequence 28425, A	c 996	314.5	13.3	80557	18	US-10-080-170-647	Sequence 647, App
923	362.5	15.3	404	10	US-09-803-719-335	Sequence 335, App	997	314.5	13.3	80557	18	US-10-468-356-647	Sequence 190, App
924	362	15.3	1616	18	US-10-437-963-78180	Sequence 78180, A	998	314	13.3	349	10	US-09-764-891-190	Sequence 9375, Ap
925	361.5	15.3	1751	18	US-10-437-963-9763	Sequence 9763, Ap	999	313.5	13.3	629	18	US-10-021-323-9375	Sequence 13684, A
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1500	241.5	10.2	2407	9	US-09-764-847-1095	Sequence 1095, Ap

Search completed: May 15, 2005, 08:59:27  
Job time : 761 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2005, 18:11:50 ; Search time 7392 Seconds  
(without alignments)  
11366.524 Million cell updates/sec

Title: US-10-063-699-51

Perfect score: 1734

Sequence: 1 gtgactctgagagccag.....aaaaaaaaaaaaaaaaa 1734

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1734	100.0	1734	6	AX092320 Sequence
2	1734	100.0	1734	6	AX358902 Sequence
3	1734	100.0	1734	6	AX362395 Sequence
4	1734	100.0	1734	6	AX376134 Sequence
5	1734	100.0	1734	6	AX403750 Sequence
6	1734	100.0	1734	6	AX454564 Sequence
7	1734	100.0	1734	6	AX491042 Sequence
8	1734	100.0	1734	6	AX696983 Sequence
9	1734	100.0	1734	6	AX358412 Homo sapi
10	1244.4	71.8	1441	6	BD275935 62 Human
11	1192.2	68.8	1982	9	BC035311 Homo sapi
12	1015.2	58.5	1431	9	AY622965 Homo sapi
13	607.2	35.0	11311	9	AC138125 Homo sapi
14	607.2	35.0	46275	9	AC002389 Human DNA
15	426.2	24.6	888	6	CQ721208
16	383.2	22.1	2044	10	BC064724 Mus muscu
17	370.8	21.4	914	6	BD206280 Human nuc
18	370.8	21.4	914	6	AR400595 Sequence
19	370.8	21.4	914	6	AX013099 Sequence

20	365	21.0	1554	10	AY622963
21	357	20.6	1947	10	AY444557
22	240	13.8	2811	6	CQ842751 Sequence
23	240	13.8	2811	9	AK125695 Homo sapi
24	209	12.1	410	6	AX245107 Sequence
25	208	12.0	342	6	AR421870 Sequence
26	208	12.0	342	6	AX982564 Sequence
27	208	12.0	342	6	BD117423 Sequence
28	204	11.8	337	6	AR421887 Sequence
29	204	11.8	337	6	AX982581 Sequence
30	204	11.8	337	6	BD117440 Sequence
31	200.4	11.6	940	9	BC004493 Homo sapi
32	189.8	10.9	326	6	AR421901 Sequence
33	189.8	10.9	326	6	AX982595 Sequence
34	189.8	10.9	326	6	BD117454 Sequence
35	178.8	10.3	154673	2	AC079472
36	163.8	9.4	365	6	AR421931 Sequence
37	163.8	9.4	365	6	AX982625 Sequence
38	163.8	9.4	365	6	BD117484 Sequence
39	160.6	9.3	253523	2	AC126062
40	160	9.2	293	6	AR421862 Sequence
41	160	9.2	293	6	AX982556 Sequence
42	160	9.2	293	6	BD117415 Sequence
43	158.8	9.2	361	6	AR421895 Sequence
44	158.8	9.2	361	6	AX982589 Sequence
45	158.8	9.2	361	6	BD117448 Sequence
46	151.8	8.8	357	6	AR421910 Sequence
47	151.8	8.8	357	6	AX982604 Sequence
48	151.8	8.8	357	6	BD117463 Sequence
49	149	8.6	351	6	AR421923 Sequence
50	149	8.6	351	6	AX982617 Sequence
51	149	8.6	351	6	BD117476 Sequence
52	146.4	8.4	44679	9	CH19F21246
53	145.4	8.4	349	6	AR421878 Sequence
54	145.4	8.4	349	6	AX982572 Sequence
55	145.4	8.4	349	6	BD117431 Sequence
56	132.4	7.6	346	6	AR421946 Sequence
57	132.4	7.6	346	6	AX982640 Sequence
58	132.4	7.6	346	6	BD117499 Sequence
59	132	7.6	349980	6	AX344553 Sequence
60	132	7.6	349980	6	AX344554 Sequence
61	127.6	7.4	614	8	AF165421 Mesembrya
62	126.8	7.3	368	10	BC049735 Mus muscu
63	126.6	7.3	15954	6	AX344491 Sequence
64	126.6	7.3	15954	6	AX348900 Sequence
65	126.2	7.3	396	6	AR391193 Sequence
66	126.2	7.3	396	6	AR392898 Sequence
67	126.2	7.3	396	6	AR489628 Sequence
68	126.2	7.3	396	6	AX493869 Sequence
69	126.2	7.3	396	6	AX093198 Sequence
70	125	7.2	602	9	BC008488 Homo sapi
71	125	7.2	1464	9	IR2005397 AL389978 Homo sapi
72	124.6	7.2	539	10	BC031454 Mus muscu
73	124.6	7.2	1044	10	BC049565 Mus muscu
74	124.4	7.2	2754	10	BC066817 Mus muscu
75	124.2	7.2	2230	5	BC078288 Danio rer
76	124.2	7.2	2350	9	BC063427 Homo sapi
77	124.2	7.2	2404	9	BC042542 Homo sapi
78	123.8	7.1	658	6	BD275413 50 Human
79	123.8	7.1	686	10	BC064030 Rattus no
80	123.8	7.1	3836	9	BC063854 Homo sapi
81	123.8	7.1	261316	2	AC095371 Rattus no
82	123.6	7.1	868	9	BC065714 Homo sapi
83	123.6	7.1	1612	9	BC044235 Homo sapi
84	123.6	7.1	2487	6	BD074862 Secreted
85	123.6	7.1	5586	6	AX348391 Sequence
86	123.6	7.1	15832	6	AX277943 Sequence
87	123.6	7.1	15832	6	AX323630 Sequence
88	123.6	7.1	15832	6	AX346245 Sequence
89	123.2	7.1	1432	10	BC062239 Rattus no
90	123.2	7.1	1472	9	BC017724 Homo sapi
91	123.2	7.1	8946	6	AX345813 Sequence
92	123.2	7.1	349980	6	AX344565 Sequence

c 93	123	7.1	392	6	CQ395758	Sequence
c 94	123	7.1	392	6	CQ402088	Sequence
c 95	123	7.1	894	9	BC044257	Homo sapi
96	123	7.1	1004	10	BC025458	Mus muscu
97	122.8	7.1	547	9	BC070202	Homo sapi
98	122.8	7.1	935	10	BC049693	Mus muscu
99	122.8	7.1	953	10	BC049732	Mus muscu
100	122.8	7.1	3394	9	BC050550	Homo sapi
101	122.4	7.1	2886	10	BC025599	Mus muscu
102	122.2	7.0	816	9	HSM805738	Homo sapi
103	122.2	7.0	1487	4	AY423736	Tachyglis
104	122.2	7.0	1493	9	BC032462	Homo sapi
105	122.2	7.0	1715	5	BC067176	Danio rer
106	122.2	7.0	2924	6	AX683129	Sequence
107	122.2	7.0	2924	10	S68736	Rattus sp.
108	122.2	7.0	3353	9	HSM803622	Sequence
109	122	7.0	3329	10	BC054371	Mus muscu
110	122	7.0	4663	9	HSM808808	Sequence
111	121.8	7.0	404	6	AX245405	Sequence
112	121.8	7.0	615	10	BC043668	Mus muscu
113	121.8	7.0	686	6	BD210474	Human gen
114	121.8	7.0	700	6	AX135555	Sequence
115	121.8	7.0	935	10	BC061157	Mus muscu
116	121.8	7.0	991	9	BC011886	Homo sapi
117	121.8	7.0	1579	6	AX834018	Sequence
118	121.8	7.0	1579	9	AK096215	Homo sapi
119	121.8	7.0	1742	9	HSM806670	Sequence
120	121.8	7.0	2337	9	HSM800876	Sequence
121	121.8	7.0	2846	6	HSM802834	Sequence
122	121.8	7.0	11416	6	AX251758	Sequence
123	121.8	7.0	11416	6	AX345020	Sequence
124	121.8	7.0	11416	6	AX348567	Sequence
125	121.8	7.0	21354	6	AX251544	Sequence
126	121.6	7.0	1657	10	BC057688	Mus muscu
127	121.6	7.0	1885	9	HSM807866	Sequence
128	121.6	7.0	2003	9	BC051760	Homo sapi
129	121.6	7.0	2788	9	AF111847	Homo sapi
130	121.6	7.0	2905	3	AK174395	Ciona int
c 131	121.6	7.0	3001	6	CQ787448	Sequence
132	121.6	7.0	4438	10	BC067016	Mus muscu
c 133	121.6	7.0	37973	6	AX347098	Sequence
c 134	121.6	7.0	34980	6	AX344572	Sequence
135	121.4	7.0	1795	5	BC068985	Sequence
136	121.2	7.0	1265	10	BC061243	Mus muscu
137	121.2	7.0	1608	10	BC057455	Mus muscu
138	121.2	7.0	2329	9	HSM805883	Sequence
139	121.2	7.0	3305	10	BC040407	Mus muscu
140	121	7.0	277	6	CQ671217	Sequence
141	121	7.0	1285	9	HSM801947	Sequence
142	121	7.0	1526	9	BC041705	Homo sapi
143	121	7.0	2006	10	BC083579	Rattus no
144	121	7.0	2464	9	HSM807471	Homo sapi
145	121	7.0	2684	9	HSM805935	Sequence
146	121	7.0	5359	10	BC054082	Sequence
c 147	120.8	7.0	810	6	CQ398775	Sequence
c 148	120.8	7.0	810	6	CQ405056	Sequence
149	120.8	7.0	2235	9	BC022267	Homo sapi
150	120.8	7.0	2929	10	BC053441	Mus muscu
151	120.8	7.0	3723	9	HSM808935	Sequence
c 152	120.8	7.0	34980	6	AX344555	Sequence
c 153	120.6	7.0	501	6	CQ411817	Sequence
154	120.6	7.0	819	10	BC064002	Mus muscu
155	120.6	7.0	1053	10	BC049595	Mus muscu
156	120.6	7.0	1080	9	BC063605	Homo sapi
157	120.6	7.0	1164	8	BT009497	Triticum
158	120.6	7.0	1732	9	HSM806991	Sequence
159	120.6	7.0	1940	9	HSM807445	Sequence
160	120.6	7.0	1941	9	BC051758	Homo sapi
161	120.6	7.0	2841	10	BC045601	Mus muscu
c 162	120.6	7.0	5306	6	AX345413	Sequence
c 163	120.6	7.0	6486	6	AX458534	Sequence
c 164	120.6	7.0	8899	6	AX345739	Sequence
c 165	120.6	7.0	8899	6	AX348461	Sequence

c 166	120.6	7.0	34980	6	AX344551	Sequence
c 167	120.6	7.0	34980	6	AX344563	Sequence
168	120.4	6.9	490	6	CQ525211	Sequence
169	120.4	6.9	727	9	BC024701	Homo sapi
170	120.4	6.9	758	9	BC062750	Homo sapi
171	120.4	6.9	762	9	BC070287	Homo sapi
172	120.4	6.9	1319	9	BC003683	Homo sapi
173	120.4	6.9	1377	5	BC063336	Xenopus t
174	120.4	6.9	1608	9	AY358187	Homo sapi
175	120.4	6.9	1684	10	BC055910	Mus muscu
176	120.4	6.9	1931	10	BC036150	Mus muscu
177	120.4	6.9	3930	9	BC027963	Homo sapi
178	120.2	6.9	625	10	BC059134	Rattus no
179	120.2	6.9	705	10	BC059084	Mus muscu
180	120.2	6.9	1329	9	AF544398	Homo sapi
181	120.2	6.9	1464	9	BC021958	Homo sapi
182	120.2	6.9	1725	9	HSM806934	Homo sapi
183	120.2	6.9	2002	9	BC068030	Homo sapi
184	120.2	6.9	2039	10	BC050804	Mus muscu
185	120.2	6.9	2237	10	BC059191	Mus muscu
186	120.2	6.9	2439	10	BC061540	Rattus no
187	120.2	6.9	2728	5	BC081323	Xenopus t
188	120.2	6.9	3315	9	AB056768	Macaca fa
c 189	120.2	6.9	4316	6	CQ807088	Sequence
c 190	120.2	6.9	4316	6	AX795868	Sequence
c 191	120.2	6.9	4316	6	AX822388	Sequence
c 192	120.2	6.9	4316	6	AX826028	Sequence
193	120	6.9	580	6	CQ526169	Sequence
194	120	6.9	942	9	BC043511	Homo sapi
195	120	6.9	1181	10	BC049768	Mus muscu
196	120	6.9	1588	9	BC070183	Homo sapi
197	120	6.9	2371	9	HSM805927	Sequence
198	120	6.9	2415	9	BC028002	Homo sapi
c 199	120	6.9	2508	10	BC079036	Rattus no
c 200	120	6.9	3001	6	CQ787464	Sequence
c 201	120	6.9	5387	6	AX344633	Sequence
c 202	120	6.9	7061	6	AX251886	Sequence
c 203	120	6.9	7061	6	AX345898	Sequence
c 204	120	6.9	7061	6	AX348679	Sequence
c 205	120	6.9	8186	6	AX344682	Sequence
c 206	120	6.9	15518	6	AX281513	Sequence
c 207	120	6.9	15518	6	AX347074	Sequence
c 208	120	6.9	15518	6	AX349039	Sequence
c 209	120	6.9	34980	6	AX344552	Sequence
c 210	119.8	6.9	425	6	CQ408472	Sequence
211	119.8	6.9	749	9	BC008417	Homo sapi
212	119.8	6.9	1034	9	AK026865	Homo sapi
213	119.8	6.9	1576	9	HSM806260	Homo sapi
214	119.8	6.9	1853	10	BC052346	Mus muscu
215	119.8	6.9	2000	9	BC063423	Homo sapi
216	119.8	6.9	2321	9	BC017105	Homo sapi
217	119.8	6.9	2406	9	BC017107	Homo sapi
218	119.8	6.9	3275	6	BD237099	Compounds
219	119.8	6.9	3275	6	AR225499	Sequence
220	119.8	6.9	3275	6	AR562922	Sequence
221	119.8	6.9	3275	6	AX321620	Sequence
222	119.8	6.9	4942	9	HSM808887	Homo sapi
223	119.8	6.9	7609	9	HSM807874	Homo sapi
224	119.8	6.9	7765	6	CQ412109	Sequence
225	119.8	6.9	7765	6	CQ433934	Sequence
c 226	119.8	6.9	24259	6	AX251447	Sequence
227	119.6	6.9	308	6	CQ517578	Sequence
228	119.6	6.9	319	6	CQ670102	Sequence
229	119.6	6.9	661	10	BC051629	Sequence
230	119.6	6.9	788	5	BC072244	Xenopus l
231	119.6	6.9	844	9	BC009571	Homo sapi
232	119.6	6.9	971	10	BC030946	Mus muscu
233	119.6	6.9	1019	10	BC043927	Mus muscu
234	119.6	6.9	1319	9	BC015490	Homo sapi
235	119.6	6.9	1331	6	CQ776637	Sequence
236	119.6	6.9	1359	5	BC053194	Danio rer
237	119.6	6.9	1696	5	BC067590	Danio rer
238	119.6	6.9	1788	9	BC044944	Homo sapi

239	119.6	6.9	2592	3	AK173351	AK173351 Ciona int	312	118.6	6.8	394	6	CQ481688	CQ481688 Sequence
240	119.6	6.9	3180	10	BC041774	BC041774 Mus muscu	313	118.6	6.8	408	6	CQ502830	CQ502830 Sequence
241	119.6	6.9	3623	10	BC034092	BC034092 Mus muscu	314	118.6	6.8	408	6	CQ511687	CQ511687 Sequence
242	119.4	6.9	515	6	CQ522671	CQ522671 Sequence	315	118.6	6.8	809	6	BD252094	BD252094 47 secret
243	119.4	6.9	863	10	BC061014	BC061014 Mus muscu	316	118.6	6.8	861	10	BC049709	BC049709 Mus muscu
244	119.4	6.9	967	9	HSN802777	AL390157 Homo sapi	317	118.6	6.8	887	9	AB125184	AB125184 Macaca fa
245	119.4	6.9	981	9	BC041179	AL390157 Homo sapi	318	118.6	6.8	1018	9	BC022044	BC022044 Homo sapi
246	119.4	6.9	1000	9	HSN806624	BS571179 Homo sapi	319	118.6	6.8	1130	10	BC043698	BC043698 Mus muscu
247	119.4	6.9	1692	8	BT009528	BT009528 Triticum	320	118.6	6.8	1182	10	BC049567	BC049567 Mus muscu
248	119.4	6.9	1760	9	BC051807	BC051807 Homo sapi	321	118.6	6.8	1257	9	BC043535	BC043535 Homo sapi
249	119.4	6.9	1946	9	HSN808123	BX647977 Homo sapi	322	118.6	6.8	1284	3	AK113775	AK113775 Ciona int
250	119.4	6.9	2005	9	HSN803426	AL832119 Homo sapi	323	118.6	6.8	1286	10	BC062175	BC062175 Mus muscu
251	119.4	6.9	2165	5	BC054602	BC054602 Danio rer	324	118.6	6.8	1445	9	BC063545	BC063545 Homo sapi
252	119.4	6.9	2501	6	AX599024	AX599024 Sequence	325	118.6	6.8	1580	5	BC067146	BC067146 Danio rer
253	119.4	6.9	2593	9	HSN807470	BX647326 Homo sapi	326	118.6	6.8	1661	9	BC025753	BC025753 Homo sapi
254	119.4	6.9	2868	10	BC006583	BC006583 Mus muscu	327	118.6	6.8	1838	10	BC083573	BC083573 Rattus no
255	119.4	6.9	2936	5	BC077828	BC077828 Xenopus l	328	118.6	6.8	2094	9	BC044310	BC044310 Homo sapi
256	119.4	6.9	3002	6	AX354181	AX354181 Sequence	329	118.6	6.8	2265	9	BC063477	BC063477 Homo sapi
257	119.4	6.9	3005	10	BC034271	BC034271 Mus muscu	330	118.6	6.8	2883	9	HSN808647	HSN808647 Sequence
258	119.4	6.9	4154	9	HSN803629	AL832322 Homo sapi	331	118.6	6.8	4255	6	AX346935	AX346935 Sequence
259	119.4	6.9	4680	9	BC042624	BC042624 Homo sapi	332	118.6	6.8	4316	6	CQ806814	CQ806814 Sequence
260	119.4	6.9	35962	6	AX598904	AX598904 Sequence	333	118.6	6.8	4316	6	AX795752	AX795752 Sequence
261	119.2	6.9	409	9	BC060322	BC060322 Homo sapi	334	118.6	6.8	4316	6	AX822260	AX822260 Sequence
262	119.2	6.9	1562	5	BC054329	BC054329 Xenopus l	335	118.6	6.8	4316	6	AX825900	AX825900 Sequence
263	119.2	6.9	1598	9	BC013323	BC013323 Homo sapi	336	118.6	6.8	5195	6	AX345823	AX345823 Sequence
264	119.2	6.9	1604	9	BC044260	BC044260 Homo sapi	337	118.6	6.8	6944	6	AX347467	AX347467 Sequence
265	119.2	6.9	2013	9	AB070201	AB070201 Macaca fa	338	118.6	6.8	6944	6	AX349188	AX349188 Sequence
266	119.2	6.9	2214	9	HSN807772	BX647626 Homo sapi	339	118.6	6.8	6944	6	AX657867	AX657867 Sequence
267	119.2	6.9	2447	6	AR079032	AR079032 Sequence	340	118.6	6.8	6944	6	AX659141	AX659141 Sequence
268	119.2	6.9	2447	6	BD190886	BD190886 Secreted	341	118.6	6.8	8900	6	CQ807251	CQ807251 Sequence
269	119.2	6.9	3288	10	BC021457	BC021457 Mus muscu	342	118.6	6.8	73778	6	AX344575	AX344575 Sequence
270	119.2	6.9	4636	10	BC057352	BC057352 Mus muscu	343	118.6	6.8	34980	6	AX344573	AX344573 Sequence
271	119.2	6.9	5365	9	HSN807518	BX647373 Homo sapi	344	118.4	6.8	472	6	CQ518059	CQ518059 Sequence
272	119.2	6.9	7306	6	AX346539	AX346539 Sequence	345	118.4	6.8	607	5	BC049055	BC049055 Danio rer
273	119	6.9	317	6	CQ526915	CQ526915 Sequence	346	118.4	6.8	746	10	BC061195	BC061195 Mus muscu
274	119	6.9	676	10	BC049769	BC049769 Mus muscu	347	118.4	6.8	824	9	BC070291	BC070291 Homo sapi
275	119	6.9	805	10	BC063183	BC063183 Rattus no	348	118.4	6.8	873	6	AX780227	AX780227 Sequence
276	119	6.9	1319	9	BC068029	BC068029 Homo sapi	349	118.4	6.8	1000	10	BC038055	BC038055 Mus muscu
277	119	6.9	1433	5	BC082836	BC082836 Xenopus l	350	118.4	6.8	1030	5	BC054286	BC054286 Xenopus l
278	119	6.9	1765	9	BC063438	BC063438 Homo sapi	351	118.4	6.8	1087	5	BC083541	BC083541 Danio rer
279	119	6.9	1788	9	HSN806673	BX640627 Homo sapi	352	118.4	6.8	1132	6	BD131068	BD131068 Secreted
280	119	6.9	2016	10	BC063147	BC063147 Rattus no	353	118.4	6.8	1350	10	BC072695	BC072695 Rattus no
281	119	6.9	2029	10	BC050265	BC050265 Mus muscu	354	118.4	6.8	1582	10	BC055609	BC055609 Mus muscu
282	119	6.9	2648	10	BC031180	BC031180 Mus muscu	355	118.4	6.8	1619	10	BC058767	BC058767 Mus muscu
283	119	6.9	2677	9	BC050385	BC050385 Homo sapi	356	118.4	6.8	2084	9	AB072761	AB072761 Macaca fa
284	119	6.9	2730	9	BC053349	BC053349 Homo sapi	357	118.4	6.8	2134	5	XLCTG	XL4990 X.laervis Cc
285	119	6.9	2920	3	AK174466	AK174466 Ciona int	358	118.4	6.8	2409	10	BC061477	BC061477 Mus muscu
286	119	6.9	3328	10	BC005512	BC005512 Mus muscu	359	118.4	6.8	2578	9	AB049758	AB049758 Homo sapi
287	118.8	6.9	580	10	BC006049	BC006049 Mus muscu	360	118.4	6.8	2654	3	AK174482	AK174482 Ciona int
288	118.8	6.9	805	6	CQ395292	CQ395292 Sequence	361	118.4	6.8	2777	5	BC063344	BC063344 Xenopus t
289	118.8	6.9	805	6	CQ401630	BC041630 Sequence	362	118.4	6.8	2815	9	BC038597	BC038597 Homo sapi
290	118.8	6.9	1017	10	BC049561	BC049561 Mus muscu	363	118.4	6.8	2846	6	AX252533	AX252533 Sequence
291	118.8	6.9	1065	10	BC049675	BC049675 Mus muscu	364	118.4	6.8	2846	6	AX092306	AX092306 Sequence
292	118.8	6.9	1159	9	BC043507	BC043507 Homo sapi	365	118.4	6.8	2846	6	AX376102	AX376102 Sequence
293	118.8	6.9	1383	5	BC056115	BC056115 Xenopus l	366	118.4	6.8	2846	6	AX403343	AX403343 Sequence
294	118.8	6.9	1409	10	BC049776	BC049776 Mus muscu	367	118.4	6.8	2846	9	AX358346	AX358346 Homo sapi
295	118.8	6.9	1966	9	HSN808069	BX647923 Homo sapi	368	118.4	6.8	2869	9	HSN804689	HSN804689 Mus muscu
296	118.8	6.9	1995	10	BC050759	BC050759 Mus muscu	369	118.4	6.8	3645	10	BC062916	BC062916 Mus muscu
297	118.8	6.9	2026	9	BC022399	BC022399 Homo sapi	370	118.4	6.8	4116	9	HSN807269	HSN807269 Homo sapi
298	118.8	6.9	2030	10	BC058229	BC058229 Mus muscu	371	118.4	6.8	4306	10	BC059824	BC059824 Mus muscu
299	118.8	6.9	2082	6	AR059958	AR059958 Sequence	372	118.4	6.8	4562	9	HSN805779	HSN805779 Sequence
300	118.8	6.9	2393	5	BC070538	BC070538 Xenopus l	373	118.4	6.8	5368	6	AX344691	AX344691 Sequence
301	118.8	6.9	2500	9	BC065207	BC065207 Homo sapi	374	118.4	6.8	6161	6	AX345313	AX345313 Sequence
302	118.8	6.9	2777	9	BC023532	BC023532 Homo sapi	375	118.4	6.8	8079	6	AX356488	AX356488 Sequence
303	118.8	6.9	3080	9	HSN807488	BX647344 Homo sapi	376	118.2	6.8	500	9	BC070218	BC070218 Homo sapi
304	118.8	6.9	3605	9	HSN808524	BX648376 Homo sapi	377	118.2	6.8	510	9	BC070217	BC070217 Homo sapi
305	118.8	6.9	4169	10	BC053919	BC053919 Mus muscu	378	118.2	6.8	794	9	BC058920	BC058920 Homo sapi
306	118.8	6.9	4498	10	BC075723	BC075723 Mus muscu	379	118.2	6.8	1289	10	BC049691	BC049691 Mus muscu
307	118.8	6.9	4726	9	HSN808619	BX648668 Homo sapi	380	118.2	6.8	1460	9	BC017009	BC017009 Homo sapi
308	118.8	6.9	5198	6	AX345181	AX345181 Sequence	381	118.2	6.8	2173	5	BC068406	BC068406 Danio rer
309	118.8	6.9	6171	6	AX345690	AX345690 Sequence	382	118.2	6.8	2233	9	BC040959	BC040959 Homo sapi
310	118.8	6.9	34980	6	AX344567	AX344567 Sequence	383	118.2	6.8	2435	9	BC050387	BC050387 Homo sapi
311	118.6	6.8	237	6	AX284920	AX284920 Sequence	384	118.2	6.8	2835	9	BC068211	BC068211 Homo sapi

385	118.2	6.8	3232	9	AF090901	AF090901 Homo sapi	C 458	117.6	6.8	267	6	CQ410745	CQ410745 Sequence
386	118.2	6.8	3459	9	BC052964	BC052964 Homo sapi	C 459	117.6	6.8	396	6	AR391210	AR391210 Sequence
387	118.2	6.8	4459	9	HSM804634	AL833321 Homo sapi	C 460	117.6	6.8	396	6	AR392915	AR392915 Sequence
388	118.2	6.8	5344	9	HSM807425	BX647281 Homo sapi	C 461	117.6	6.8	396	6	AR489645	AR489645 Sequence
389	118	6.8	431	9	BC070144	BC070144 Homo sapi	C 462	117.6	6.8	396	6	AR493886	AR493886 Sequence
390	118	6.8	543	10	BC055944	BC055944 Mus muscu	C 463	117.6	6.8	396	6	AX093215	AX093215 Sequence
391	118	6.8	774	10	BC013457	BC013457 Mus muscu	C 464	117.6	6.8	675	10	BC059112	BC059112 Rattus no
392	118	6.8	899	5	BC060392	BC060392 Xenopus l	465	117.6	6.8	681	5	BC055187	BC055187 Danio rer
393	118	6.8	910	10	BC049687	BC049687 Mus muscu	466	117.6	6.8	859	9	BC043551	BC043551 Homo sapi
394	118	6.8	1054	10	BC049758	BC049758 Mus muscu	467	117.6	6.8	1108	10	BC032259	BC032259 Mus muscu
395	118	6.8	1100	9	BC063599	BC063599 Homo sapi	468	117.6	6.8	1128	9	BC071732	BC071732 Homo sapi
396	118	6.8	1129	10	BC060535	BC060535 Rattus no	469	117.6	6.8	1319	9	BC034528	BC034528 Homo sapi
397	118	6.8	1137	10	BC062232	BC062232 Rattus no	470	117.6	6.8	1337	3	AY118704	AY118704 Drosophila
398	118	6.8	1287	10	BC061031	BC061031 Mus muscu	471	117.6	6.8	1384	10	BC052146	BC052146 Mus muscu
399	118	6.8	1343	9	BC052989	BC052989 Homo sapi	472	117.6	6.8	1568	10	BC048399	BC048399 Mus muscu
400	118	6.8	1402	9	BC040630	BC040630 Homo sapi	473	117.6	6.8	1591	9	HSM807298	BX647154 Homo sapi
401	118	6.8	1424	5	BC063367	BC063367 Xenopus t	474	117.6	6.8	1616	10	BC043714	BC043714 Mus muscu
402	118	6.8	1555	9	AB063070	AB063070 Macaca fa	475	117.6	6.8	1741	9	AB063008	AB063008 Macaca fa
403	118	6.8	1650	9	BC063391	BC063391 Homo sapi	476	117.6	6.8	1803	9	HSM807650	BX647504 Homo sapi
404	118	6.8	1959	9	BC043548	BC043548 Homo sapi	477	117.6	6.8	1869	9	HSM807550	BX647405 Homo sapi
405	118	6.8	1985	10	BC049351	BC049351 Mus muscu	478	117.6	6.8	1985	6	BD275145	BD275145 48 Human
406	118	6.8	1993	9	HSM803801	AL832493 Homo sapi	479	117.6	6.8	2217	9	BC073932	BC073932 Homo sapi
407	118	6.8	2441	3	AK174351	AK174351 Clona int	480	117.6	6.8	2344	9	BC050578	BC050578 Homo sapi
408	118	6.8	2470	10	BC027800	BC027800 Mus muscu	481	117.6	6.8	2385	6	BD186882	BD186882 Nucleic a
409	118	6.8	2620	5	BC077100	BC077100 Danio rer	482	117.6	6.8	2499	9	HSM801350	AL133016 Homo sapi
410	118	6.8	2770	9	HSM807752	BX647606 Homo sapi	483	117.6	6.8	2607	9	BC053734	BC053734 Homo sapi
411	118	6.8	2804	9	HSM807489	BX647345 Homo sapi	484	117.6	6.8	2752	9	HSM806735	BX641046 Homo sapi
412	118	6.8	2809	9	HSM802470	AL157431 Homo sapi	485	117.6	6.8	2991	9	BC030556	BC030556 Homo sapi
413	118	6.8	3383	9	HSM803701	BC832393 Homo sapi	486	117.6	6.8	3002	6	AK571883	AK571883 Sequence
414	118	6.8	3525	10	BC034207	BC034207 Mus muscu	487	117.6	6.8	3141	3	AK116783	AK116783 Clona int
415	118	6.8	3530	10	BC053732	BC053732 Mus muscu	488	117.6	6.8	3660	10	BC051069	BC051069 Mus muscu
416	118	6.8	3870	9	HSM806049	BX537527 Homo sapi	489	117.6	6.8	5338	9	HSM808825	BX648674 Homo sapi
417	118	6.8	4362	9	HSM805498	AL834414 Homo sapi	490	117.6	6.8	6644	6	E23355	E23355 Virus vecto
418	118	6.8	4818	9	HSM807492	BX647348 Homo sapi	491	117.6	6.8	7372	6	E23357	E23357 Virus vecto
419	118	6.8	4930	9	HSM807373	AL832066 Homo sapi	492	117.6	6.8	7996	6	E23359	E23359 Virus vecto
420	118	6.8	5517	9	HSM807238	BX647094 Homo sapi	493	117.6	6.8	7996	6	E23359	E23359 Virus vecto
421	118	6.8	7216	9	HSM805762	BX537480 Homo sapi	494	117.4	6.8	267	6	AX338096	AX338096 Sequence
422	118	6.8	7369	6	AX598791	AX598791 Sequence	495	117.4	6.8	575	6	CQ526566	CQ526566 Sequence
423	118	6.8	7369	6	AX705365	AX705365 Sequence	496	117.4	6.8	575	10	BC040513	BC040513 Mus muscu
424	118	6.8	10369	6	AX251057	AX251057 Sequence	497	117.4	6.8	711	9	BC051802	BC051802 Homo sapi
425	118	6.8	10369	6	AX345294	AX345294 Sequence	498	117.4	6.8	940	10	BC060548	BC060548 Rattus no
426	118	6.8	12178	10	AF466694	AF466694 Rattus no	499	117.4	6.8	995	9	BC043534	BC043534 Homo sapi
427	118	6.8	40324	6	AX458633	AX458633 Sequence	500	117.4	6.8	1191	9	BC014547	BC014547 Homo sapi
428	117.8	6.8	439	6	CQ518358	CQ518358 Sequence	501	117.4	6.8	1245	10	BC049747	BC049747 Mus muscu
429	117.8	6.8	633	10	BC059147	BC059147 Rattus no	502	117.4	6.8	1332	10	BC060992	BC060992 Mus muscu
430	117.8	6.8	1084	9	AB019565	AB019565 Homo sapi	503	117.4	6.8	1382	10	BC068658	BC068658 Mus muscu
431	117.8	6.8	1084	9	BC026265	BC026265 Homo sapi	504	117.4	6.8	1383	9	BC032432	BC032432 Homo sapi
432	117.8	6.8	1219	10	BC049717	BC049717 Mus muscu	505	117.4	6.8	1581	9	BC034284	BC034284 Homo sapi
433	117.8	6.8	1372	9	BC024221	BC024221 Homo sapi	506	117.4	6.8	1673	6	BD138829	BD138829 Secreted
434	117.8	6.8	1381	5	BC063358	BC063358 Xenopus t	507	117.4	6.8	1701	9	BC071665	BC071665 Homo sapi
435	117.8	6.8	1652	9	BC028121	BC028121 Homo sapi	508	117.4	6.8	1706	5	BC082351	BC082351 Xenopus l
436	117.8	6.8	1728	9	AB070110	AB070110 Macaca fa	509	117.4	6.8	1711	9	BC032509	BC032509 Homo sapi
437	117.8	6.8	1887	10	BC050801	BC050801 Mus muscu	510	117.4	6.8	1767	9	HSM800099	AL049314 Homo sapi
438	117.8	6.8	1889	9	BC073841	BC073841 Homo sapi	511	117.4	6.8	1850	9	BC040123	BC040123 Homo sapi
439	117.8	6.8	2190	9	BC048340	BC048340 Homo sapi	512	117.4	6.8	1886	9	AX025084	AX025084 Homo sapi
440	117.8	6.8	2789	9	HSM804418	AL833107 Homo sapi	513	117.4	6.8	1889	9	HSM805887	BX537794 Homo sapi
441	117.8	6.8	3006	9	BC039068	BC039068 Homo sapi	514	117.4	6.8	2048	9	BC044243	BC044243 Homo sapi
442	117.8	6.8	3189	9	BC002830	BC002830 Homo sapi	515	117.4	6.8	2132	9	AB072776	AB072776 Macaca fa
443	117.8	6.8	3454	9	HSM802993	AL713659 Homo sapi	516	117.4	6.8	2161	6	CQ414527	CQ414527 Sequence
444	117.8	6.8	3850	10	BC063749	BC063749 Mus muscu	517	117.4	6.8	2167	10	BC028325	BC028325 Mus muscu
445	117.8	6.8	3973	6	AX345073	AX345073 Sequence	518	117.4	6.8	2465	9	BC013348	BC013348 Homo sapi
446	117.8	6.8	4086	9	HSM803439	AL832132 Homo sapi	519	117.4	6.8	2563	9	AF125949	AF125949 Homo sapi
447	117.8	6.8	4436	10	BC058961	BC058961 Mus muscu	520	117.4	6.8	2611	9	BC041438	BC041438 Homo sapi
448	117.8	6.8	4670	9	AF104032	AF104032 Homo sapi	521	117.4	6.8	2782	9	HSM803706	AL832398 Homo sapi
449	117.8	6.8	4990	6	CQ493127	CQ493127 Sequence	522	117.4	6.8	2820	10	BC062390	BC062390 Rattus no
450	117.8	6.8	4990	6	CQ493522	BC065072 Mus muscu	523	117.4	6.8	2968	10	BC058408	BC058408 Mus muscu
451	117.8	6.8	5251	10	BC038061	BC038061 Mus muscu	524	117.4	6.8	3328	10	BC052770	BC052770 Mus muscu
452	117.8	6.8	5405	10	BC038061	BC038061 Mus muscu	525	117.4	6.8	3724	5	BC068927	BC068927 Xenopus l
453	117.8	6.8	6577	6	AX251920	AX251920 Sequence	526	117.4	6.8	4057	10	BC067005	BC067005 Mus muscu
454	117.8	6.8	6577	6	AX346258	AX346258 Sequence	527	117.4	6.8	5152	6	AR453070	AR453070 Sequence
455	117.8	6.8	6577	6	AX348993	AX348993 Sequence	528	117.4	6.8	5152	6	AX281182	AX281182 Sequence
456	117.8	6.8	15528	6	A93016	A93016 Sequence 4	529	117.4	6.8	16033	6	AX346306	AX346306 Sequence
457	117.8	6.8	15528	12	PEAVGEN	Y07862 Cloning vec	530	117.4	6.8	34980	6	AX344570	AX344570 Sequence

531	117.2	6.8	733	9	BC009801	BC009801 Homo sapi	604	117	6.7	2922	9	BC032692	BC032692 Homo sapi
532	117.2	6.8	812	10	BC061144	BC061144 Mus muscu	605	117	6.7	3010	6	AX358754	AX358754 Sequence
533	117.2	6.8	1090	10	BC049543	BC049543 Mus muscu	606	117	6.7	3010	6	AX362247	AX362247 Sequence
534	117.2	6.8	1271	9	AF090934	AF090934 Homo sapi	607	117	6.7	3010	9	AX358753	AX358753 Homo sapi
535	117.2	6.8	1426	10	BC043720	BC043720 Mus muscu	608	117	6.7	3230	9	BC063118	BC063118 Homo sapi
536	117.2	6.8	1430	5	BC064202	BC064202 Xenopus t	609	117	6.7	3686	10	BC043709	BC043709 Mus muscu
537	117.2	6.8	1665	9	BC041446	BC041446 Homo sapi	610	117	6.7	3916	10	BC018439	BC018439 Mus muscu
538	117.2	6.8	1769	9	BC025749	BC025749 Homo sapi	611	117	6.7	3937	5	BC068837	BC068837 Xenopus l
539	117.2	6.8	1870	9	AK002598	AK002598 Homo sapi	612	117	6.7	4259	9	HSB05206	AL833900 Homo sapi
540	117.2	6.8	1990	9	AK000212	AK000212 Homo sapi	613	117	6.7	4389	10	BC058345	BC058345 Mus muscu
541	117.2	6.8	2065	5	BC066376	BC066376 Danio rer	614	117	6.7	4619	9	HSB06714	BC040525 Homo sapi
542	117.2	6.8	2081	5	HSB086272	BSX537592 Homo sapi	615	117	6.7	4725	9	BC040525	AX458643 Sequence
543	117.2	6.8	2238	5	BC063964	BC063964 Danio rer	616	117	6.7	6775	6	AX458643	AX458643 Sequence
544	117.2	6.8	2356	10	BC061208	AX598878 Mus muscu	617	117	6.7	6794	6	AX251872	AX251872 Sequence
545	117.2	6.8	2501	6	AX598878	AX598878 Sequence	618	117	6.7	6794	6	AX344260	AX344260 Sequence
546	117.2	6.8	2610	6	BC038448	BC038448 Homo sapi	619	117	6.7	6794	6	AX348651	AX348651 Sequence
547	117.2	6.8	3223	6	CQ806938	CQ806938 Sequence	620	117	6.7	7165	9	HSB03503	AL832196 Homo sapi
548	117.2	6.8	3223	6	CQ807212	CQ807212 Sequence	621	117	6.7	7240	9	HSB08174	BSX648028 Homo sapi
549	117.2	6.8	3626	9	BC012147	BC012147 Homo sapi	622	117	6.7	8900	6	CQ806577	CQ806577 Sequence
550	117.2	6.8	4001	6	AX347363	AX347363 Sequence	623	117	6.7	11394	6	AX323608	AX323608 Sequence
551	117.2	6.8	4001	6	AX349084	AX349084 Sequence	624	116.8	6.7	266	6	CQ484216	CQ484216 Sequence
552	117.2	6.8	4001	6	AX657851	AX657851 Sequence	625	116.8	6.7	421	6	CQ526039	CQ526039 Sequence
553	117.2	6.8	4001	6	AX659125	AX659125 Sequence	626	116.8	6.7	446	3	AF146743	AF146743 Mesobuthu
554	117.2	6.8	4081	9	HSB0807531	BSX647386 Homo sapi	627	116.8	6.7	460	6	CQ527342	CQ527342 Sequence
555	117.2	6.8	4237	6	BD057918	BD057918 Secreterd	628	116.8	6.7	502	6	CQ525317	CQ525317 Sequence
556	117.2	6.8	4969	9	HSB0806817	BC052198 Mus muscu	629	116.8	6.7	532	10	BC049701	BC049701 Mus muscu
557	117.2	6.8	5280	10	HSB052198	BC052198 Homo sapi	630	116.8	6.7	549	10	BC048536	BC048536 Mus muscu
558	117.2	6.8	6134	6	AX458624	AX458624 Sequence	631	116.8	6.7	682	10	BC049545	BC049545 Mus muscu
559	117.2	6.8	3562	6	AX598758	AX598758 Sequence	632	116.8	6.7	793	9	BC018189	BC018189 Homo sapi
560	117.2	6.8	56153	6	AX251552	AX251552 Sequence	633	116.8	6.7	806	5	CR405924	CR405924 Gallus ga
561	117	6.7	346	6	CQ398070	CQ398070 Sequence	634	116.8	6.7	822	9	BC006807	BC006807 Homo sapi
562	117	6.7	346	6	CQ404361	CQ404361 Sequence	635	116.8	6.7	889	10	BC049685	BC049685 Mus muscu
563	117	6.7	360	6	CQ324586	CQ324586 Sequence	636	116.8	6.7	920	10	BC027780	BC027780 Mus muscu
564	117	6.7	527	9	BC032225	BC032225 Homo sapi	637	116.8	6.7	970	10	BC061464	BC061464 Mus muscu
565	117	6.7	553	10	BC039566	BC039566 Mus muscu	638	116.8	6.7	973	9	BC043578	BC043578 Homo sapi
566	117	6.7	701	5	BC075162	BC075162 Xenopus l	639	116.8	6.7	997	9	BC047943	BC047943 Homo sapi
567	117	6.7	760	6	CQ497632	CQ497632 Sequence	640	116.8	6.7	1071	9	HSB0805733	BSX537431 Homo sapi
568	117	6.7	772	6	BD191024	BD191024 Secreterd	641	116.8	6.7	1073	9	BC032697	BC032697 Rattus no
569	117	6.7	818	9	BC043527	BC043527 Homo sapi	642	116.8	6.7	1076	10	BC062802	BC062802 Rattus no
570	117	6.7	893	6	CQ472917	CQ472917 Sequence	643	116.8	6.7	1080	10	BC049655	BC049655 Mus muscu
571	117	6.7	948	10	BC031442	BC031442 Mus muscu	644	116.8	6.7	1331	10	BC030915	BC030915 Mus muscu
572	117	6.7	970	10	BC064826	BC064826 Mus muscu	645	116.8	6.7	1352	3	AK115954	AK115954 Ciona int
573	117	6.7	1048	9	BC063640	BC063640 Homo sapi	646	116.8	6.7	1433	3	AK174181	AK174181 Ciona int
574	117	6.7	1081	9	BC043527	BC043527 Homo sapi	647	116.8	6.7	1456	5	BC077897	BC077897 Xenopus l
575	117	6.7	1092	10	BC0005748	BC0005748 Mus muscu	648	116.8	6.7	1647	9	HSB0806060	BSX537936 Homo sapi
576	117	6.7	1132	10	BC060558	BC060558 Rattus no	649	116.8	6.7	1719	3	AK116650	AK116650 Ciona int
577	117	6.7	1171	9	BC056889	BC056889 Homo sapi	650	116.8	6.7	1740	9	BC042437	BC042437 Homo sapi
578	117	6.7	1288	9	BC033582	BC033582 Homo sapi	651	116.8	6.7	1770	9	BC025717	BC025717 Homo sapi
579	117	6.7	1311	5	BC075786	BC075786 Danio rer	652	116.8	6.7	1802	9	BC025776	BC025776 Homo sapi
580	117	6.7	1414	5	BC049767	BC049767 Mus muscu	653	116.8	6.7	1846	9	BC038379	BC038379 Homo sapi
581	117	6.7	1614	5	BC071086	BC071086 Xenopus l	654	116.8	6.7	1959	10	BC060504	BC060504 Mus muscu
582	117	6.7	1627	9	BC039584	BC039584 Homo sapi	655	116.8	6.7	2072	9	BC044245	BC044245 Homo sapi
583	117	6.7	1851	10	BC024872	BC024872 Mus muscu	656	116.8	6.7	2173	9	HSB0806315	BSX538120 Homo sapi
584	117	6.7	1670	9	HSB069699	BSX640854 Homo sapi	657	116.8	6.7	2360	9	BC063595	BC063595 Homo sapi
585	117	6.7	1694	9	BC012597	BC012597 Homo sapi	658	116.8	6.7	2435	9	AX028219	BC028219 Homo sapi
586	117	6.7	1763	10	BC061098	BC061098 Mus muscu	659	116.8	6.7	2511	6	AX768355	AX768355 Sequence
587	117	6.7	1883	10	BC022165	BC022165 Mus muscu	660	116.8	6.7	2612	10	BC053749	BC053749 Mus muscu
588	117	6.7	1923	9	AB093671	AB093671 Macaca fa	661	116.8	6.7	2641	9	BC020219	BC020219 Homo sapi
589	117	6.7	1953	9	AB056420	AB056420 Macaca fa	662	116.8	6.7	2683	10	BC052924	BC052924 Mus muscu
590	117	6.7	1960	10	BC061459	BC061459 Mus muscu	663	116.8	6.7	2709	10	BC054846	BC054846 Mus muscu
591	117	6.7	1968	10	BC006016	BC006016 Mus muscu	664	116.8	6.7	2722	9	HSB0806004	BSX537897 Homo sapi
592	117	6.7	1976	9	BC040113	BC040113 Homo sapi	665	116.8	6.7	2789	10	BC026672	BC026672 Mus muscu
593	117	6.7	2039	9	HSB0806781	BSX640711 Homo sapi	666	116.8	6.7	2840	10	BC052769	BC052769 Mus muscu
594	117	6.7	2081	10	BC043712	BC043712 Mus muscu	667	116.8	6.7	3000	9	BC036812	BC036812 Homo sapi
595	117	6.7	2246	6	AR212256	AR212256 Sequence	668	116.8	6.7	3045	9	HSB080843	BSX648692 Homo sapi
596	117	6.7	2246	6	AR265251	AR265251 Sequence	669	116.8	6.7	3250	5	BC068779	BC068779 Xenopus l
597	117	6.7	2246	10	AF017152	AF017152 Mus muscu	670	116.8	6.7	3345	9	HSB0802955	BC041132 Homo sapi
598	117	6.7	2325	5	BC065681	BC065681 Danio rer	671	116.8	6.7	3446	9	HSB0802955	AL713742 Homo sapi
599	117	6.7	2545	9	BC063430	BC063430 Homo sapi	672	116.8	6.7	3492	5	BC078645	BC078645 Danio rer
600	117	6.7	2627	9	BC027919	BC027919 Homo sapi	673	116.8	6.7	3914	9	HSB0803724	AL832416 Homo sapi
601	117	6.7	2688	10	BC021912	BC021912 Mus muscu	674	116.8	6.7	3997	6	AX086658	AX086658 Sequence
602	117	6.7	2790	9	BC048292	BC048292 Homo sapi	675	116.8	6.7	4265	9	HSB0807603	BSX647458 Homo sapi
603	117	6.7	2832	10	BC052176	BC052176 Mus muscu	676	116.8	6.7	4385	9	HSB0806219	BSX538049 Homo sapi

677	116.8	6.7	4505	9	HSMB03050	AL173778 Homo sapi	750	116.4	6.7	1511	10	BC061104	BC061104 Mus muscu
c 678	116.8	6.7	4877	6	AX285067	AX285067 Sequence	751	116.4	6.7	1549	9	HSMB08772	BX648621 Homo sapi
c 679	116.8	6.7	4877	6	AX285068	AX285068 Sequence	752	116.4	6.7	1549	10	BC005509	BC005509 Mus muscu
c 680	116.8	6.7	4877	6	AX285079	AX285079 Sequence	753	116.4	6.7	1560	9	BC032420	BC032420 Homo sapi
c 681	116.8	6.7	6003	10	AY426635	AY426635 Mus muscu	754	116.4	6.7	1568	5	BC050177	BC050177 Danio rer
c 682	116.8	6.7	6025	6	AX2277881	AX2277881 Sequence	755	116.4	6.7	1601	9	BC050451	BC050451 Homo sapi
c 683	116.8	6.7	6112	6	AX345565	AX345565 Sequence	756	116.4	6.7	1620	10	BC046622	BC046622 Mus muscu
c 684	116.8	6.7	7906	6	AX277935	AX277935 Sequence	757	116.4	6.7	1642	5	BC064224	BC064224 Xenopus t
c 685	116.8	6.7	7906	6	AX323622	AX323622 Sequence	758	116.4	6.7	1727	5	BC071446	BC071446 Danio rer
c 686	116.8	6.7	7906	6	AX344771	AX344771 Sequence	759	116.4	6.7	1762	9	AF258575	AF258575 Homo sapi
c 687	116.8	6.7	9747	9	HSMB06689	BX640641 Homo sapi	760	116.4	6.7	1773	9	BC037559	BC037559 Homo sapi
c 688	116.6	6.7	231	6	CQ685486	CQ685486 Sequence	761	116.4	6.7	1775	5	BC053257	BC053257 Danio rer
c 689	116.6	6.7	240	6	CQ663206	CQ663206 Sequence	762	116.4	6.7	1786	9	AB070107	AB070107 Macaca fa
c 690	116.6	6.7	407	6	CQ523526	CQ523526 Sequence	763	116.4	6.7	1816	9	BC050396	BC050396 Homo sapi
c 691	116.6	6.7	408	6	CQ524818	CQ524818 Sequence	764	116.4	6.7	1842	9	BC024042	BC024042 Homo sapi
c 692	116.6	6.7	484	6	CQ526860	CQ526860 Sequence	765	116.4	6.7	1860	9	BC058897	BC058897 Homo sapi
c 693	116.6	6.7	514	10	BC061178	BC061178 Mus muscu	766	116.4	6.7	1880	6	CQ769491	CQ769491 Sequence
c 694	116.6	6.7	800	10	BC034163	BC034163 Mus muscu	767	116.4	6.7	1880	10	BC083571	BC083571 Rattus no
c 695	116.6	6.7	1071	9	AF078844	AF078844 Homo sapi	768	116.4	6.7	1994	3	AK116078	AK116078 Ciona int
c 696	116.6	6.7	1254	9	BC054506	BC054506 Homo sapi	769	116.4	6.7	2005	9	BC013372	BC013372 Homo sapi
c 697	116.6	6.7	1448	10	BC052344	BC052344 Mus muscu	770	116.4	6.7	2012	9	AY125488	AY125488 Homo sapi
c 698	116.6	6.7	1499	9	BC042195	BC042195 Homo sapi	771	116.4	6.7	2027	9	BC063512	BC063512 Homo sapi
c 699	116.6	6.7	1510	9	BC037973	BC037973 Homo sapi	772	116.4	6.7	2040	9	HSMB07056	HSMB07056 Homo sapi
c 700	116.6	6.7	1690	9	BC049211	BC049211 Homo sapi	773	116.4	6.7	2085	9	BC029120	BC029120 Homo sapi
c 701	116.6	6.7	1692	3	AK174216	AK174216 Ciona int	774	116.4	6.7	2130	10	BC062005	BC062005 Rattus no
c 702	116.6	6.7	1798	6	AR366535	AR366535 Sequence	775	116.4	6.7	2138	9	BC067301	BC067301 Homo sapi
c 703	116.6	6.7	2073	9	BC068024	BC068024 Homo sapi	776	116.4	6.7	2201	5	BC068355	BC068355 Danio rer
c 704	116.6	6.7	2287	9	BC044220	BC044220 Homo sapi	777	116.4	6.7	2205	3	AK115544	AK115544 Ciona int
c 705	116.6	6.7	2604	8	BT009473	BT009473 Triticum	778	116.4	6.7	2245	9	BC037547	BC037547 Homo sapi
c 706	116.6	6.7	2724	9	HSMB06666	BX641033 Homo sapi	779	116.4	6.7	2247	9	BC009648	BC009648 Homo sapi
c 707	116.6	6.7	2943	9	HSMB03526	AL832219 Homo sapi	780	116.4	6.7	2280	9	BC047310	BC047310 Homo sapi
c 708	116.6	6.7	3353	6	AX086952	AX086952 Sequence	781	116.4	6.7	2439	9	HSMB07466	HSMB07466 Homo sapi
c 709	116.6	6.7	3399	9	BC063840	BC063840 Homo sapi	782	116.4	6.7	2453	9	HSMB07676	HSMB07676 Homo sapi
c 710	116.6	6.7	15649	6	AX348976	AX348976 Sequence	783	116.4	6.7	2511	3	AK174016	AK174016 Ciona int
c 711	116.6	6.7	31656	2	AC149363	AC149363 Phakopsor	784	116.4	6.7	2530	10	BC063267	BC063267 Mus muscu
c 712	116.6	6.7	153567	2	AC087135	AC087135 Mus muscu	785	116.4	6.7	2610	10	BC063261	BC063261 Sequence
c 713	116.4	6.7	212	6	CQ677317	CQ677317 Sequence	786	116.4	6.7	2674	6	AR183261	AR183261 Sequence
c 714	116.4	6.7	401	3	AF543047	AF543047 Mesobuthu	787	116.4	6.7	2674	6	AR456323	AR456323 Sequence
c 715	116.4	6.7	452	6	CQ527434	CQ527434 Sequence	788	116.4	6.7	2674	10	BC083550	BC083550 Rattus no
c 716	116.4	6.7	472	6	CQ525172	CQ525172 Sequence	789	116.4	6.7	2946	5	BC076976	BC076976 Xenopus t
c 717	116.4	6.7	543	6	CQ524637	CQ524637 Sequence	790	116.4	6.7	3269	5	BC073066	BC073066 Xenopus l
c 718	116.4	6.7	589	10	BC049706	BC049706 Mus muscu	791	116.4	6.7	3498	5	BC065688	BC065688 Danio rer
c 719	116.4	6.7	608	5	BD075124	BD075124 Xenopus l	792	116.4	6.7	3564	10	BSMB5123	BSMB5123 Mus muscu
c 720	116.4	6.7	667	6	BD249950	BD249950 50 human	793	116.4	6.7	3596	9	HSMB06341	BX538140 Homo sapi
c 721	116.4	6.7	674	6	AR283453	AR283453 Sequence	794	116.4	6.7	3747	10	BC064447	BC064447 Mus muscu
c 722	116.4	6.7	674	6	AR344221	AR344221 Sequence	795	116.4	6.7	4062	5	BC070004	BC070004 Danio rer
c 723	116.4	6.7	674	6	AR351422	AR351422 Sequence	796	116.4	6.7	4421	10	BC042512	BC042512 Mus muscu
c 724	116.4	6.7	674	6	AR454002	AR454002 Sequence	797	116.4	6.7	4457	10	BC070435	BC070435 Mus muscu
c 725	116.4	6.7	674	6	AR561590	AR561590 Sequence	798	116.4	6.7	4651	9	BC042656	BC042656 Homo sapi
c 726	116.4	6.7	674	6	AX282972	AX282972 Sequence	799	116.4	6.7	4744	5	BC066770	BC066770 Xenopus l
c 727	116.4	6.7	674	6	AX303145	AX303145 Sequence	800	116.4	6.7	5567	10	BC052164	BC052164 Mus muscu
c 728	116.4	6.7	685	10	BC049720	BC049720 Mus muscu	801	116.4	6.7	5686	9	HSMB08430	BX648282 Homo sapi
c 729	116.4	6.7	749	10	BC060563	BC060563 Rattus no	802	116.4	6.7	6192	6	AX251440	AX251440 Sequence
c 730	116.4	6.7	819	9	HSMB07474	BX647330 Homo sapi	803	116.4	6.7	6436	6	AX345583	AX345583 Sequence
c 731	116.4	6.7	939	10	BC049689	BC049689 Mus muscu	804	116.4	6.7	6458	9	HSMB06837	BX641067 Homo sapi
c 732	116.4	6.7	972	10	BC049738	BC049738 Mus muscu	805	116.4	6.7	6484	6	AX344730	AX344730 Sequence
c 733	116.4	6.7	1047	5	BC027974	BC027974 Homo sapi	806	116.4	6.7	6668	6	AX346598	AX346598 Sequence
c 734	116.4	6.7	1062	5	BC084361	BC084361 Xenopus l	807	116.4	6.7	7369	6	AX705937	AX705937 Sequence
c 735	116.4	6.7	1100	10	BC061092	BC061092 Mus muscu	808	116.4	6.7	7369	6	AX705937	AX705937 Sequence
c 736	116.4	6.7	1119	9	BC071717	BC071717 Homo sapi	809	116.4	6.7	9021	6	AX347134	AX347134 Sequence
c 737	116.4	6.7	1166	9	BC043545	BC043545 Homo sapi	810	116.4	6.7	9021	6	AX347426	AX347426 Sequence
c 738	116.4	6.7	1200	5	BC077122	BC077122 Danio rer	811	116.4	6.7	9021	6	AX348462	AX348462 Sequence
c 739	116.4	6.7	1201	9	BC050586	BC050586 Homo sapi	812	116.4	6.7	9021	6	AX349147	AX349147 Sequence
c 740	116.4	6.7	1270	5	BC066642	BC066642 Danio rer	813	116.4	6.7	9021	6	AX657808	AX657808 Sequence
c 741	116.4	6.7	1287	3	BT009948	BT009948 Drosophill	814	116.4	6.7	9021	6	AX659082	AX659082 Sequence
c 742	116.4	6.7	1343	10	BC061103	BC061103 Mus muscu	815	116.4	6.7	12007	6	AX345619	AX345619 Sequence
c 743	116.4	6.7	1344	5	BC056074	BC056074 Xenopus l	816	116.4	6.7	133276	2	AC087147	AC087147 Mus muscu
c 744	116.4	6.7	1347	10	BC008980	BC008980 Mus muscu	817	116.4	6.7	189682	2	AC107855	AC107855 Mus muscu
c 745	116.4	6.7	1373	10	BC049731	BC049731 Homo sapi	818	116.2	6.7	267	6	CQ525163	CQ525163 Sequence
c 746	116.4	6.7	1387	9	BC032568	BC032568 Homo sapi	819	116.2	6.7	738	9	HSMB06309	BX538116 Homo sapi
c 747	116.4	6.7	1409	5	BC064261	BC064261 Xenopus t	820	116.2	6.7	756	6	CQ399155	CQ399155 Sequence
c 748	116.4	6.7	1419	9	BC032340	BC032340 Homo sapi	821	116.2	6.7	756	6	CQ405433	CQ405433 Sequence
c 749	116.4	6.7	1500	10	BC049755	BC049755 Mus muscu	822	116.2	6.7	789	9	BC061900	BC061900 Homo sapi



823	116.2	6.7	854	5	BC084189	BC084189 Xenopus t	c	896	116	6.7	5908	6	AX345499	AX345499 Sequence
824	116.2	6.7	911	10	BC061126	BC061126 Mus muscu	c	897	116	6.7	9095	6	AX458545	AX458545 Sequence
825	116.2	6.7	977	9	BC051846	BC051846 Homo sapi		898	115.8	6.7	325	6	CQ527169	CQ527169 Sequence
826	116.2	6.7	1198	10	BC033305	BC033305 Mus muscu		899	115.8	6.7	458	10	BC061002	BC061002 Mus muscu
827	116.2	6.7	1305	9	BC039058	BC039058 Homo sapi		900	115.8	6.7	500	6	CQ408389	CQ408389 Sequence
828	116.2	6.7	1273	10	BC049640	BC049640 Mus muscu		901	115.8	6.7	504	6	CQ526778	CQ526778 Sequence
829	116.2	6.7	1280	9	BC047365	BC047365 Homo sapi		902	115.8	6.7	549	6	CQ524814	CQ524814 Sequence
830	116.2	6.7	1368	6	BC083654	BC083654 Rattus no	c	903	115.8	6.7	606	6	CQ503221	CQ503221 Sequence
831	116.2	6.7	1403	9	BC043542	BC043542 Homo sapi	c	904	115.8	6.7	606	6	CQ512068	CQ512068 Sequence
832	116.2	6.7	1408	10	BC048693	BC048693 Mus muscu		905	115.8	6.7	625	9	BC032803	BC032803 Homo sapi
833	116.2	6.7	1498	10	BC065779	BC065779 Mus muscu		906	115.8	6.7	732	5	AY522586	AY522586 Oreochrom
834	116.2	6.7	1517	9	BC016152	BC016152 Homo sapi		907	115.8	6.7	848	5	BC062495	BC062495 Xenopus t
835	116.2	6.7	1538	5	BC051777	BC051777 Danio rer	c	908	115.8	6.7	870	6	CQ482086	CQ482086 Sequence
836	116.2	6.7	1560	9	BC073173	BC073173 Homo sapi		909	115.8	6.7	879	9	BC007021	BC007021 Homo sapi
837	116.2	6.7	1610	9	BC064141	BC064141 Homo sapi		910	115.8	6.7	1010	10	BC061971	BC061971 Rattus no
838	116.2	6.7	1630	9	BC039130	BC039130 Homo sapi		911	115.8	6.7	1038	9	BC038366	BC038366 Homo sapi
839	116.2	6.7	1673	10	BC010324	BC010324 Mus muscu		912	115.8	6.7	1084	9	BC022290	BC022290 Homo sapi
840	116.2	6.7	1680	10	AF528194	AF528194 Mus muscu		913	115.8	6.7	1173	10	BC061094	BC061094 Mus muscu
841	116.2	6.7	1691	3	AF044679	AF044679 Leishmani		914	115.8	6.7	1310	9	HSM807559	HSM807559 Mus muscu
842	116.2	6.7	1719	10	BC045148	BC045148 Mus muscu		915	115.8	6.7	1429	10	BC022990	BC022990 Mus muscu
843	116.2	6.7	1727	10	BC050800	BC050800 Mus muscu		916	115.8	6.7	1646	9	BC051812	BC051812 Homo sapi
844	116.2	6.7	1733	6	BD062047	BD062047 Novel tum		917	115.8	6.7	1650	9	AB047615	AB047615 Macaca fa
845	116.2	6.7	1946	5	BC077411	BC077411 Xenopus l		918	115.8	6.7	1782	9	BC050531	BC050531 Homo sapi
846	116.2	6.7	2194	10	BC031202	BC031202 Mus muscu		919	115.8	6.7	1820	5	BC066434	BC066434 Danio rer
847	116.2	6.7	2316	10	BC064469	BC064469 Mus muscu		920	115.8	6.7	1933	6	BD270058	BD270058 Secreted
848	116.2	6.7	2553	10	BC061558	BC061558 Rattus no		921	115.8	6.7	2012	10	AF362952	AF362952 Mus muscu
849	116.2	6.7	2713	5	BC060926	BC060926 Danio rer		922	115.8	6.7	2012	6	AX664375	AX664375 Sequence
850	116.2	6.7	2800	9	BC053596	BC053596 Homo sapi		923	115.8	6.7	2087	10	BC054081	BC054081 Mus muscu
851	116.2	6.7	3159	10	BC030921	BC030921 Mus muscu		924	115.8	6.7	2095	5	BC084410	BC084410 Xenopus l
852	116.2	6.7	3326	9	HSM808512	HSM808512 Mus muscu		925	115.8	6.7	2178	9	BC046358	BC046358 Homo sapi
853	116.2	6.7	3332	10	HSM805392	HSM805392 Mus muscu		926	115.8	6.7	2223	5	BC067619	BC067619 Danio rer
854	116.2	6.7	3422	9	HSM805920	HSM805920 Homo sapi		927	115.8	6.7	2270	9	HSM806047	HSM806047 Homo sapi
855	116.2	6.7	3884	9	HSM806337	HSM806337 Homo sapi		928	115.8	6.7	2319	9	HSM805518	HSM805518 Homo sapi
856	116.2	6.7	4066	10	BC048824	BC048824 Mus muscu		929	115.8	6.7	2320	10	BC046962	BC046962 Mus muscu
857	116.2	6.7	4180	10	BC042645	BC042645 Mus muscu		930	115.8	6.7	2394	5	BC063911	BC063911 Xenopus t
858	116.2	6.7	4454	9	HSM806344	HSM806344 Mus muscu		931	115.8	6.7	2556	9	HSM805953	HSM805953 Homo sapi
859	116.2	6.7	4753	10	BC058514	BC058514 Mus muscu		932	115.8	6.7	2633	9	HSM804701	HSM804701 Homo sapi
860	116.2	6.7	5339	3	AY119181	AY119181 Drosophill		933	115.8	6.7	2666	9	BC027972	BC027972 Homo sapi
861	116.2	6.7	34980	6	AX344558	AX344558 Sequence		934	115.8	6.7	3117	10	BC043717	BC043717 Mus muscu
862	116	6.7	235	6	CQ677257	CQ677257 Sequence		935	115.8	6.7	3482	9	HSM800550	HSM800550 Homo sapi
863	116	6.7	270	6	CQ655781	CQ655781 Sequence		936	115.8	6.7	3502	9	HSM807726	HSM807726 Homo sapi
864	116	6.7	466	11	BV090989	BV090989 RPAMMSQ0		937	115.8	6.7	3582	10	BC053927	BC053927 Mus muscu
865	116	6.7	466	11	BV098168	BV098168 RPAMMSQ0		938	115.8	6.7	3669	10	BC038376	BC038376 Mus muscu
866	116	6.7	481	6	CQ524400	CQ524400 Sequence		939	115.8	6.7	3758	9	HSM801755	HSM801755 Homo sapi
867	116	6.7	481	9	BC070219	BC070219 Homo sapi		940	115.8	6.7	4064	10	BC072632	BC072632 Mus muscu
868	116	6.7	525	9	BC034020	BC034020 Homo sapi		941	115.8	6.7	4851	10	BC062121	BC062121 Mus muscu
869	116	6.7	827	10	BC049729	BC049729 Mus muscu		942	115.8	6.7	5123	10	BC064466	BC064466 Mus muscu
870	116	6.7	936	6	BD107846	BD107846 36 human	c	943	115.8	6.7	5216	6	AX281348	AX281348 Sequence
871	116	6.7	950	9	BC063550	BC063550 Homo sapi		944	115.8	6.7	5216	6	AX345249	AX345249 Sequence
872	116	6.7	1083	9	HSM800561	HSM800561 Homo sapi		945	115.8	6.7	5395	10	BC078662	BC078662 Homo sapi
873	116	6.7	1113	9	BC030277	BC030277 Homo sapi		946	115.8	6.7	5595	10	BC082548	BC082548 Mus muscu
874	116	6.7	1126	6	BD275148	BD275148 48 Human	c	947	115.8	6.7	11097	6	AX826974	AX826974 Sequence
875	116	6.7	1216	10	BC052782	BC052782 Mus muscu		948	115.6	6.7	144	6	BD138840	BD138840 Secreted
876	116	6.7	1233	10	BC058696	BC058696 Mus muscu		949	115.6	6.7	144	6	I89947	I89947 Sequence 26
877	116	6.7	1269	9	BC072684	BC072684 Homo sapi		950	115.6	6.7	144	6	BD005387	BD005387 Secreted
878	116	6.7	1426	5	BC054250	BC054250 Xenopus l		951	115.6	6.7	240	6	I48979	I48979 Sequence 6
879	116	6.7	1720	9	BC036875	BC036875 Homo sapi		952	115.6	6.7	484	6	CQ426160	CQ426160 Sequence
880	116	6.7	1743	10	BC051150	BC051150 Mus muscu	c	953	115.6	6.7	508	6	CQ411440	CQ411440 Sequence
881	116	6.7	1756	9	BC029848	BC029848 Homo sapi		954	115.6	6.7	565	6	CQ526051	CQ526051 Sequence
882	116	6.7	2009	3	AK116580	AK116580 Clona inc		955	115.6	6.7	603	6	CQ526797	CQ526797 Sequence
883	116	6.7	2090	9	BC049196	BC049196 Homo sapi		956	115.6	6.7	931	10	BC049725	BC049725 Mus muscu
884	116	6.7	2139	5	BC054626	BC054626 Danio rer		957	115.6	6.7	1109	10	BC063150	BC063150 Rattus no
885	116	6.7	2186	5	BC077623	BC077623 Xenopus l		958	115.6	6.7	1251	10	BC038552	BC038552 Mus muscu
886	116	6.7	2207	10	BC066857	BC066857 Mus muscu		959	115.6	6.7	1299	6	BD227288	BD227288 Secreted
887	116	6.7	2475	3	AY296116	AY296116 Ixodes sc		960	115.6	6.7	1462	10	BC060618	BC060618 Mus muscu
888	116	6.7	2852	6	AX574786	AX574786 Sequence		961	115.6	6.7	1500	9	BC056861	BC056861 Homo sapi
889	116	6.7	3117	9	BC043528	BC043528 Homo sapi		962	115.6	6.7	1661	9	BC025755	BC025755 Homo sapi
890	116	6.7	3221	9	BC015893	BC015893 Homo sapi		963	115.6	6.7	1782	10	BC050802	BC050802 Mus muscu
891	116	6.7	3640	9	HSM806825	HSM806825 Homo sapi		964	115.6	6.7	1876	10	BC053422	BC053422 Mus muscu
892	116	6.7	4283	9	BC042496	BC042496 Homo sapi		965	115.6	6.7	1889	9	BC050462	BC050462 Homo sapi
893	116	6.7	4675	9	HSM803445	HSM803445 Homo sapi		966	115.6	6.7	1906	10	BC063161	BC063161 Rattus no
894	116	6.7	5277	9	HSM808645	HSM808645 Homo sapi		967	115.6	6.7	1913	3	AY069281	AY069281 Drosophill
895	116	6.7	5366	6	AX345435	AX345435 Sequence		968	115.6	6.7	1973	9	BC022780	BC022780 Homo sapi

969	115.6	6.7	1999	9	HS24242859	AJ242859 Homo sapi	1042	115.4	6.7	4358	10	BC060187	BC060187 Mus muscu
970	115.6	6.7	2045	5	BC047761	BC047761 Homo sapi	1043	115.4	6.7	4518	9	HS2802971	AL713745 Homo sapi
971	115.6	6.7	2106	5	BC075571	BC075571 Xenopus t	1044	115.4	6.7	4574	9	HS2803437	AL832130 Homo sapi
972	115.6	6.7	2245	9	HS2803715	BC024407 Homo sapi	1045	115.4	6.7	4606	10	BC058089	BC058089 Mus muscu
973	115.6	6.7	2313	10	BC021410	BC021410 Mus muscu	1046	115.4	6.7	4812	5	BC068296	BC068296 Xenopus t
974	115.6	6.7	2878	9	HS2805674	BX537379 Homo sapi	1047	115.4	6.7	5219	9	BC057396	BC057396 Homo sapi
975	115.6	6.7	2917	9	BC054514	BC054514 Homo sapi	c1048	115.4	6.7	6171	6	AX345691	AX345691 Sequence
976	115.6	6.7	2972	9	BC023549	BC023549 Homo sapi	c1049	115.4	6.7	6522	6	AX345952	AX345952 Sequence
977	115.6	6.7	3401	9	BC040376	BC040376 Homo sapi	c1050	115.4	6.7	349980	6	AX344566	AX344566 Sequence
978	115.6	6.7	3796	5	BC066783	BC066783 Xenopus t	c1051	115.2	6.6	375	6	CQ513063	CQ513063 Sequence
979	115.6	6.7	4413	10	BC053035	BC053035 Mus muscu	1052	115.2	6.6	488	6	CQ522468	CQ522468 Sequence
c 980	115.6	6.7	4670	9	BC072849	BC072849 Homo sapi	1053	115.2	6.6	539	10	BC061539	BC061539 Rattus no
c 981	115.6	6.7	5908	6	AX251914	AX251914 Sequence	1054	115.2	6.6	554	6	CQ526772	CQ526772 Sequence
c 982	115.6	6.7	5908	6	AX277930	AX277930 Sequence	1055	115.2	6.6	562	10	BC049688	BC049688 Mus muscu
c 983	115.6	6.7	5908	6	AX232617	AX232617 Sequence	1056	115.2	6.6	637	9	BC024914	BC024914 Homo sapi
c 984	115.6	6.7	66993	2	AC138074	AC138074 Homo sapi	1057	115.2	6.6	686	10	BC060302	BC060302 Mus muscu
c 985	115.6	6.7	193988	2	AC102269	AC102269 Mus muscu	1058	115.2	6.6	691	5	BC071138	BC071138 Xenopus l
c 986	115.4	6.7	260	6	CQ695445	CQ695445 Sequence	1059	115.2	6.6	720	10	BC083088	BC083088 Mus muscu
987	115.4	6.7	335	10	BC048511	BC048511 Mus muscu	1060	115.2	6.6	723	9	HS2808728	BX648577 Homo sapi
988	115.4	6.7	384	3	AF155365	AF155365 Buthus na	1061	115.2	6.6	837	9	S78214	S78214 APC=tumor a
989	115.4	6.7	743	10	BC034898	BC034898 Mus muscu	1062	115.2	6.6	845	9	BC044653	BC044653 Homo sapi
990	115.4	6.7	791	9	BC038970	BC038970 Homo sapi	1063	115.2	6.6	909	10	BC035323	BC035323 Mus muscu
991	115.4	6.7	847	9	BC053571	BC053571 Homo sapi	1064	115.2	6.6	1078	9	BC035314	BC035314 Homo sapi
992	115.4	6.7	860	9	BC038839	BC038839 Homo sapi	1065	115.2	6.6	1080	9	BC022354	BC022354 Homo sapi
993	115.4	6.7	865	10	BC060948	BC060948 Mus muscu	1066	115.2	6.6	1119	9	BC070137	BC070137 Homo sapi
994	115.4	6.7	872	6	AX068322	AX068322 Sequence	1067	115.2	6.6	1175	10	BC049596	BC049596 Mus muscu
995	115.4	6.7	890	8	AY735693	AY735693 Arabidops	1068	115.2	6.6	1348	9	BC070154	BC070154 Homo sapi
996	115.4	6.7	911	10	BC061108	BC061108 Mus muscu	1069	115.2	6.6	1388	9	BC016332	BC016332 Homo sapi
997	115.4	6.7	959	9	BC031674	BC031674 Homo sapi	1070	115.2	6.6	1400	9	BC063708	BC063708 Homo sapi
998	115.4	6.7	1001	10	BC049605	BC049605 Mus muscu	1071	115.2	6.6	1468	10	BC068202	BC068202 Rattus no
999	115.4	6.7	1038	10	BC013496	BC013496 Mus muscu	1072	115.2	6.6	1487	9	BC026303	BC026303 Homo sapi
1000	115.4	6.7	1248	5	BC071085	BC071085 Xenopus l	1073	115.2	6.6	1500	5	XLNKAATP	Y11587 X.laevia nr
1001	115.4	6.7	1469	6	BD260697	BD260697 50 human	1074	115.2	6.6	1502	9	BC009739	BC009739 Homo sapi
1002	115.4	6.7	1500	3	AK174058	AK174058 Clona int	1075	115.2	6.6	1615	9	AF218014	AF218014 Homo sapi
1003	115.4	6.7	1545	10	BC062173	BC062173 Mus muscu	1076	115.2	6.6	1650	9	BC036926	BC036926 Homo sapi
1004	115.4	6.7	1562	10	BC063181	BC063181 Rattus no	1077	115.2	6.6	1660	9	BC032309	BC032309 Homo sapi
1005	115.4	6.7	1589	9	BC043543	BC043543 Homo sapi	1078	115.2	6.6	1752	9	BC042090	BC042090 Homo sapi
1006	115.4	6.7	1739	9	AK026045	AK026045 Homo sapi	1079	115.2	6.6	1805	9	AB070053	AB070053 Macaca fa
1007	115.4	6.7	1755	9	BC031825	BC031825 Homo sapi	1080	115.2	6.6	1890	9	HS2807434	AX647290 Homo sapi
1008	115.4	6.7	1770	9	BC063419	BC063419 Homo sapi	1081	115.2	6.6	1941	5	BC053250	BC053250 Danio rer
1009	115.4	6.7	1894	9	AB063046	AB063046 Macaca fa	1082	115.2	6.6	1975	10	BC052682	BC052682 Mus muscu
1010	115.4	6.7	1904	6	AR528502	AR528502 Sequence	1083	115.2	6.6	1985	6	BD172402	BD172402 Secretd
1011	115.4	6.7	1904	6	AX463966	AX463966 Sequence	1084	115.2	6.6	1985	6	BD172721	BD172721 Secretd
1012	115.4	6.7	1904	9	AY358614	AY358614 Homo sapi	1085	115.2	6.6	1985	6	BD173040	BD173040 Secretd
1013	115.4	6.7	1924	9	AK026741	AK026741 Homo sapi	1086	115.2	6.6	1985	6	BD173359	BD173359 Secretd
1014	115.4	6.7	1963	10	BC083817	BC083817 Rattus no	1087	115.2	6.6	1985	6	BD175393	BD175393 Secretd
1015	115.4	6.7	1986	10	BC050807	BC050807 Mus muscu	1088	115.2	6.6	1985	6	CQ881212	CQ881212 Sequence
1016	115.4	6.7	2058	6	BD276055	BD276055 48 Human	1089	115.2	6.6	1985	6	AR410771	AR410771 Sequence
1017	115.4	6.7	2074	9	BC014433	BC014433 Homo sapi	1090	115.2	6.6	1985	6	AR439135	AR439135 Sequence
1018	115.4	6.7	2095	5	BC067676	BC067676 Danio rer	1091	115.2	6.6	1985	6	AR473155	AR473155 Sequence
1019	115.4	6.7	2098	9	BC017717	BC017717 Homo sapi	1092	115.2	6.6	1985	6	AR527141	AR527141 Sequence
1020	115.4	6.7	2161	9	BC025768	BC025768 Homo sapi	1093	115.2	6.6	1985	6	AR566174	AR566174 Sequence
1021	115.4	6.7	2172	9	AB096991	AB096991 Macaca fa	1094	115.2	6.6	1985	6	AX375960	AX375960 Sequence
1022	115.4	6.7	2178	6	AX099370	AX099370 Sequence	1095	115.2	6.6	1985	6	AX697621	AX697621 Sequence
1023	115.4	6.7	2262	6	AR487911	AR487911 Sequence	1096	115.2	6.6	1985	6	BD075542	BD075542 Secretary
1024	115.4	6.7	2312	9	HS2803723	AL832415 Homo sapi	1097	115.2	6.6	1985	6	AY358500	AY358500 Homo sapi
1025	115.4	6.7	2334	3	AK116665	AK116665 Clona int	1098	115.2	6.6	1999	9	BC020684	BC020684 Homo sapi
1026	115.4	6.7	2403	9	HS2808752	BX648601 Homo sapi	1099	115.2	6.6	2060	10	BC038004	BC038004 Mus muscu
1027	115.4	6.7	2562	9	HS2808661	BX648513 Homo sapi	1100	115.2	6.6	2108	5	BC084490	BC084490 Xenopus t
1028	115.4	6.7	2910	9	BC042070	BC042070 Homo sapi	1101	115.2	6.6	2150	9	BC025715	BC025715 Homo sapi
1029	115.4	6.7	2924	9	BC063554	BC063554 Homo sapi	1102	115.2	6.6	2196	9	HS2805743	BX537439 Homo sapi
1030	115.4	6.7	2986	9	HS2807768	BX647622 Homo sapi	1103	115.2	6.6	2216	5	BC054636	BC054636 Danio rer
1031	115.4	6.7	2989	9	HS2807541	BX647396 Homo sapi	1104	115.2	6.6	2246	9	BC051820	BC051820 Homo sapi
1032	115.4	6.7	3084	10	BC058950	BC058950 Mus muscu	1105	115.2	6.6	2277	3	AK116699	AK116699 Clona int
1033	115.4	6.7	3186	5	BC068331	BC068331 Danio rer	1106	115.2	6.6	2377	8	AY080711	AY080711 Arabidops
1034	115.4	6.7	3245	9	HS2805849	BX537493 Homo sapi	1107	115.2	6.6	2387	10	BC048933	BC048933 Mus muscu
1035	115.4	6.7	3274	9	BC0207371	BX647227 Homo sapi	1108	115.2	6.6	2390	9	AF090900	AF090900 Homo sapi
1036	115.4	6.7	3307	9	BC025714	BC025714 Homo sapi	1109	115.2	6.6	2429	10	BC049167	BC049167 Mus muscu
1037	115.4	6.7	3686	10	BC023773	BC023773 Mus muscu	1110	115.2	6.6	2474	3	AY220909	AY220909 Helicover
1038	115.4	6.7	3983	9	HS2803572	AL832265 Homo sapi	1111	115.2	6.6	2607	5	BC054610	BC054610 Danio rer
1039	115.4	6.7	4064	6	AR526951	AR526951 Sequence	1112	115.2	6.6	2672	9	HS2806308	BX538115 Homo sapi
1040	115.4	6.7	4064	10	AF438405	AF438405 Mus muscu	1113	115.2	6.6	2747	9	HS2803601	AL832294 Homo sapi
1041	115.4	6.7	4158	9	HS2805995	BX537514 Homo sapi	1114	115.2	6.6	2750	5	BC084264	BC084264 Xenopus l

1115	115.2	6.6	2776	10	BC034120	BC034120 Mus muscu	c1188	114.8	6.6	445	6	CQ402005	CQ402005 Sequence
1116	115.2	6.6	2780	10	BC021914	BC021914 Mus muscu	c1189	114.8	6.6	476	6	CQ410349	CQ410349 Sequence
1117	115.2	6.6	3082	10	BC046972	BC046972 Mus muscu	1190	114.8	6.6	501	6	CQ527244	CQ527244 Sequence
1118	115.2	6.6	3183	9	BC044242	BC044242 Homo sapi	1191	114.8	6.6	579	6	CQ526842	CQ526842 Sequence
1119	115.2	6.6	3380	9	BSM807223	BSM807223 Homo sapi	1192	114.8	6.6	596	9	BC008387	BC008387 Homo sapi
1120	115.2	6.6	3358	9	BSM803467	BSM803467 Homo sapi	1193	114.8	6.6	612	10	BC061085	BC061085 Mus muscu
1121	115.2	6.6	3894	10	BC053925	BC053925 Mus muscu	1194	114.8	6.6	663	10	BC058460	BC058460 Rattus no
1122	115.2	6.6	4043	10	BC020177	BC020177 Mus muscu	1195	114.8	6.6	878	6	AX482482	AX482482 Sequence
1123	115.2	6.6	4286	9	BSM807052	BSM807052 Homo sapi	1196	114.8	6.6	932	9	BC043537	BC043537 Homo sapi
1124	115.2	6.6	4659	9	BSM806121	BSM806121 Homo sapi	1197	114.8	6.6	942	5	BC049498	BC049498 Danio rer
1125	115.2	6.6	4946	9	BSM805863	BSM805863 Homo sapi	1198	114.8	6.6	1004	9	BC043536	BC043536 Homo sapi
1126	115.2	6.6	5249	9	BSM803431	BSM803431 Homo sapi	1199	114.8	6.6	1007	10	BC049682	BC049682 Mus muscu
1127	115.2	6.6	5325	9	BSM806205	BSM806205 Homo sapi	1200	114.8	6.6	1030	10	BC049544	BC049544 Mus muscu
1128	115.2	6.6	5599	10	BC049182	BC049182 Mus muscu	1201	114.8	6.6	1065	10	BC049634	BC049634 Mus muscu
1129	115.2	6.6	6251	10	BC050823	BC050823 Mus muscu	1202	114.8	6.6	1110	9	BC063695	BC063695 Homo sapi
c1130	115.2	6.6	6960	6	AX347301	AX347301 Sequence	1203	114.8	6.6	1117	8	AF243375	AF243375 Glycine m
c1131	115.2	6.6	8712	6	AX344694	AX344694 Sequence	1204	114.8	6.6	1122	10	BC049644	BC049644 Mus muscu
c1132	115.2	6.6	113515	6	AX347077	AX347077 Sequence	1205	114.8	6.6	1156	5	BC049488	BC049488 Danio rer
1133	115.2	6.6	256673	2	AC087146	AC087146 Mus muscu	1206	114.8	6.6	1232	10	BC060554	BC060554 Rattus no
1134	115	6.6	381	6	CQ526814	CQ526814 Sequence	1207	114.8	6.6	1259	6	E03348	E03348 cDNA sequen
1135	115	6.6	423	6	CQ523358	CQ523358 Sequence	1208	114.8	6.6	1286	9	BC044234	BC044234 Homo sapi
1136	115	6.6	439	6	CQ525664	CQ525664 Sequence	1209	114.8	6.6	1286	9	BC010296	BC010296 Mus muscu
1137	115	6.6	490	6	CQ523744	CQ523744 Sequence	1210	114.8	6.6	1333	10	BC010296	BC010296 Mus muscu
1138	115	6.6	569	6	BD223440	BD223440 94 human	1211	114.8	6.6	1339	9	BC016710	BC016710 Homo sapi
1139	115	6.6	569	6	AR243074	AR243074 Sequence	1212	114.8	6.6	1405	9	BC044934	BC044934 Homo sapi
1140	115	6.6	569	6	AR404255	AR404255 Sequence	1213	114.8	6.6	1414	10	BC005487	BC005487 Mus muscu
1141	115	6.6	1093	9	BC043577	BC043577 Homo sapi	1214	114.8	6.6	1416	9	AF090943	AF090943 Homo sapi
1142	115	6.6	1124	9	BC025950	BC025950 Homo sapi	1215	114.8	6.6	1457	6	BD231695	BD231695 31 human
1143	115	6.6	1383	5	BC074687	BC074687 Xenopus t	1215	114.8	6.6	1493	9	BC042547	BC042547 Homo sapi
1144	115	6.6	1501	10	BC039998	BC039998 Mus muscu	1216	114.8	6.6	1498	10	BC083575	BC083575 Rattus no
1145	115	6.6	1641	9	BC043576	BC043576 Homo sapi	1217	114.8	6.6	1501	5	BC080019	BC080019 Xenopus l
1146	115	6.6	1648	9	BSM808551	BSM808551 Homo sapi	1218	114.8	6.6	1573	9	BSM801268	BSM801268 Homo sapi
1147	115	6.6	1656	5	BC064161	BC064161 Xenopus t	1219	114.8	6.6	1590	9	BSM803698	BSM803698 Homo sapi
1148	115	6.6	1671	10	BC022180	BC022180 Mus muscu	1220	114.8	6.6	1591	9	BC050659	BC050659 Homo sapi
1149	115	6.6	1800	9	BC053634	BC053634 Homo sapi	1221	114.8	6.6	1591	10	AB041801	AB041801 Mus muscl
1150	115	6.6	1802	9	AB071113	AB071113 Macaca fa	1222	114.8	6.6	1605	10	BC039750	BC039750 Mus muscu
1151	115	6.6	1802	9	BC016828	BC016828 Homo sapi	1223	114.8	6.6	1667	10	BC013215	BC013215 Mus muscu
1152	115	6.6	1813	6	AR164089	AR164089 Sequence	1224	114.8	6.6	1743	9	AB070131	AB070131 Macaca fa
1153	115	6.6	2104	9	BSM806838	BSM806838 Homo sapi	1225	114.8	6.6	1755	10	BC060516	BC060516 Rattus no
1154	115	6.6	2190	9	BC063454	BC063454 Homo sapi	1226	114.8	6.6	1790	9	BC042674	BC042674 Homo sapi
1155	115	6.6	2208	10	BC052921	BC052921 Mus muscu	1227	114.8	6.6	1827	5	BC049315	BC049315 Danio rer
1156	115	6.6	2321	9	BC058898	BC058898 Homo sapi	1228	114.8	6.6	1831	6	CQ498497	CQ498497 Sequence
1157	115	6.6	2496	6	BD191411	BD191411 Secreted	1229	114.8	6.6	1844	6	CQ412894	CQ412894 Sequence
1158	115	6.6	2514	9	BC044863	BC044863 Homo sapi	1230	114.8	6.6	1926	5	BSM804091	BSM804091 Xenopus l
1159	115	6.6	2548	9	BC040371	BC040371 Homo sapi	1231	114.8	6.6	1933	9	BSM806724	BSM806724 Homo sapi
1160	115	6.6	2765	9	BC044240	BC044240 Homo sapi	1232	114.8	6.6	1954	6	BD270057	BD270057 Secreted
1161	115	6.6	2943	10	BC005526	BC005526 Mus muscu	1233	114.8	6.6	1985	5	BC053414	BC053414 Danio rer
1162	115	6.6	2977	5	BC070986	BC070986 Xenopus l	1234	114.8	6.6	2001	3	AK112791	AK112791 Clona int
1163	115	6.6	3060	6	AR252731	AR252731 Sequence	1235	114.8	6.6	2010	10	BC046588	BC046588 Mus muscu
1164	115	6.6	3060	6	AX055476	AX055476 Sequence	1236	114.8	6.6	2053	9	BC030196	BC030196 Homo sapi
1165	115	6.6	3060	6	AX089948	AX089948 Sequence	1237	114.8	6.6	2054	10	BC039272	BC039272 Mus muscu
1166	115	6.6	3060	6	AX358962	AX358962 Sequence	1238	114.8	6.6	2096	10	BC034131	BC034131 Mus muscu
1167	115	6.6	3060	6	AX362455	AX362455 Sequence	1239	114.8	6.6	2108	9	AB047801	AB047801 Homo sapi
1168	115	6.6	3060	6	AX403617	AX403617 Sequence	1240	114.8	6.6	2112	5	BC076765	BC076765 Xenopus l
1169	115	6.6	3060	6	AX454694	AX454694 Sequence	1241	114.8	6.6	2158	5	BC082415	BC082415 Xenopus l
1170	115	6.6	3060	6	AX491172	AX491172 Sequence	1242	114.8	6.6	2164	10	BC005513	BC005513 Mus muscu
1171	115	6.6	3232	10	BC082299	BC082299 Mus muscu	1243	114.8	6.6	2202	10	BC052362	BC052362 Mus muscu
1172	115	6.6	3300	9	BC011656	BC011656 Homo sapi	1244	114.8	6.6	2325	10	BC051401	BC051401 Mus muscu
1173	115	6.6	4494	10	BC063058	BC063058 Mus muscu	1245	114.8	6.6	2325	9	BSM800967	BSM800967 Homo sapi
1174	115	6.6	4828	9	BSM808886	BSM808886 Homo sapi	1246	114.8	6.6	2485	10	BC064470	BC064470 Mus muscu
1175	115	6.6	5402	9	BSM804677	BSM804677 Homo sapi	1247	114.8	6.6	2500	10	BC050384	BC050384 Homo sapi
1176	115	6.6	6931	9	BSM803520	BSM803520 Homo sapi	1248	114.8	6.6	2507	9	BC053747	BC053747 Mus muscu
c1177	115	6.6	14006	6	AX346860	AX346860 Sequence	1249	114.8	6.6	2549	10	BC032289	BC032289 Mus muscu
1178	114.8	6.6	221	6	CQ685593	CQ685593 Sequence	1250	114.8	6.6	2549	10	BC061563	BC061563 Rattus no
1179	114.8	6.6	263	6	CQ683258	CQ683258 Sequence	1251	114.8	6.6	2661	10	BC026137	BC026137 Mus muscu
1180	114.8	6.6	299	6	CQ669036	CQ669036 Sequence	1252	114.8	6.6	2686	5	AJ719361	AJ719361 Gallus ga
1181	114.8	6.6	309	6	CQ513146	CQ513146 Sequence	1253	114.8	6.6	2789	3	AK114441	AK114441 Clona int
c1182	114.8	6.6	327	6	CQ408014	CQ408014 Sequence	1254	114.8	6.6	2840	5	BC056558	BC056558 Danio rer
1183	114.8	6.6	381	3	AF159974	AF159974 Butus ma	1255	114.8	6.6	3050	5	BC066571	BC066571 Danio rer
1184	114.8	6.6	396	6	CQ525748	CQ525748 Sequence	1256	114.8	6.6	3255	9	BSM803224	BSM803224 Homo sapi
1185	114.8	6.6	436	6	CQ397977	CQ397977 Sequence	1257	114.8	6.6	3317	9	BC039313	BC039313 Homo sapi
c1186	114.8	6.6	436	6	CQ404269	CQ404269 Sequence	1258	114.8	6.6	3491	5	BC059285	BC059285 Xenopus l
c1187	114.8	6.6	445	6	CQ395672	CQ395672 Sequence	1259	114.8	6.6	3518	9	BSM807510	BSM807510 Homo sapi
							1260	114.8	6.6	3547	5	BC084146	BC084146 Xenopus t

1261	114.8	6.6	3676	10	BC0622923	BC0629233 Mus muscu	1334	114.4	6.6	268	6	CQ526263	CQ526263 Sequence
1262	114.8	6.6	3899	6	BD191414	Secreted	1335	114.4	6.6	300	6	BD213699	BD213699 Novel hum
1263	114.8	6.6	3901	9	BSM803363	AL811956 Homo sapi	1336	114.4	6.6	323	6	CQ524910	CQ524910 Sequence
1264	114.8	6.6	4004	9	BC041086	BC041086 Homo sapi	1337	114.4	6.6	380	6	CQ526811	CQ526811 Sequence
1265	114.8	6.6	4298	9	BSM804564	AL833251 Homo sapi	1338	114.4	6.6	430	6	BC062435	BC062435 Homo sapi
1266	114.8	6.6	5155	9	BSM805801	BSX53723 Homo sapi	1339	114.4	6.6	454	3	AF150012	AF150012 Mesobuthu
1267	114.8	6.6	5586	6	AX345551	AX345551 Sequence	1340	114.4	6.6	515	6	CQ526571	CQ526571 Sequence
1268	114.8	6.6	5845	6	AX346564	AX346564 Sequence	1341	114.4	6.6	544	6	CQ524776	CQ524776 Sequence
1269	114.8	6.6	5966	9	BSM808164	BSX648018 Homo sapi	1342	114.4	6.6	585	6	CQ526237	CQ526237 Sequence
1270	114.8	6.6	6748	9	BSM807852	BSX647706 Homo sapi	1343	114.4	6.6	601	5	BC082936	BC082936 Xenopus 1
1271	114.8	6.6	6976	9	BSM808639	BSX648491 Homo sapi	1344	114.4	6.6	664	6	CQ397668	CQ397668 Sequence
1272	114.8	6.6	13606	6	AX251315	AX251315 Sequence	1345	114.4	6.6	664	6	CQ403965	CQ403965 Sequence
1273	114.8	6.6	13606	6	AX278002	AX278002 Sequence	1346	114.4	6.6	687	10	BC049765	BC049765 Mus muscu
1274	114.8	6.6	13606	6	AX323699	AX323699 Sequence	1347	114.4	6.6	706	10	BC055114	BC055114 Mus muscu
1275	114.8	6.6	13606	6	AX346712	AX346712 Sequence	1348	114.4	6.6	745	10	BC049606	BC049606 Mus muscu
1276	114.8	6.6	14920	6	AX344738	AX344738 Sequence	1349	114.4	6.6	763	9	BC040916	BC040916 Homo sapi
1277	114.8	6.6	17137	6	AX345092	AX345092 Sequence	1350	114.4	6.6	778	9	BC047942	BC047942 Homo sapi
1278	114.8	6.6	18624	6	AX346605	AX346605 Sequence	1351	114.4	6.6	782	9	BC040860	BC040860 Homo sapi
1279	114.8	6.6	113515	6	AX347076	AX347076 Sequence	1352	114.4	6.6	870	6	BD231669	BD231669 31 human
1280	114.8	6.6	349980	6	AX344571	AX344571 Sequence	1353	114.4	6.6	898	10	BC026633	BC026633 Mus muscu
1281	114.6	6.6	208	6	CQ677600	CQ677600 Sequence	1354	114.4	6.6	1037	10	BC061131	BC061131 Mus muscu
1282	114.6	6.6	231	6	CQ526354	CQ526354 Sequence	1355	114.4	6.6	1408	9	BC065718	BC065718 Homo sapi
1283	114.6	6.6	351	6	CQ410508	CQ410508 Sequence	1356	114.4	6.6	1457	9	BC056863	BC056863 Homo sapi
1284	114.6	6.6	397	3	AF135818	AF135818 Mesobuthu	1357	114.4	6.6	1561	9	BC040443	BC040443 Homo sapi
1285	114.6	6.6	462	6	CQ523723	CQ523723 Sequence	1358	114.4	6.6	1684	9	BC064148	BC064148 Homo sapi
1286	114.6	6.6	489	6	CQ524523	CQ524523 Sequence	1359	114.4	6.6	1929	10	BC058811	BC058811 Mus muscu
1287	114.6	6.6	539	6	CQ523463	CQ523463 Sequence	1360	114.4	6.6	1983	10	BC005510	BC005510 Mus muscu
1288	114.6	6.6	544	6	CQ410812	CQ410812 Sequence	1361	114.4	6.6	2004	9	BC043556	BC043556 Homo sapi
1289	114.6	6.6	757	9	BC051791	BC051791 Homo sapi	1362	114.4	6.6	2019	10	BC063758	BC063758 Mus muscu
1290	114.6	6.6	760	9	BC052336	BC052336 Homo sapi	1363	114.4	6.6	2035	9	BC063696	BC063696 Homo sapi
1291	114.6	6.6	843	10	BC026460	BC026460 Mus muscu	1364	114.4	6.6	2085	5	BC077186	BC077186 Xenopus 1
1292	114.6	6.6	860	9	BC039722	BC039722 Homo sapi	1365	114.4	6.6	2250	5	BC061708	BC061708 Danio rer
1293	114.6	6.6	881	10	BC049733	BC049733 Mus muscu	1366	114.4	6.6	2328	9	BC043587	BC043587 Homo sapi
1294	114.6	6.6	901	10	BC055108	BC055108 Sequence	1367	114.4	6.6	2400	5	BC056284	BC056284 Danio rer
1295	114.6	6.6	1026	6	CQ708603	CQ708603 Sequence	1368	114.4	6.6	2557	9	BC042875	BC042875 Homo sapi
1296	114.6	6.6	1138	10	BC062234	BC062234 Rattus no	1369	114.4	6.6	2585	9	BSM805677	BSM805677 Mus muscu
1297	114.6	6.6	1250	9	BC033385	BC033385 Homo sapi	1370	114.4	6.6	2630	9	BC038222	BC038222 Homo sapi
1298	114.6	6.6	1309	5	BC067650	BC067650 Danio rer	1371	114.4	6.6	2735	9	BC046366	BC046366 Homo sapi
1299	114.6	6.6	1470	9	BC072387	BC072387 Homo sapi	1372	114.4	6.6	2765	3	AK115430	AK115430 Ciona int
1300	114.6	6.6	1498	5	BC077743	BC077743 Xenopus 1	1373	114.4	6.6	2827	6	CQ491125	CQ491125 Sequence
1301	114.6	6.6	1527	5	BC064182	BC064182 Xenopus t	1374	114.4	6.6	2827	6	CQ496990	CQ496990 Sequence
1302	114.6	6.6	1527	6	BD227255	BD227255 Secreted	1375	114.4	6.6	2909	3	AK116710	AK116710 Ciona int
1303	114.6	6.6	1570	6	BC036920	BC036920 Homo sapi	1376	114.4	6.6	2922	3	AF479582	AF479582 Boophilus
1304	114.6	6.6	1603	6	CQ490224	CQ490224 Homo sapi	1377	114.4	6.6	3030	3	AK116919	AK116919 Ciona int
1305	114.6	6.6	1603	6	CQ491236	CQ491236 Sequence	1378	114.4	6.6	3336	5	BC054630	BC054630 Danio rer
1306	114.6	6.6	1603	6	CQ496086	CQ496086 Sequence	1379	114.4	6.6	4268	9	BC071594	BC071594 Homo sapi
1307	114.6	6.6	1603	6	CQ497104	CQ497104 Sequence	1380	114.4	6.6	4679	9	BSM808418	BSM808418 Homo sapi
1308	114.6	6.6	1606	10	BC051176	BC051176 Mus muscu	1381	114.4	6.6	4740	10	BC054557	BC054557 Mus muscu
1309	114.6	6.6	1626	9	BC050587	BC050587 Homo sapi	1382	114.4	6.6	4838	10	BC082542	BC082542 Mus muscu
1310	114.6	6.6	1722	5	BC063371	BC063371 Xenopus t	1383	114.4	6.6	5378	6	AX346781	AX346781 Sequence
1311	114.6	6.6	1732	10	BC033364	BC033364 Mus muscu	1384	114.4	6.6	5426	10	BC066037	BC066037 Mus muscu
1312	114.6	6.6	1756	9	BC069223	BC069223 Homo sapi	1385	114.4	6.6	61940	2	AC109312	AC109312 Homo sapi
1313	114.6	6.6	1789	9	BC070134	BC070134 Homo sapi	1386	114.2	6.6	358	6	CQ671266	CQ671266 Sequence
1314	114.6	6.6	1793	10	BC062171	BC062171 Mus muscu	1387	114.2	6.6	372	9	BC071808	BC071808 Homo sapi
1315	114.6	6.6	1835	9	BC040063	BC040063 Homo sapi	1388	114.2	6.6	487	10	BC069220	BC069220 Mus muscu
1316	114.6	6.6	1913	9	BC030546	BC030546 Homo sapi	1389	114.2	6.6	508	9	BC017744	BC017744 Homo sapi
1317	114.6	6.6	1930	5	BC066725	BC066725 Danio rer	1390	114.2	6.6	516	6	CQ524041	CQ524041 Sequence
1318	114.6	6.6	2240	5	BC084150	BC084150 Xenopus t	1391	114.2	6.6	547	6	CQ526009	CQ526009 Sequence
1319	114.6	6.6	2265	10	BC051639	BC051639 Mus muscu	1392	114.2	6.6	570	6	CQ527266	CQ527266 Sequence
1320	114.6	6.6	2284	9	AB055303	AB055303 Macaca fa	1393	114.2	6.6	606	6	CQ524188	CQ524188 Sequence
1321	114.6	6.6	2302	5	BC079972	BC079972 Xenopus 1	1394	114.2	6.6	610	6	CQ427732	CQ427732 Sequence
1322	114.6	6.6	2379	9	AB060887	AB060887 Macaca fa	1395	114.2	6.6	633	9	BC032625	BC032625 Homo sapi
1323	114.6	6.6	2420	5	BC066695	BC066695 Danio rer	1396	114.2	6.6	704	10	BC049749	BC049749 Mus muscu
1324	114.6	6.6	2598	5	BC044109	BC044109 Xenopus 1	1397	114.2	6.6	1155	9	BC036792	BC036792 Homo sapi
1325	114.6	6.6	2820	9	BC065198	BC065198 Homo sapi	1398	114.2	6.6	1345	9	BC073861	BC073861 Homo sapi
1326	114.6	6.6	3149	9	BSM807648	BSX67502 Homo sapi	1399	114.2	6.6	1493	9	BSM805897	BSM805897 Homo sapi
1327	114.6	6.6	3226	9	AY189289	AY189289 Homo sapi	1400	114.2	6.6	1725	9	BC028081	BC028081 Homo sapi
1328	114.6	6.6	3375	9	BC038406	BC038406 Homo sapi	1401	114.2	6.6	1781	9	BC041173	BC041173 Homo sapi
1329	114.6	6.6	3956	9	BSM805531	AL834437 Homo sapi	1402	114.2	6.6	1793	9	BC071757	BC071757 Homo sapi
1330	114.6	6.6	4940	9	BSM806769	BSX649189 Homo sapi	1403	114.2	6.6	1819	5	BC076769	BC076769 Xenopus 1
1331	114.6	6.6	5524	9	BSM807226	BSX647082 Homo sapi	1404	114.2	6.6	1820	8	BT009533	BT009533 Triticum
1332	114.6	6.6	349980	6	AX344559	AX344559 Sequence	1405	114.2	6.6	1832	5	BC084269	BC084269 Xenopus 1
1333	114.4	6.6	247	6	CQ524931	CQ524931 Sequence	1406	114.2	6.6	1885	9	BSM808768	BSM808768 Homo sapi

1407	114.2	1407	114.2	6.6	1910	9	BC0433519	BC043519 Homo sapi	1480	114	6.6	3110	10	BC057617	BC057617 Mus muscu
1408	114.2	1408	114.2	6.6	1953	10	BC034135	BC04135 Mus muscu	1481	114	6.6	3251	5	BC074658	BC074658 Xenopus t
1409	114.2	1409	114.2	6.6	2209	10	BC040761	BC040761 Mus muscu	1482	114	6.6	3310	10	BC061486	BC061486 Mus muscu
1410	114.2	1410	114.2	6.6	2224	6	BD189940	BD189940 Tumor ant	1483	114	6.6	3375	9	BSM806552	BSM806552 Homo sapi
1411	114.2	1411	114.2	6.6	2224	6	AB062292	AB062292 Homo sapi	1484	114	6.6	4124	3	AK112284	AK112284 Ciona int
1412	114.2	1412	114.2	6.6	2269	6	BD136822	BD136822 Podocalyx	1485	114	6.6	4829	10	BC060175	BC060175 Mus muscu
1413	114.2	1413	114.2	6.6	2269	6	AF212112	AF212112 Sequence	1486	114	6.6	5154	9	BSM805947	BSM805947 Homo sapi
1414	114.2	1414	114.2	6.6	2269	6	AF219137	AF219137 Homo sapi	1487	114	6.6	5165	6	CQ413028	CQ413028 Sequence
1415	114.2	1415	114.2	6.6	2432	9	BSM808545	BSM808545 Homo sapi	1488	114	6.6	5355	9	BSM806819	BSM806819 Homo sapi
1416	114.2	1416	114.2	6.6	2445	9	BC019562	BC019562 Homo sapi	1489	114	6.6	5439	9	BSM805827	BSM805827 Homo sapi
1417	114.2	1417	114.2	6.6	2608	6	BD230959	BD230959 49 human	1490	114	6.6	5627	10	BSM807499	BSM807499 Homo sapi
1418	114.2	1418	114.2	6.6	2608	6	AR337254	AR337254 Sequence	1491	114	6.6	5703	10	BC054080	BC054080 Mus muscu
1419	114.2	1419	114.2	6.6	2734	5	BC076749	BC076749 Xenopus l	1492	114	6.6	12177	6	AX345553	AX345553 Sequence
1420	114.2	1420	114.2	6.6	2740	9	BC053595	BC053595 Homo sapi	1493	114	6.6	12669	6	AX252150	AX252150 Sequence
1421	114.2	1421	114.2	6.6	2968	9	BC060758	BC060758 Homo sapi	1494	114	6.6	12669	6	AX344518	AX344518 Sequence
1422	114.2	1422	114.2	6.6	3059	10	BSM805182	BSM805182 Mus muscu	1495	114	6.6	12669	6	AX348921	AX348921 Sequence
1423	114.2	1423	114.2	6.6	3134	9	BSM805794	BSM805794 Homo sapi	1496	114	6.6	110000	8	CR382134_12	Continuation (13 o
1424	114.2	1424	114.2	6.6	3178	9	BSM803719	BSM803719 Homo sapi	1497	113.8	6.6	267	6	CQ526755	CQ526755 Sequence
1425	114.2	1425	114.2	6.6	4339	9	AF106862	AF106862 Homo sapi	1498	113.8	6.6	321	6	AX361391	AX361391 Sequence
1426	114.2	1426	114.2	6.6	4345	9	BSM808518	BSM808518 Homo sapi	1499	113.8	6.6	393	6	CQ408183	CQ408183 Sequence
1427	114.2	1427	114.2	6.6	4630	9	BSM807495	BSM807495 Homo sapi	1500	113.8	6.6	412	6	CQ522434	CQ522434 Sequence
1428	114.2	1428	114.2	6.6	4825	9	BSM802973	BSM802973 Homo sapi							
1429	114.2	1429	114.2	6.6	4864	9	BSM807992	BSM807992 Homo sapi							
1430	114.2	1430	114.2	6.6	5763	9	BSM808699	BSM808699 Homo sapi							
c1431	114.2	c1431	114.2	6.6	9580	14	AF054250	AF054250 Hepatitis							
c1432	114.2	c1432	114.2	6.6	13469	6	AX2511348	AX2511348 Sequence							
1433	114.2	1433	114.2	6.6	173854	2	AC073047	AC073047 Homo sapi							
1434	114.2	1434	114.2	6.6	191531	2	AC113984	AC113984 Mus muscu							
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LOCUS AX092320 1734 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 51 from Patent WO0116318.  
ACCESSION AX092320  
VERSION AX092320.1 GI:13444474  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and  
Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0116318-A 51 08-MAR-2001;  
Genentech, Inc. (US)  
FEATURES  
source 1..1734  
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Query Match 100.0%; Score 1734; DB 6; Length 1734;  
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DB 61 GAGGAGACAGAGGAGTCCGAG 120  
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QY 181 GAGATGAAGTTCCAGGGGCCCTTGGCCCTCTGCTTGGCCCTCTGCTTGGCCCTCTGCTTGGCC 240  
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QY 241 GAGGCTGGCCCCCTTGCAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

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Db	301	GGACATGGCCTTGGGAGAGCGCCTCGAGCGAAGGGGTGGGAAAGGCCATTTGGCAAGAGAGGCC	360	
Qy	361	GGAGGGGAGCTGGCTCTAAAGTCAGTGAAGGCCCTTGGCCAAAGGGACCCAGAGAACGAGTT	420	
Db	361	GGAGGGGAGCTGGCTCTAAAGTCAGTGAAGGCCCTTGGCCAAAGGGACCCAGAGAACGAGTT	420	
Qy	421	GGCACTGAAGTCAGGCAGGTTCCAGGCTTTGGCGGACGAGATGCTTTGGGGCAACAGGGTC	480	
Db	421	GGCACTGAAGTCAGGCAGGTTCCAGGCTTTGGCGGACGAGATGCTTTGGGGCAACAGGGTC	480	
Qy	481	GGGGAAAGCAGCCCATGCTCTCGGAAAAACACTGGGCACGAGATTGGCAGACAGGCAGAGAAT	540	
Db	481	GGGGAAAGCAGCCCATGCTCTCGGAAAAACACTGGGCACGAGATTGGCAGACAGGCAGAGAAT	540	
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Db	1141	AACCACGGTGGAGCGCGGAGGAAATGGACATAAAACCGGGTGTAAGAACCCAGGGAAT	1200	
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Db	1201	GAAGCCCGGGAGCGGGGATCTGGGATTCAGGGCTTCAGAGACAGGGAGTTCCAGC	1260	
Qy	1261	AACATGAGGGAAAATAAGCAAGAGGGCAATCGCCTCTCTGGAGGCTCTGGAGACAATTAT	1320	
Db	1261	AACATGAGGGAAAATAAGCAAGAGGGCAATCGCCTCTCTGGAGGCTCTGGAGACAATTAT	1320	
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[illegible]





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DEFINITION	Sequence 201 from Patent WO0168848.		
ACCESSION	AX376134		
VERSION	AX376134.1	GI:19170459	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Baker, K. P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P. J., Gurney, A. L., Pan, J., Smith, V., Watanabe, C. K., Wood, W. I. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0168848-A 201 20-SEP-2001; Genentech, Inc. (US)		
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Qy	121	GGCGGCAAGGAGGAGCCCTGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTCGGCA	180
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## RESULT 5

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AX403750
LOCUS AX403750
DEFINITION Sequence 105 from Patent WO0077037.
ACCESSION AX403750
VERSION AX403750.1 GI:21437185
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A., Baker,K., Botstein,D., Desnovers,L., Eaton,D.L.,
Ferrara,N., Fong,S., Gao,W.Q., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
Williams,P.M., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 105 21-DEC-2000;
Genentech Inc. (US)
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Location/Qualifiers
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Query Match 100.0%; Score 1734; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 6.6e-273;
Matches 1734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GTGGACTCTGAGAACCCAGGCGAGTTGAGGACAGAGAGAGAGAGGCTGCAGACCCAGAG 60
Qy 61 GAGGAGACAGCGGAGTCCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGAGAGCAAG 120
Db 61 GAGGAGACAGCGGAGTCCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGAGAGCAAG 120
Qy 121 GCGGCGAGGAGGAGACCCCTGGTGGGAGGAGACACTCTGGAGAGAGAGGGGGCTGGGCA 180
Db 121 GCGGCGAGGAGGAGACCCCTGGTGGGAGGAGACACTCTGGAGAGAGAGGGGGCTGGGCA 180
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QY 181 GAGATGAAGTTCAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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QY 241 GAGGCTGGCCCCCTGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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Db 721 TCAGCAGGAGGAGTTCGATGAATCTCAGGAGGAGTTCGATGAATCTCAGGAGGAGGAG 780
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LOCUS AX696983 1734 bp DNA linear PAT 02-APR-2003  
DEFINITION Sequence 51 from Patent WO0078961.  
ACCESSION AX696983  
VERSION AX696983.1 GI:29497984

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
1 Ferrar, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Pong, S., Goddard, A.,  
Goddard, P.J., Gurney, A.L., Smith, V., Tamas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 51 28-DEC-2000;  
Genentech Inc. (US)

FEATURES  
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1. .1734  
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Best Local Similarity 100.0%; Pred. No. 6.6e-273;  
Matches 1734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GAGATGAAGTTCCAGGGGCCCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
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DB 1621 ACAA 1680  
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LOCUS AY358412  
DEFINITION AY358412  
ACCESSION AY358412.1 GI:37181948  
VERSION AY358412.1  
KEYWORDS FLI CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1734)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL 12975309  
PUBMED 2 (bases 1 to 1734)  
AUTHORS Clark,H.F.



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Db 1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1734

RESULT 10
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LOCUS BD275935 1441 bp DNA linear PAT 17-JUL-2003
DEFINITION 62 Human secreted proteins.
ACCESSION BD275935
VERSION BD275935.1 GI:33085703
KEYWORDS JP 2002543771-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1441)
Birze,C.E., Mouret,P.A., Florence,K.A., Ruben,S.M.,
Komatsoulis,G.A., Ni,J.J., Ebner,R., W.D., Lafleur, Olsen,H.S.,
Shi,Y., Soppet,D.R., Rosen,C.A. and Young,P.E.
62 Human secreted proteins
Patent: JP 2002543771-A 13 24-DEC-2002;
Human Genome Sciences Inc
OS Homo sapiens
PN JP 2002543771-A/13
PD 24-DEC-2002
PF 06-APR-2000 JP 2000611564
PR 09-APR-1999 US 60/128693,26-APR-1999 US 60/130991 PI
Charles e birze,paul a mouret,kimberly a florence,steven m pi
ruben.
PI george a komatsoulis,jian ni,reinhard ebner,david w pi
lafleur,henrik s olsen,
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FH Key Location/Qualifiers
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ORIGIN

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Matches 1427; Conservative 0; Mismatches 3; Indels 162; Gaps 2;

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QY 101 GCACAGAGACGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 160
DB 72 GCACAGAGACGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 131
QY 161 GAGAGAGGGGGCTGGGACAGAGATGAAGTTCAGGGGGCCCTGGCCCTGCTGCTG 220
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QY 221 CCCTTGCTGGGACAGTGGGAGGCTGGCCCTGCGAGGCGGAGGAGGAGGAGGAGG 280
DB 192 CCCTTGCTGGGACAGTGGGAGGCTGGCCCTGCGAGGCGGAGGAGGAGGAGGAGG 251
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QY 341 AGGCCATTGGCAAGAGGCGGAGGGGACAGTGGCTCTAAAGTCAGTAGGGCCCTTGGCC 400
DB 312 AGGCCATTGGCAAGAGGCGGAGGGGACAGTGGCTCTAAAGTCAGTAGGGCCCTTGGCC 371
QY 401 AAGGACACAGAGAGCAGTGGCACTGGAGTCAGGAGGTTCCAGGCTTTGGCGGAGGAG 460
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DEFINITION Homo sapiens chromosome 19 clone LLNL-228H6, complete sequence.
ACCESSION AC138125
VERSION AC138125.1 GI:27151356
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 11311)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (17-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This is not the entire sequence of the clone (entire
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The number of bases overlapped is 2919.
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Matches 615; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db 5428 GGTGCTTGGGAGTGGTGTGGGGCTG 5401

RESULT 14
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LOCUS Human DNA from chromosome 19 specific cosmid R28461, genomic
DEFINITION sequence, complete sequence.
ACCESSION AC002389
VERSION AC002389.1 GI:2282012
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lamerdin, J.E., McCready, P.M., Adamson, A.W., Burkhardt-Schultz, K.,
Garcia, E., Kyle, A., Ramirez, M., Stillwagen, S., Barnes, J.,
Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A.,
Olsen, A.O. and Carrano, A.V.
TITLE Sequence analysis of a 1Mb region in 19q13.1
JOURNAL Unpublished
2 (bases 1 to 46275)
Lamerdin, J.E.
Direct Submission
Submitted (28-JUL-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
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clone 788214 5' similar to WP:ZK418.5 CE00807"
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clone 788214 5' similar to WP:ZK418.5 CE00807"
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frame: 1, quality: excellent, score: 100.000"
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  QY 61 GAGGAGGACAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
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  QY 121 GCGCGCAAGGAGGAGACCTGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
  Db 3063 GCGCGCAAGGAGGAGACCTGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3004

  QY 181 GAGATGAAGTTCAGGGGGCCCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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  QY 241 GAGGCTGGCCCTCGCAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
  Db 2943 GAGGCTGGCCCTCGCAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2884

  QY 301 GGACATGGCTCGGAGAGCGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
  Db 2883 GGACATGGCTCGGAGAGCGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2824

  QY 361 GGAGGGGCGAGCTGGCTCTAAAGTCAGTGAGGCGCTTGGCAGAGGAGGAGGAGGAGGAG 420
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  Db 2763 GGCATCTGGAGTCAGGAGGAGTTCAGGCTTTGGCGAGGAGGAGGAGGAGGAGGAGGAG 2704

  QY 481 GGGGAAGCAGCCCATCTCTGGGAAACACTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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  QY 541 GTCATTGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
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DEFINITION Sequence 7142 from Patent WO02068579.
ACCESSION CQ721208
VERSION CQ721208.1 GI:42282065
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 7142 06-SEP-2002;
PE Corporation (NY) (US)
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  QY 244 GCTGCCCCCTGCAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
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  QY 304 CATGCGCTGGGAGAGCGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAGAGGCCGGA 363
  Db 121 CATGCGCTGGGAGAGCGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAGAGGCCGGA 180

  QY 364 GGGGAGCTGGCTCTAAAGTCAGTGAGGCGCTTGGCCAAAGGAGCCAGAGAGCAGTTGGC 423
  Db 181 GGGGAGCTGGCTCTAAAGTCAGTGAGGCGCTTGGCCAAAGGAGCCAGAGAGCAGTTGGC 240

  QY 424 ACTGGAGTCAGGAGGTTCCAGGCTTTGCGCGCAGCAGATGCTTTGGGCAACAGGGGTGCG 483
  Db 241 ACTGGAGTCAGGAGGTTCCAGGCTTTGCGCGCAGCAGATGCTTTGGGCAACAGGGGTGCG 300

  QY 484 GAAGCAGCCCATGCTCTGGGAAACACTGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
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Search completed: May 16, 2005, 22:19:19
Job time : 7415 secs
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Gapop 10'-0 , Gapext 1.0
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description
RESULT 1
ID AAC87038 standard; cDNA; 1734 BP.
DE Nucleotide sequence of human polypeptide PRO1411.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 2
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DE Human DNA encoding PRO polypeptide sequence #101.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 3
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DE Human PRO1411 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 4; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 4
ID ABK33613 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO protein, Seq ID No 155.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 6; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 5
ID ABS74403 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.

Title: US-10-063-699-51
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Gapop 10'-0 , Gapext 1.0
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : N_Geneseq_16Dec04.*
1: Geneseqn19806.*
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13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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PN WO200077037-A2.
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DE Human DNA encoding PRO polypeptide sequence #101.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
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PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.9e-243;
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DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
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RESULT 6
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DE Human angiogenesis related cDNA PRO1411 SEQ ID NO: 149.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERR ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
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Best Local Similarity 100.0%; Pred. No. 1.9e-243;
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DE cDNA encoding human PRO polypeptide #101.
PN US2003036141-A1.
PD 20-FEB-2003.
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Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 8
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DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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PN US2003036162-A1.
PD 20-FEB-2003.
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PN US2003036137-A1.
PD 20-FEB-2003.
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DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 12
ID ACDB1566 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO411.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
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RESULT 13
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PN US2003040063-A1.  
PD 27-FEB-2003.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
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PN US2003040064-A1.  
PD 27-FEB-2003.  
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ID ACD1893 standard; cDNA; 1734 BP.  
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PN US2003027267-A1.  
PD 06-FEB-2003.  
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Pred. No. 1.9e-243;  
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PN US2003036160-A1.  
PD 20-FEB-2003.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
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PN US2003044925-A1.  
PD 06-MAR-2003.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
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ID ACF02000 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 19  
ID ACA60388 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
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ID ACA72257 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
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DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
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Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
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PN US2003036124-A1.  
PD 20-FEB-2003.  
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PN US2003040054-A1.  
PD 27-FEB-2003.  
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ID ACA8683 standard; cDNA; 1734 BP.  
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PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003036134-A1.  
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PN US2003027275-A1.  
PD 06-FEB-2003.  
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PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 30  
ID ACD25458 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 31  
ID ACD17935 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 32  
ID ACC88222 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 33  
ID ACD21576 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.

PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 34  
ID ACD19643 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US200304916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 35  
ID ACA58935 standard; cDNA; 1734 BP.  
DE cDNA encoding human secreted polypeptide PRO1411.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 36  
ID ABX98253 standard; cDNA; 1734 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 201.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 37  
ID ACD14004 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 38  
ID ACD09784 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 39  
ID ACC68529 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 40  
ID ACD21269 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 41  
ID ABX75641 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1411.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 42  
ID ACA64011 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #26.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 43  
ID ABX97844 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.

PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 44  
ID ACA97320 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 45  
ID ACA57783 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 46  
ID ACD14311 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 47  
ID ACC91094 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 48  
ID ACC68836 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 49  
ID ACD07033 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 50  
ID ACA67484 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 51  
ID ACC81539 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 52  
ID ACA91275 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #26.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 53  
ID ACC89143 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 54  
ID ACC86499 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 55  
ID ACC89757 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 56  
ID ACC92936 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 57  
ID ACAT2564 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 58  
ID ACA89082 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 59  
ID ACA69818 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 60  
ID ACA96961 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 61  
ID ACA90957 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 62  
ID ACA70739 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 63  
ID ACA95249 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 64  
ID ACC86192 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 65  
ID ACD45174 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO411 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 66  
ID ACC90064 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 67  
ID ACD12672 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 68  
ID ACF19902 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 69  
ID ABX76846 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 70  
ID ACA60527 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 71  
ID ACA73178 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 72  
ID ACA68721 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 73  
ID ACA74565 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003036138-A1.  
PD 20-FEB-2003.



Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 74  
ID ACA04517 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 DNA.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 75  
ID ACA70432 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 76  
ID ACD14618 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 77  
ID ACA93722 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 78  
ID ACA68290 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 79  
ID ABX98755 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 80  
ID ACA67296 standard; cDNA; 1734 BP.  
DE cDNA encoding human secreted polypeptide PRO1411.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 81  
ID ACC81232 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 82  
ID ACA95556 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 83  
ID ACD04474 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 84  
ID ACA68574 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 85  
ID ACC87915 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 86  
ID ACF12577 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 87  
ID ACH66269 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 88  
ID ACA96292 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 89  
ID ACA5066 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 90  
ID ACA73792 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 91  
ID ACA74204 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 92  
ID ACA96599 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 8; Length 1734;  
RESULT 93  
ID ACD10705 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003032107-A1.  
PD 13-FEB-2003.



RESULT 114  
ID ACA94942 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 115  
ID AC016504 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 116  
ID AC015593 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 117  
ID ACA98473 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 118  
ID ABX16686 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein #101.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 8; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 119  
ID ACAG3398 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #26.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 120  
ID ACA97627 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 121  
ID ACA65658 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 122  
ID ACA99076 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 123  
ID ACC91708 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 124  
ID AC011119 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 125  
ID AC014969 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US200304922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 126  
ID AC011733 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 127  
ID ACC95862 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 128  
ID ACF16425 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 129  
ID ACF02543 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 130  
ID ACF02850 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 131  
ID ACF21437 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 132  
ID ACF10121 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 133  
ID ACF78014 standard; cDNA; 1734 BP.

DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 134  
ID ACD46719 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 135  
ID ACD49482 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 136  
ID ACF28249 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 137  
ID ACD88939 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 138  
ID ACD84334 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 139  
ID ACD99108 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 140  
ID ADA77953 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 141  
ID ACP48850 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 142  
ID ACD09170 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036131-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 143  
ID ACF11963 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 144  
ID ACF41197 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 145  
ID ACF15811 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 146  
ID ACF16118 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 147  
ID ABR44303 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 148  
ID ADB17108 standard; cDNA; 1734 BP.  
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 149  
ID ACD31945 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 150  
ID ACF18753 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 151  
ID ACF09200 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

RESULT 152  
ID ACF78321 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054473-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 153  
ID ACF51920 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064440-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 154  
ID ACF26407 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068704-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 155  
ID ACF24200 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068722-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 156  
ID ACF63511 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073183-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 157  
ID ACF50385 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104549-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 158  
ID ACH07856 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049749-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 159  
ID ACF13662 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064462-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 160  
ID ACD41588 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003065159-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 161  
ID ACF32001 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064447-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 162  
ID ACF23279 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073184-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 163  
ID ACF3969 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064463-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 164  
ID ACD45491 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064451-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 165  
ID ACF53148 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068721-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 166  
ID ACF27328 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068699-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 167  
ID ACF45166 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068707-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 168  
ID ACF29784 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073175-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 169  
ID ACD89860 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068695-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 170  
ID ACD84641 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.

PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 171  
ID ACD9801 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 172  
ID ACF77093 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 173  
ID ACF76786 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 174  
ID ACF49771 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 175  
ID ACF50078 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 176  
ID ACD09477 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 177  
ID ACD08556 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 178  
ID ACH03601 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 179  
ID ACF12270 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 180  
ID ACC94778 standard; cDNA; 1734 BP.

DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 181  
ID ACD22497 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 182  
ID ACF15197 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 183  
ID ACC97292 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 184  
ID ACC92322 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 185  
ID ACF13969 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 186  
ID ACF14276 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 187  
ID ACF09507 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 188  
ID ACD68275 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 189  
ID ACD45798 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064454-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 190  
ID ACD47947 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 191  
ID ACD67678 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 192  
ID ACF25486 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 193  
ID ACF29170 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 194  
ID ACD84948 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 195  
ID ACD84027 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 196  
ID ACD88018 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 197  
ID ACF30705 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 198  
ID ACF32308 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 199  
ID ACHI1968 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 200  
ID ACHI2275 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 201  
ID ADA19913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 202  
ID ACD40667 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 203  
ID ADB17296 standard; cDNA; 1734 BP.  
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 204  
ID ACF18139 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 205  
ID ACF08586 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 206  
ID ACF31387 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 207  
ID ACF52227 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

RESULT 208  
ID ACD50096 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003088733-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 209  
ID ACF38799 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 210  
ID ACF26714 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 211  
ID ACF24814 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003088716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 212  
ID ACF46394 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 213  
ID ACF27942 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 214  
ID ACD89246 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 215  
ID ACF63818 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 216  
ID ACF60458 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 217  
ID ACH12582 standard; cDNA; 1734 BP.

DE cDNA encoding human PRO polypeptide #101.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 218  
ID ACH10005 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 219  
ID ACD03860 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 220  
ID ACD10398 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 221  
ID ACD12040 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 222  
ID ACF42425 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 223  
ID ACF18446 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 224  
ID ACF02236 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 225  
ID ACF21744 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 226  
ID ACF10428 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;



Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 227  
ID ACF33880 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 228  
ID ACF44842 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 229  
ID ACD90474 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 230  
ID ACD91087 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 231  
ID ACF30398 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 232  
ID ACD87097 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 233  
ID ACF60151 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 234  
ID ACF46701 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003083733-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 235  
ID ACF75558 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 236  
ID ADA79745 standard; cDNA; 1734 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 237  
ID ACF17218 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 238  
ID ACF22972 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 239  
ID ACF07972 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 240  
ID ACF08279 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 241  
ID ACF40583 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 242  
ID ACF53762 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 243  
ID ACD47026 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 244  
ID ACF47929 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 245  
ID ACF47315 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068753-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 246  
ID ADA47277 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 247  
ID ACF46087 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 248  
ID ACD96176 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 249  
ID ACF52534 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 250  
ID ACF52841 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 251  
ID ACF64834 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 252  
ID ACF76479 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 253  
ID ACF61379 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 254  
ID ACF61686 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

RESULT 255  
ID ACD30717 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 256  
ID ACD31638 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 257  
ID ACD32559 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 258  
ID ADA20085 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 259  
ID ACD82115 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 260  
ID ACF17525 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 261  
ID ACF07358 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 262  
ID ACF20516 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 263  
ID ACF21130 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 264  
ID ACF20823 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073172-A1.

PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 265  
ID ACDA7640 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 266  
ID ACFA7622 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 267  
ID ACP53455 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 268  
ID ACDB6790 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 269  
ID ACH05038 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 270  
ID ACP44535 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 271  
ID ADA61472 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 272  
ID ACD22190 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 273  
ID ACD24537 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

RESULT 274  
ID ACD39740 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 275  
ID ACDA0047 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 276  
ID ACP13355 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 277  
ID ACF03157 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 278  
ID ACF78628 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 279  
ID ACF11349 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 280  
ID ACP50692 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 281  
ID ACF34187 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 282  
ID ACDA6412 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 283  
ID ACD48254 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064464-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 284  
ID ACF27635 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 285  
ID ACF24507 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 286  
ID ACD85562 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 287  
ID ACD90167 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 288  
ID ACD83720 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 289  
ID ACF49157 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 290  
ID ACH07242 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 291  
ID ACH07549 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 292  
ID ACH08163 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 293  
ID ACH11354 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 294  
ID ACH11661 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 295  
ID ACH10312 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 296  
ID ACF01315 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 297  
ID ACF40890 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 298  
ID ACD24230 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 299  
ID ACD31331 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 300  
ID ACF17832 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 301  
ID ACF32615 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 302  
ID ACF40276 standard; cDNA; 1734 BP.

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DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 303
ID ACF48236 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 304
ID ACF38185 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 305
ID ACF25121 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 306
ID ACF27021 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 307
ID ACF29477 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 308
ID ACD87711 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 309
ID ACF76172 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 310
ID ACF49464 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 311
ID ACF43921 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 312
ID ACH06266 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 313
ID ACH06573 standard; cDNA; 1734 BP.
DE cDNA encoding human PRO polypeptide #101.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 314
ID ADA83270 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 315
ID ACC92629 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 316
ID ACC93243 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 317
ID ACF19288 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 318
ID ACD12979 standard; cDNA; 1734 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #101.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 319
ID ACF06437 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 320
ID ACC94471 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;
RESULT 321
ID ACC97899 standard; cDNA; 1734 BP.
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.
PN US2003044932-A1.
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ID 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 322  
ID ACC94164 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 323  
ID ABT44586 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 324  
ID ACF42118 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 325  
ID ACD31024 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 326  
ID ACD43053 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 327  
ID ACD43360 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 328  
ID ACF14890 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 329  
ID ACF01622 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 330  
ID ACF31694 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 331

ID ACD57371 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 332  
ID ACD48561 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 333  
ID ACD4868 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 334  
ID ACF51306 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 335  
ID ACF54069 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 336  
ID ACF25793 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 337  
ID ACF39106 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 338  
ID ACF28863 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 339  
ID ACD90780 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 340  
ID ACD86483 standard; cDNA; 1734 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PD US2003068765-A1.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 341  
ID ACH05345 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 342  
ID ACF65141 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 343  
ID ADB20313 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 344  
ID ACF43614 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 345  
ID ACH09084 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 346  
ID ACH09391 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 347  
ID ADA78565 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 348  
ID ACD82253 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 1411 cDNA.  
PN US2003044334-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 349  
ID ACF09814 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068720-A1.

PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 350  
ID ADA00382 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO 411 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 351  
ID ACF50999 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 352  
ID ACF23893 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 353  
ID ACD88325 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 354  
ID ACH09698 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 355  
ID ACH10619 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 356  
ID ACD11426 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 357  
ID ACC96476 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 358  
ID ACH04377 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;

Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 359  
ID ACC98506 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 360  
ID ACF1811 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 361  
ID ACF16732 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 362  
ID ACD32252 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 363  
ID ACD30410 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 364  
ID ACD1281 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 365  
ID ACF07665 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 366  
ID ACF31080 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 367  
ID ACF77400 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 368  
ID ACF11042 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073170-A1.

PD 17-APR-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 369  
ID ACF32922 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 370  
ID ACF26100 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 371  
ID ACD83413 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 372  
ID ACF23586 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 373  
ID ACF43000 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 374  
ID ACF43307 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 375  
ID ACH05959 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 376  
ID ACH08777 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 377  
ID ACC90371 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;



Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 378  
ID ACF10735 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 379  
ID ACC93550 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 380  
ID ACC96169 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 381  
ID ACD24844 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US200304921-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 382  
ID ACF01929 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 383  
ID ACF22051 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 384  
ID ACF22655 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 385  
ID ACF08893 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 386  
ID ACF33229 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 387  
ID ACF54683 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.

PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 388  
ID ACF48543 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 389  
ID ACD47333 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 390  
ID ACD49175 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 391  
ID ACF37878 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 392  
ID ACF30091 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 393  
ID ACD87404 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 394  
ID ACF61993 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 395  
ID ACHI0926 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 396  
ID ACD10091 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036158-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 397  
ID ACD16816 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003036151-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 398  
ID ACC99113 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040067-A1.  
PD 27-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 399  
ID ACF00507 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054456-A1.  
PD 20-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 400  
ID ACD40974 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054482-A1.  
PD 20-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 401  
ID ACF14583 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003054457-A1.  
PD 20-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 402  
ID ACF22358 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003059883-A1.  
PD 27-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 403  
ID ACF78935 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049764-A1.  
PD 13-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 404  
ID ACD67921 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073129-A1.  
PD 17-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 405  
ID ACF11656 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003073177-A1.  
PD 17-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 406  
ID ACF51613 standard; cDNA; 1734 BP.

DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064442-A1.  
PD 03-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 407  
ID ACF33536 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003064450-A1.  
PD 03-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 408  
ID ACD49789 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068731-A1.  
PD 10-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 409  
ID ACF37571 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068683-A1.  
PD 10-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 410  
ID ACF28556 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068754-A1.  
PD 10-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 411  
ID ACD88632 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068681-A1.  
PD 10-APR-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 412  
ID ACF75251 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096351-A1.  
PD 22-MAY-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 413  
ID ACF61072 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096358-A1.  
PD 22-MAY-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 414  
ID ACF44228 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104556-A1.  
PD 05-JUN-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 415  
ID ACH08470 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049756-A1.  
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 416  
ID ACC93857 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 417  
ID ACD20962 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 418  
ID ACF06744 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 419  
ID ACD20655 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 420  
ID ACD22804 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 421  
ID ACD30274 standard; cDNA; 1734 BP.  
DE Human cDNA encoding Pro1411.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 422  
ID ACF41504 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 423  
ID ABT43959 standard; cDNA; 1734 BP.  
DE Human membrane bound receptor/protein PRO1411 cDNA sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 424  
ID ACF07051 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 425  
ID ACF77707 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.

PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 426  
ID ACD46105 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 427  
ID ACF47008 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 428  
ID ACF54376 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 429  
ID ACF45780 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 430  
ID ACF45473 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 431  
ID ACF38492 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 432  
ID ACD89553 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 433  
ID ACD85255 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 9; Length 1734;  
RESULT 434  
ID ACD85869 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003068726-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 435  
ID ACF75865 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 436  
ID ACF60765 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 437  
ID ACH05652 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 438  
ID ADA82636 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 439  
ID ADB85624 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 440  
ID ADB83645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 441  
ID ADB80751 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 442  
ID ADB73292 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 443  
ID ACF55911 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 444  
ID ADB78374 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 9; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 445  
ID ACF55297 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 446  
ID ADB85022 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 447  
ID ADB78128 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 448  
ID ADB85944 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 449  
ID ACF56218 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 450  
ID ACF56525 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 451  
ID ADB87194 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 452  
ID ADB84776 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 453  
ID ACF55911 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 453  
ID ADB68303 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 454  
ID ADB68110 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 455  
ID ACF55604 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 456  
ID ACF54990 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 457  
ID ADB83891 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 458  
ID ADB73046 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 459  
ID ADB90927 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 460  
ID ADC07007 standard; cDNA; 1734 BP.  
DE Human PRO1411 cDNA.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 461  
ID ADC17920 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #15.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

RESULT 462  
ID ADC17186 standard; cDNA; 1734 BP.  
DE cDNA sequence encoding a PRO polypeptide (SeqID 51).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 463  
ID ADC14884 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 464  
ID ADC36884 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 465  
ID ADC52379 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 466  
ID ADC21874 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 467  
ID ADC49905 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 468  
ID ADC49104 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 469  
ID ADC49621 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 470  
ID ADC47482 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 471  
ID ADC47482 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;

ID ADC47227 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 472  
ID ADC78102 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 473  
ID ADD06337 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 474  
ID ADD05674 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 475  
ID ADD10438 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #75.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 476  
ID ADC77856 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 477  
ID ADD11398 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #75.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 478  
ID ADD50819 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 479  
ID ADD51065 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 480  
ID ADD70566 standard; cDNA; 1734 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 481  
ID ADD39643 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 482  
ID ADD70089 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 483  
ID ADD37191 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #75.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 484  
ID ADD36055 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 485  
ID ADD38210 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 486  
ID ADD39166 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 487  
ID ADD50546 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 488  
ID ADD50300 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 489  
ID ADD38689 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.

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PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 490
ID ADD40120 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 491
ID ADD51311 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 492
ID ADE50341 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 493
ID ADE19953 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 494
ID ADE49864 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 495
ID ADE21422 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 496
ID ADF29847 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 497
ID ADF55740 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 498
ID ADG01056 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003078387-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 499
ID ADG08609 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 500
ID ADG02669 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 501
ID ADG01376 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 502
ID ADF95551 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 503
ID ADF95230 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 504
ID ADG12366 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 505
ID ADH24083 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 506
ID ADH34109 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 507
ID ADH29942 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 508  
ID ADH3913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 509  
ID ADH09026 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 510  
ID ADG85317 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 511  
ID ADH4593 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 512  
ID ADH37449 standard; cDNA; 1734 BP.  
DE Human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 513  
ID ADH02038 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 514  
ID ADH37619 standard; cDNA; 1734 BP.  
DE Human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 515  
ID ADG85657 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 516  
ID ADH24253 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;

Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 517  
ID ADH38547 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 518  
ID ADG63786 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 519  
ID ADG83668 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 520  
ID ADH29476 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 521  
ID ADH27592 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 522  
ID ADH37789 standard; cDNA; 1734 BP.  
DE Human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 523  
ID ADH37966 standard; cDNA; 1734 BP.  
DE Human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 524  
ID ADH57386 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 525  
ID ADH53528 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
Pred. No. 1.9e-243;



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RESULT 526
ID ADH53698 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 527
ID ADH52034 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 528
ID ADH9889 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 529
ID ADI25399 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 530
ID ADH90192 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 531
ID ADI25569 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 532
ID ADH97743 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 533
ID ADH99244 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 534
ID ADI03591 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 535
ID ADH53698 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 536
ID ADH90022 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 537
ID ADH98423 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 538
ID ADI11098 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 539
ID ADI11608 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 540
ID ADH98253 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 541
ID ADH98593 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 542
ID ADH98083 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 543
ID ABX78628 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1734; DB 10; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 544
ID ACA75600 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
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PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 545  
ID ACA71080 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 546  
ID ACC87608 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 547  
ID ACC86994 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 548  
ID ACD04167 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 549  
ID ACA69498 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #101.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 550  
ID ACA90343 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 551  
ID ACC89450 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 552  
ID ACA98241 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 553  
ID ACA93883 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 554  
ID ACA66918 standard; cDNA; 1734 BP.  
DE cDNA encoding human PRO polypeptide #78.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 555  
ID ACD15276 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 556  
ID ACD08863 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 557  
ID ACC96783 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 558  
ID ACF15504 standard; cDNA; 1734 BP.  
DE Human secreted polypeptide PRO1411-encoding cDNA, SEQ ID NO:201.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 559  
ID ACD42388 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO141 cDNA.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 560  
ID ACD86670 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 561  
ID ACA72871 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 562  
ID ACD03043 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US200303153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 563  
ID ACD01858 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 564  
ID ACA92050 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 565  
ID ADI05071 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 566  
ID ADI03421 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO411 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 567  
ID ADI04816 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 568  
ID ADH78270 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181688-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 569  
ID ADI19614 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 570  
ID ADH90362 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 571  
ID ADI03081 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 572  
ID ADH77930 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 573  
ID ADH97913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;

Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 574  
ID ADI01298 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 575  
ID ADI01993 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 576  
ID ADI03251 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 577  
ID ADI11438 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 578  
ID ADI02340 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 579  
ID ADI11778 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 580  
ID ADI05415 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 581  
ID ADH79487 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 582  
ID ADI19444 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;  
RESULT 583  
ID ADH97913 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 10; Length 1734;

RESULT 583  
ID ADI05245 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 584  
ID ADH79657 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 585  
ID ADI01483 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 586  
ID ADI01653 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 587  
ID ADI01823 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 588  
ID ADH79827 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 589  
ID ADI04645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 590  
ID ADI02781 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 591  
ID ADH78100 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 592  
ID ADC52189 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 593  
ID ADI25909 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 594  
ID ADK65421 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 595  
ID ADH98763 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 596  
ID ADH80004 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 10; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 597  
ID ADL32807 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 11; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 598  
ID ADM30341 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 11; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 599  
ID ADL93735 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 11; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 600  
ID ADC4858 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 601  
ID ADC52189 standard; cDNA; 1734 BP.

DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003130483-A1.
PD	10-JUL-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 602	
ID	ADE21029 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100735-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 603	
ID	ADE05873 standard; cDNA; 1734 BP.
DE	Human PRO polynucleotide #78.
PN	US2003100728-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 604	
ID	ADE75102 standard; cDNA; 1734 BP.
DE	Human PRO polynucleotide #78.
PN	US2003100712-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 605	
ID	ADD75848 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100717-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 606	
ID	ADD85080 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100722-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 607	
ID	ADD86906 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100738-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 608	
ID	ADE20783 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100734-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 609	
ID	ADE33080 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003096362-A1.
PD	22-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 610	
ID	ADE05627 standard; cDNA; 1734 BP.
DE	Human PRO polynucleotide #78.
PN	US2003100708-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 611	
ID	ADD73612 standard; cDNA; 1734 BP.
DE	Human PRO polynucleotide #78.
PN	US2003100711-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 612	
ID	ADD78452 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100737-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 613	
ID	ADE41399 standard; cDNA; 1734 BP.
DE	Human secreted/transmembrane PRO polypeptide cDNA #75.
PN	US2003100497-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 614	
ID	ADE74338 standard; cDNA; 1734 BP.
DE	Human secreted/transmembrane protein (PRO) cDNA #101.
PN	US2003211572-A1.
PD	13-NOV-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 615	
ID	ADE21275 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100736-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 616	
ID	ADD77390 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100732-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 617	
ID	ADE20537 standard; cDNA; 1734 BP.
DE	Novel human secreted and transmembrane protein PRO1411 cDNA.
PN	US2003100733-A1.
PD	29-MAY-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity	100.0%; Pred. No. 1.9e-243;
RESULT 618	
ID	ADD75602 standard; cDNA; 1734 BP.
DE	Human PRO polynucleotide #78.
PN	US20031000

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 620  
ID ADD74364 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 621  
ID ADD76094 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 622  
ID ADD85586 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 623  
ID ADE05135 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 624  
ID ADD75348 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 625  
ID ADD76892 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 626  
ID ADD86660 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 627  
ID ADE41200 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 628  
ID ADD78128 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 629  
ID ADE74950 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #101.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 630  
ID ADD77636 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 631  
ID ADD77882 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 632  
ID ADD85340 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 633  
ID ADD73872 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 634  
ID ADD74610 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 635  
ID ADD77138 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 636  
ID ADD85832 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 637  
ID ADE05381 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 638  
ID ADD78128 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.

RESULT 638  
ID ADD74856 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 639  
ID ADE96424 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 640  
ID ADF25735 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 641  
ID ADF24634 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 642  
ID ADF29370 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 643  
ID ADE96901 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 644  
ID ADG05668 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 645  
ID ADG27222 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 646  
ID ADF96163 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 647  
ID ADG11285 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 648  
ID ADG04434 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 649  
ID ADG12064 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 650  
ID ADG00594 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 651  
ID ADF94621 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 652  
ID ADG06717 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 653  
ID ADH06621 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 654  
ID ADH06451 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 655  
ID ADG68872 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 656  
ID ADH27762 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 657  
ID ADH25103 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 658  
ID ADH33735 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 659  
ID ADG82850 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 660  
ID ADH02939 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 661  
ID ADH02378 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 662  
ID ADH07985 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 663  
ID ADG69382 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 664  
ID ADH39203 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 665  
ID ADH03893 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003220471-A1.

PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 666  
ID ADH03416 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 667  
ID ADH26131 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 668  
ID ADG83943 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 669  
ID ADH39061 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 670  
ID ADG85487 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 671  
ID ADG63635 standard; cDNA; 1734 BP.  
DE Human secreted/transmembrane polypeptide PRO1411 cDNA.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 672  
ID ADH06281 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 673  
ID ADH30111 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 674  
ID ADH24423 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.



PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 675  
ID ADH33100 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 676  
ID ADG69552 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 677  
ID ADH07815 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 678  
ID ADG5827 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 679  
ID ADH39373 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 680  
ID ADH33565 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 681  
ID ADH33905 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 682  
ID ADH01115 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 683  
ID ADG69722 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 684  
ID ADH02208 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 685  
ID ADG69212 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 686  
ID ADG85997 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 687  
ID ADH24933 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 688  
ID ADH39550 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 689  
ID ADH02548 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 690  
ID ADG69042 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 691  
ID ADH07645 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 692  
ID ADG86167 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1734; DB 12; Length 1734;  
Pred. No. 1.9e-243;  
RESULT 693  
ID ADG69722 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 693
ID ADH24763 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 694
ID ADH25811 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 695
ID ADH38377 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 696
ID ADH57216 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 697
ID ADH43582 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #75.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 698
ID ADG34151 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 699
ID ADH04370 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 700
ID ADH49570 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 701
ID ADH90532 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 702
ID ADI11268 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #26.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 703
ID ADH98933 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 704
ID ADI33621 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #78.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 705
ID ADI02163 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 706
ID ADH69715 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #78.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 707
ID ADH61371 standard; cDNA; 1734 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1411.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 708
ID ADH90702 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 709
ID ADI29876 standard; cDNA; 1734 BP.
DE Novel human secreted and transmembrane protein PRO1411 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 710
ID ADJ54839 standard; cDNA; 1734 BP.
DE Human PRO polynucleotide #101.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1734; DB 12; Length 1734;
Best Local Similarity 100.0%; Pred. No. 1.9e-243;
RESULT 711
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ID ADJ98577 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 712  
ID ADJ98747 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 713  
ID ADH78906 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 714  
ID ADJ99140 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 715  
ID ADJ99310 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 716  
ID ADJ98928 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 717  
ID ADH79076 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 718  
ID ADK00936 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 719  
ID ADK14457 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 720  
ID ADM27273 standard; cDNA; 1734 BP.

DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 721  
ID ADR82927 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #75.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 722  
ID ADJ64610 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #101.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 723  
ID ADK66631 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #78.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 724  
ID ADM31506 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 725  
ID ADM36553 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 726  
ID ADM40358 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 727  
ID ADM80906 standard; cDNA; 1734 BP.  
DE Human PRO polynucleotide #26.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 728  
ID ADL94570 standard; cDNA; 1734 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1411.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 729  
ID ADN37966 standard; cDNA; 1734 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.

PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1734; DB 12; Length 1734;  
Best Local Similarity 100.0%; Pred. No. 1.9e-243;  
RESULT 730  
ID AAA37036 standard; cDNA; 1733 BP.  
DE Human PRO1411 (UNQ729) cDNA sequence SEQ ID NO:51.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 99.9%; Score 1733; DB 3; Length 1733;  
Best Local Similarity 100.0%; Pred. No. 2.6e-243;  
RESULT 731  
ID AAF54238 standard; DNA; 1733 BP.  
DE DNA encoding protein of the invention #15.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 99.9%; Score 1733; DB 4; Length 1733;  
Best Local Similarity 100.0%; Pred. No. 2.6e-243;  
RESULT 732  
ID ADH52204 standard; cDNA; 1629 BP.  
DE Novel human secreted and transmembrane protein PRO1411 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 81.2%; Score 1408; DB 12; Length 1629;  
Best Local Similarity 94.7%; Pred. No. 4.9e-196;  
RESULT 733  
ID ABL88146 standard; cDNA; 1320 BP.  
DE Human PRO1411 cDNA sequence SEQ ID NO:149.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 76.1%; Score 1320; DB 6; Length 1320;  
Best Local Similarity 100.0%; Pred. No. 3.1e-183;  
RESULT 734  
ID AAZ43802 standard; cDNA; 1493 BP.  
DE Human adult skin cDNA clone vd3\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 71.8%; Score 1244.8; DB 3; Length 1493;  
Best Local Similarity 87.3%; Pred. No. 2.7e-172;  
RESULT 735  
ID AAC69515 standard; DNA; 1441 BP.  
DE Human secreted protein gene 4 clone HKAJK47.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 71.8%; Score 1244.4; DB 3; Length 1441;  
Best Local Similarity 89.6%; Pred. No. 3.1e-172;  
RESULT 736  
ID AAZ43803 standard; cDNA; 1897 BP.  
DE Human adult skin cDNA clone vd4\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 61.4%; Score 1065.2; DB 3; Length 1897;  
Best Local Similarity 88.0%; Pred. No. 3.6e-146;  
RESULT 737  
ID AAZ42019 standard; cDNA; 914 BP.  
DE Human endometrium tumour cDNA derived EST 39.  
PN DE19817948-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 21.4%; Score 370.8; DB 2; Length 914;  
Best Local Similarity 95.7%; Pred. No. 3.6e-45;  
RESULT 738  
ID ADQ64237 standard; cDNA; 2811 BP.  
DE Novel human cDNA sequence #1398.  
PN EP1440981-A2.

PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.8%; Score 240; DB 12; Length 2811;  
Best Local Similarity 100.0%; Pred. No. 3.9e-26;  
RESULT 739  
ID AAS36979 standard; cDNA; 410 BP.  
DE Novel human diagnostic and therapeutic gene #37.  
PN WO200166753-A2.  
PD 13-SEP-2001.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 209; DB 4; Length 410;  
Best Local Similarity 99.5%; Pred. No. 1.2e-21;  
RESULT 740  
ID AAL00189 standard; cDNA; 349 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 190.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 170.4; DB 4; Length 349;  
Best Local Similarity 91.8%; Pred. No. 5.1e-16;  
RESULT 741  
ID ACH27866 standard; cDNA; 587 BP.  
DE Human adult ovary cDNA #6246.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 9.0%; Score 156.4; DB 9; Length 587;  
Best Local Similarity 61.1%; Pred. No. 5.6e-14;  
RESULT 742  
ID ADQ52666 standard; DNA; 513 BP.  
DE Novel canine microarray-related DNA sequence SeqID3969.  
PN WO2004063324-A2.  
PD 29-JUL-2004.  
PA (GENE-) GENE LOGIC INC.  
PA (PFIZ ) PFIZER PROD INC.  
Query Match 8.5%; Score 147.2; DB 13; Length 513;  
Best Local Similarity 66.3%; Pred. No. 1.2e-12;  
RESULT 743  
ID ACN58609 standard; cDNA; 313 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-010-Q6-N6-Cl1, SEQ:13390.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.4%; Score 128.2; DB 13; Length 313;  
Best Local Similarity 75.1%; Pred. No. 7e-10;  
RESULT 744  
ID ACN45357 standard; cDNA; 597 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A11, SEQ:138.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.3%; Score 126.8; DB 13; Length 597;  
Best Local Similarity 80.1%; Pred. No. 1.1e-09;  
RESULT 745  
ID ABK31495 standard; DNA; 15954 BP.  
DE Signal transduction associated gene modified complementary DNA #169.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.3%; Score 126.6; DB 6; Length 15954;  
Best Local Similarity 70.9%; Pred. No. 1.2e-09;  
RESULT 746

ID ABL70468 standard; DNA; 15954 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#179.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.3%; Score 126.6; DB 6; Length 15954;  
Best Local Similarity 70.9%; Pred. No. 1.2e-09;  
RESULT 747  
ID AAF94825 standard; cDNA; 396 BP.  
DE Human ovarian cancer associated coding sequence SEQ ID NO: 16.  
PN WO200118046-A2.  
PD 15-MAR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.3%; Score 126.2; DB 4; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 748  
ID ABL48775 standard; cDNA; 396 BP.  
DE Ovarian carcinoma sequence isolate 23660.1.  
PN. US2002004491-A1.  
PD 10-JAN-2002.  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
Query Match 7.3%; Score 126.2; DB 6; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 749  
ID ABL70468 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 16.  
PN WO200239885-A2.  
PD 23-MAY-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 7.3%; Score 126.2; DB 6; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 750  
ID ADM10685 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma-associated cDNA 23660.1.  
PN US20030206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.3%; Score 126.2; DB 11; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 751  
ID ADJ11015 standard; cDNA; 396 BP.  
DE Representative human ovarian carcinoma cDNA SeqID 16.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.3%; Score 126.2; DB 12; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 752  
ID ADM43276 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma cDNA #16.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.3%; Score 126.2; DB 12; Length 396;  
Best Local Similarity 78.7%; Pred. No. 1.4e-09;  
RESULT 753  
ID ACN52610 standard; cDNA; 574 BP.  
DE Cotton androecium tissue EST Clone ID: LTB3828-016-Q1-N6-G6, SEQ:7391.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.2%; Score 125.2; DB 13; Length 574;  
Best Local Similarity 77.8%; Pred. No. 1.9e-09;  
RESULT 754  
ID ADF7609 standard; cDNA; 602 BP.  
DE Novel human secreted and transmembrane protein cDNA SeqID 283.  
PN WO2003072035-A2.

PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 125; DB 10; Length 602;  
Best Local Similarity 82.7%; Pred. No. 2.1e-09;  
RESULT 755  
ID ADL83210 standard; cDNA; 602 BP.  
DE Human PRO52174 cDNA, SEQ ID 412.  
PN WO2004024097-A2.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 125; DB 12; Length 602;  
Best Local Similarity 82.7%; Pred. No. 2.1e-09;  
RESULT 756  
ID ADL91506 standard; cDNA; 602 BP.  
DE Human immune-related polypeptide PRO52174-encoding cDNA, SEQ ID NO:21.  
PN WO2004024072-A2.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 125; DB 12; Length 602;  
Best Local Similarity 82.7%; Pred. No. 2.1e-09;  
RESULT 757  
ID ADM41666 standard; cDNA; 602 BP.  
DE PRO52174 cDNA, associated with B-cell activation.  
PN WO2004024069-A2.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 125; DB 12; Length 602;  
Best Local Similarity 82.7%; Pred. No. 2.1e-09;  
RESULT 758  
ID AAC80551 standard; cDNA; 658 BP.  
DE Human secreted protein gene 21 SEQ ID NO:31.  
PN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 123.8; DB 3; Length 658;  
Best Local Similarity 81.7%; Pred. No. 3.1e-09;  
RESULT 759  
ID AAX33813 standard; DNA; 2487 BP.  
DE Coding sequence for human secreted protein cb213\_11.  
PN WO9913066-A1.  
PD 18-MAR-1999.  
PA (GENY) GENETICS INST INC.  
Query Match 7.1%; Score 123.6; DB 2; Length 2487;  
Best Local Similarity 80.9%; Pred. No. 3.3e-09;  
RESULT 760  
ID ABK40004 standard; DNA; 5586 BP.  
DE Human chemically pretreated gene sequence #43 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.1%; Score 123.6; DB 6; Length 5586;  
Best Local Similarity 69.4%; Pred. No. 3.3e-09;  
RESULT 761  
ID AAS45399 standard; DNA; 15832 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #52.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.1%; Score 123.6; DB 4; Length 15832;  
Best Local Similarity 69.4%; Pred. No. 3.4e-09;  
RESULT 762  
ID ABL33343 standard; DNA; 15832 BP.  
DE Human immune system associated gene SEQ ID NO: 1316.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.1%; Score 123.6; DB 6; Length 15832;  
Best Local Similarity 69.4%; Pred. No. 3.4e-09;  
RESULT 763  
ID ABK28244 standard; DNA; 15832 BP.  
DE DNA transcription associated complementary genomic DNA #59.  
PN WO200192585-A2.  
PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.1%; Score 123.6; DB 6; Length 15832;  
Best Local Similarity 69.4%; Pred. No. 3.4e-09;  
RESULT 764  
ID ABL32911 standard; DNA; 8946 BP.  
DE Human immune system associated gene SEQ ID NO: 884.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.1%; Score 123.2; DB 6; Length 8946;  
Best Local Similarity 81.2%; Pred. No. 3.8e-09;  
RESULT 765  
ID ADI70087 standard; DNA; 392 BP.  
DE Human ovarian cancer DNA marker #2829.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 7.1%; Score 123; DB 5; Length 392;  
Best Local Similarity 66.2%; Pred. No. 4e-09;  
RESULT 766  
ID ADI76417 standard; DNA; 392 BP.  
DE Human ovarian cancer DNA marker #9159.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 7.1%; Score 123; DB 5; Length 392;  
Best Local Similarity 66.2%; Pred. No. 4e-09;  
RESULT 767  
ID ADP07684 standard; DNA; 705 BP.  
DE Human secreted protein encoding DNA, seq id 167.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.1%; Score 122.8; DB 12; Length 705;  
Best Local Similarity 88.7%; Pred. No. 4.3e-09;  
RESULT 768  
ID ACN49708 standard; cDNA; 554 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.0%; Score 122.2; DB 13; Length 554;  
Best Local Similarity 77.5%; Pred. No. 5.2e-09;  
RESULT 769  
ID ADB79863 standard; DNA; 2924 BP.  
DE Rat myosin heavy chain coding sequence, SEQ ID 103.  
PN EP1279744-A2.  
PD 29-JAN-2003.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 7.0%; Score 122.2; DB 10; Length 2924;  
Best Local Similarity 94.1%; Pred. No. 5.3e-09;  
RESULT 770  
ID AAS37277 standard; cDNA; 404 BP.  
DE Novel human diagnostic and therapeutic gene #335.  
PN WO200166753-A2.  
PD 13-SEP-2001.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 121.8; DB 4; Length 404;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 771  
ID AAZ80280 standard; cDNA; 686 BP.  
DE Human colon cancer cell line SW480 cDNA clone SEQ ID NO:364.  
PN WO9964576-A2.  
PD 16-DEC-1999.  
PA (FARB) BAYER CORP.  
Query Match 7.0%; Score 121.8; DB 3; Length 686;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 772  
ID AAH23810 standard; cDNA; 700 BP.

DE Human transferase HTFS-10 cDNA, SEQ ID NO:52.  
PN WO200132888-A2.  
PD 10-MAY-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.0%; Score 121.8; DB 5; Length 700;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 773  
ID ADE28278 standard; DNA; 703 BP.  
DE Human MDDT DNA - SEQ ID 128.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.0%; Score 121.8; DB 10; Length 703;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 774  
ID ADM02457 standard; cDNA; 1579 BP.  
DE Human cDNA of the invention SEQ ID NO:1142.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.0%; Score 121.8; DB 11; Length 1579;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 775  
ID ADQ24565 standard; DNA; 1608 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7385.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.0%; Score 121.8; DB 12; Length 1608;  
Best Local Similarity 98.4%; Pred. No. 6e-09;  
RESULT 776  
ID ABL32118 standard; DNA; 11416 BP.  
DE Human immune system associated gene SEQ ID NO: 91.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.0%; Score 121.8; DB 6; Length 11416;  
Best Local Similarity 77.8%; Pred. No. 6.1e-09;  
RESULT 777  
ID ABL70135 standard; DNA; 11416 BP.  
DE Chemically treated cell signalling DNA sequence#13.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.0%; Score 121.8; DB 6; Length 11416;  
Best Local Similarity 77.8%; Pred. No. 6.1e-09;  
RESULT 778  
ID AAS61063 standard; DNA; 11416 BP.  
DE Human gene regulation-associated gene oligonucleotide #18.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.0%; Score 121.8; DB 6; Length 11416;  
Best Local Similarity 77.8%; Pred. No. 6.1e-09;  
RESULT 779  
ID AAS46815 standard; DNA; 21354 BP.  
DE Tumour suppressor gene derived chemically modified sequence #512.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.0%; Score 121.8; DB 4; Length 21354;  
Best Local Similarity 66.7%; Pred. No. 6.2e-09;  
RESULT 780  
ID ACN56061 standard; cDNA; 474 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-F7, SEQ:10842.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.0%; Score 121.6; DB 13; Length 474;  
Best Local Similarity 82.7%; Pred. No. 6.4e-09;

RESULT 781  
ID AAG4638 standard; DNA; 801 BP.  
DE Partial sequence MEL3 associated with melanoma and thyroid tumors.  
PN WO200050595-A2.  
PD 31-AUG-2000.  
PA (GOUT/) GOUT I.  
PA (RODN/) RODIN N.  
PA (FILO/) FILOENKO V.  
PA (MATS/) MATSUKA G.  
PA (SCAN/) SCANLAN M.  
PA (OLDL/) OLD L.  
PA (BILY/) BILYNSKY B.  
Query Match 7.0%; Score 121.6; DB 3; Length 801;  
Best Local Similarity 68.0%; Pred. No. 6.4e-09;  
RESULT 782  
ID ABK92244 standard; DNA; 2788 BP.  
DE Prostate cancer-associated DNA sequence #130.  
PN WO200230268-A2.  
PD 18-APR-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.0%; Score 121.6; DB 6; Length 2788;  
Best Local Similarity 85.0%; Pred. No. 6.5e-09;  
RESULT 783  
ID ABI34196 standard; DNA; 37973 BP.  
DE Human immune system associated gene SEQ ID NO: 2169.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 7.0%; Score 121.6; DB 6; Length 37973;  
Best Local Similarity 80.7%; Pred. No. 6.6e-09;  
RESULT 784  
ID ACH26439 standard; cDNA; 432 BP.  
DE Human adult ovary cDNA #4819.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 7.0%; Score 121; DB 9; Length 432;  
Best Local Similarity 80.2%; Pred. No. 7.8e-09;  
RESULT 785  
ID ACN61416 standard; cDNA; 490 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.0%; Score 121; DB 13; Length 490;  
Best Local Similarity 80.2%; Pred. No. 7.8e-09;  
RESULT 786  
ID ADJ38237 standard; DNA; 810 BP.  
DE Human ovarian cancer DNA marker #12127.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 7.0%; Score 120.8; DB 5; Length 810;  
Best Local Similarity 93.3%; Pred. No. 8.4e-09;  
RESULT 787  
ID ADI73104 standard; DNA; 810 BP.  
DE Human ovarian cancer DNA marker #5846.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 7.0%; Score 120.8; DB 5; Length 810;  
Best Local Similarity 93.3%; Pred. No. 8.4e-09;  
RESULT 788  
ID ACN51787 standard; cDNA; 480 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-N6-A12, SEQ:6568.  
PN US2004123340-A1.

PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.0%; Score 120.6; DB 13; Length 480;  
Best Local Similarity 77.0%; Pred. No. 8.9e-09;  
RESULT 789  
ID ADL44998 standard; DNA; 501 BP.  
DE Human ovarian cancer DNA marker #18888.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 7.0%; Score 120.6; DB 5; Length 501;  
Best Local Similarity 90.2%; Pred. No. 8.9e-09;  
RESULT 790  
ID AAC68125 standard; cDNA; 809 BP.  
DE Human secreted protein cDNA sequence #45.  
PN WO200058335-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 7.0%; Score 120.6; DB 3; Length 809;  
Best Local Similarity 93.3%; Pred. No. 9e-09;  
RESULT 791  
ID AAA27413 standard; cDNA; 1164 BP.  
DE Wheat histidyl-tRNA synthetase coding sequence # 1.  
PN WO200028057-A2.  
PD 18-MAY-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 7.0%; Score 120.6; DB 3; Length 1164;  
Best Local Similarity 96.9%; Pred. No. 9e-09;  
RESULT 792  
ID AAD05087 standard; cDNA; 2297 BP.  
DE Human secreted protein-encoding gene 7 cDNA clone HHMM74, SEQ ID NO: 45.  
PN WO200134768-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 120.6; DB 4; Length 2297;  
Best Local Similarity 71.0%; Pred. No. 9.1e-09;  
RESULT 793  
ID ADA40350 standard; cDNA; 2297 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 120.6; DB 8; Length 2297;  
Best Local Similarity 71.0%; Pred. No. 9.1e-09;  
RESULT 794  
ID ADA56516 standard; DNA; 2297 BP.  
DE Gene encoding human secreted protein #223.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 120.6; DB 10; Length 2297;  
Best Local Similarity 71.0%; Pred. No. 9.1e-09;  
RESULT 795  
ID AAD05059 standard; cDNA; 2612 BP.  
DE Human secreted protein-encoding gene 7 cDNA clone HHMM74, SEQ ID NO: 17.  
PN WO200134768-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 120.6; DB 4; Length 2612;  
Best Local Similarity 71.0%; Pred. No. 9.1e-09;  
RESULT 796  
ID ADJ19854 standard; cDNA; 2612 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.0%; Score 120.6; DB 8; Length 2612;  
Best Local Similarity 71.0%; Pred. No. 9.1e-09;

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RESULT 797
ID ADA56044 standard; DNA; 2612 BP.
DE Gene encoding human secreted protein #223.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.0%; Score 120.6; DB 10; Length 2612;
RESULT 798
ID ABL32511 standard; DNA; 5306 BP.
DE Human immune system associated gene SEQ ID NO: 484.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 7.0%; Score 120.6; DB 6; Length 5306;
RESULT 799
ID ABQ67050 standard; DNA; 6486 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 7.0%; Score 120.6; DB 6; Length 6486;
RESULT 800
ID ABK40074 standard; DNA; 8899 BP.
DE Human chemically pretreated gene sequence #78 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 7.0%; Score 120.6; DB 6; Length 8899;
RESULT 801
ID ABL32837 standard; DNA; 8899 BP.
DE Human immune system associated gene SEQ ID NO: 810.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 7.0%; Score 120.6; DB 6; Length 8899;
RESULT 802
ID AAI87804 standard; cDNA; 398 BP.
DE Human polynucleotide SEQ ID NO 7864.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.9%; Score 120.4; DB 4; Length 398;
RESULT 803
ID ABV57059 standard; cDNA; 490 BP.
DE Human prostate expression marker cDNA 57050.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 6.9%; Score 120.4; DB 5; Length 490;
RESULT 804
ID ADQ22774 standard; DNA; 3950 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5594.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 6.9%; Score 120.4; DB 12; Length 3950;
RESULT 805
ID ACN62572 standard; cDNA; 559 BP.
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A11, SEQ:17353.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 13; Length 559;
RESULT 806
ID AAS33148 standard; cDNA; 804 BP.
DE DNA encoding human secreted protein, Seq ID No 107.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 4; Length 804;
RESULT 807
ID AAS26005 standard; cDNA; 1074 BP.
DE Human cDNA encoding a novel secreted protein, Seq ID 184.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 4; Length 1074;
RESULT 808
ID ABX73346 standard; DNA; 1074 BP.
DE Human novel polynucleotide #174.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 8; Length 1074;
RESULT 809
ID ADQ23223 standard; DNA; 1567 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6043.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 12; Length 1567;
RESULT 810
ID AD854224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 10; Length 4316;
RESULT 811
ID ADS9522 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:538.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 6.9%; Score 120.2; DB 13; Length 4316;
RESULT 812
ID ACN51318 standard; cDNA; 545 BP.
DE Cotton androecium tissue EST Clone ID: LTB3828-014-Q1-N6-F6, SEQ:6099.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 6.9%; Score 120; DB 13; Length 545;
RESULT 813
ID ABV58017 standard; cDNA; 580 BP.
DE Human prostate expression marker cDNA 58008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 6.9%; Score 120; DB 5; Length 580;
RESULT 814
ID ADE79027 standard; DNA; 1064 BP.
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DE Human protein modification and maintenance molecule (PMM)-7 gene.  
Query Match 6.9%; Score 120; DB 10; Length 1064;  
Best Local Similarity 92.6%; Pred. No. 1.1e-08;  
RESULT 815  
ID ABL34624 standard; cDNA; 1769 BP.  
DE Human metastasis associated gene SEQ ID NO: 177.  
PN WO20017376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 120; DB 6; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 824  
ID ABL70607 standard; DNA; 15518 BP.  
DE Chemically treated cell signalling DNA sequence#249.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 120; DB 6; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 825  
ID ADS9985 standard; DNA; 15518 BP.  
DE Bisulphite treated human gene associated with metastasis #89.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 6.9%; Score 120; DB 7; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 826  
ID ADL41653 standard; DNA; 425 BP.  
DE Human ovarian cancer DNA marker #15543.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.9%; Score 119.8; DB 5; Length 425;  
Best Local Similarity 74.4%; Pred. No. 1.2e-08;  
RESULT 827  
ID AAH33241 standard; cDNA; 464 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:297.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 119.8; DB 4; Length 464;  
Best Local Similarity 88.8%; Pred. No. 1.2e-08;  
RESULT 828  
ID ACN57821 standard; cDNA; 560 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-006-Q6-K6-C12, SEQ:13602.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 6.9%; Score 119.8; DB 13; Length 560;  
Best Local Similarity 85.8%; Pred. No. 1.2e-08;  
RESULT 829  
ID AAZ07192 standard; cDNA; 3275 BP.  
DE Human lung tumour protein SAL-25 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 6.9%; Score 119.8; DB 2; Length 3275;  
Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
RESULT 830  
ID AAC79145 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific cDNA #98.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 6.9%; Score 119.8; DB 3; Length 3275;  
Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
RESULT 831  
ID AAD23220 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific protein SAL-25 cDNA.

DE Human protein modification and maintenance molecule (PMM)-7 gene.  
Query Match 6.9%; Score 120; DB 10; Length 1064;  
Best Local Similarity 92.6%; Pred. No. 1.1e-08;  
RESULT 815  
ID ABL34624 standard; cDNA; 1769 BP.  
DE Human metastasis associated gene SEQ ID NO: 177.  
PN WO20017376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 120; DB 6; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 824  
ID ABL70607 standard; DNA; 15518 BP.  
DE Chemically treated cell signalling DNA sequence#249.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 120; DB 6; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 825  
ID ADS9985 standard; DNA; 15518 BP.  
DE Bisulphite treated human gene associated with metastasis #89.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 6.9%; Score 120; DB 7; Length 15518;  
Best Local Similarity 80.1%; Pred. No. 1.1e-08;  
RESULT 826  
ID ADL41653 standard; DNA; 425 BP.  
DE Human ovarian cancer DNA marker #15543.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.9%; Score 119.8; DB 5; Length 425;  
Best Local Similarity 74.4%; Pred. No. 1.2e-08;  
RESULT 827  
ID AAH33241 standard; cDNA; 464 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:297.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.9%; Score 119.8; DB 4; Length 464;  
Best Local Similarity 88.8%; Pred. No. 1.2e-08;  
RESULT 828  
ID ACN57821 standard; cDNA; 560 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-006-Q6-K6-C12, SEQ:13602.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 6.9%; Score 119.8; DB 13; Length 560;  
Best Local Similarity 85.8%; Pred. No. 1.2e-08;  
RESULT 829  
ID AAZ07192 standard; cDNA; 3275 BP.  
DE Human lung tumour protein SAL-25 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 6.9%; Score 119.8; DB 2; Length 3275;  
Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
RESULT 830  
ID AAC79145 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific cDNA #98.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 6.9%; Score 119.8; DB 3; Length 3275;  
Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
RESULT 831  
ID AAD23220 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific protein SAL-25 cDNA.

PN WO200172295-A2.  
 PD 04-OCT-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 6.9%; Score 119.8; DB 4; Length 3275;  
 Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
 RESULT 832  
 ID ADD66459 standard; cDNA; 3275 BP.  
 DE Human lung tumour-specific related cDNA, SEQ ID No 151.  
 PN WO200292001-A2.  
 PD 21-NOV-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 6.9%; Score 119.8; DB 10; Length 3275;  
 Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
 RESULT 833  
 ID ADE87713 standard; cDNA; 3275 BP.  
 DE Human lung tumour antigen cDNA #98.  
 PN US2003118599-A1.  
 PD 26-JUN-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 6.9%; Score 119.8; DB 10; Length 3275;  
 Best Local Similarity 91.4%; Pred. No. 1.2e-08;  
 RESULT 834  
 ID AAL26497 standard; cDNA; 7765 BP.  
 DE Human breast cancer expressed polynucleotide 18954.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 6.9%; Score 119.8; DB 4; Length 7765;  
 Best Local Similarity 88.4%; Pred. No. 1.2e-08;  
 RESULT 835  
 ID ADL45290 standard; DNA; 7765 BP.  
 DE Human ovarian cancer DNA marker #19180.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 6.9%; Score 119.8; DB 5; Length 7765;  
 Best Local Similarity 88.4%; Pred. No. 1.2e-08;  
 RESULT 836  
 ID ACN88585 standard; DNA; 7765 BP.  
 DE Breast cancer related marker, seq id 9735.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 6.9%; Score 119.8; DB 11; Length 7765;  
 Best Local Similarity 88.4%; Pred. No. 1.2e-08;  
 RESULT 837  
 ID AAS46691 standard; DNA; 24259 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #414.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 6.9%; Score 119.8; DB 4; Length 24259;  
 Best Local Similarity 79.3%; Pred. No. 1.2e-08;  
 RESULT 838  
 ID ABV49426 standard; cDNA; 308 BP.  
 DE Human prostate expression marker cDNA 49417.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 6.9%; Score 119.6; DB 5; Length 308;  
 Best Local Similarity 93.3%; Pred. No. 1.2e-08;  
 RESULT 839  
 ID ADQ22074 standard; DNA; 980 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.9%; Score 119.6; DB 12; Length 980;  
 Best Local Similarity 93.3%; Pred. No. 1.3e-08;  
 RESULT 840  
 ID ADJ75071 standard; DNA; 1331 BP.  
 DE Marker gene SEQ ID NO:323.  
 PN EP1394274-A2.

PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Query Match 6.9%; Score 119.6; DB 12; Length 1331;  
 Best Local Similarity 84.8%; Pred. No. 1.3e-08;  
 RESULT 841  
 ID AAC81052 standard; cDNA; 1859 BP.  
 DE Human secreted protein cDNA sequence #25.  
 PN WO200063230-A2.  
 PD 26-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.9%; Score 119.6; DB 3; Length 1859;  
 Best Local Similarity 93.3%; Pred. No. 1.3e-08;  
 RESULT 842  
 ID ADA40158 standard; cDNA; 3466 BP.  
 DE Human secreted protein encoding cDNA.  
 PN WO2002102993-A2.  
 PD 27-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.9%; Score 119.6; DB 8; Length 3466;  
 Best Local Similarity 96.8%; Pred. No. 1.3e-08;  
 RESULT 843  
 ID ADB91280 standard; cDNA; 3466 BP.  
 DE Human secreted protein cDNA #SEQ ID 226.  
 PN WO2003004622-A2.  
 PD 16-JAN-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.9%; Score 119.6; DB 9; Length 3466;  
 Best Local Similarity 96.8%; Pred. No. 1.3e-08;  
 RESULT 844  
 ID ADA56320 standard; DNA; 3466 BP.  
 DE Gene encoding human secreted protein #499.  
 PN WO2002102994-A2.  
 PD 27-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.9%; Score 119.6; DB 10; Length 3466;  
 Best Local Similarity 96.8%; Pred. No. 1.3e-08;  
 RESULT 845  
 ID ABV54519 standard; cDNA; 515 BP.  
 DE Human prostate expression marker cDNA 54510.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 6.9%; Score 119.4; DB 5; Length 515;  
 Best Local Similarity 92.0%; Pred. No. 1.3e-08;  
 RESULT 846  
 ID ABZ10224 standard; DNA; 2501 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #364.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 6.9%; Score 119.4; DB 8; Length 2501;  
 Best Local Similarity 79.7%; Pred. No. 1.4e-08;  
 RESULT 847  
 ID ABA91228 standard; cDNA; 3002 BP.  
 DE Human DBF4 related factor 1 (DRF1) Incyte clone 3051528.  
 PN WO200196557-A2.  
 PD 20-DEC-2001.  
 PA (PHAA) PHARMACIA & UPJOHN SPA.  
 Query Match 6.9%; Score 119.4; DB 6; Length 3002;  
 Best Local Similarity 89.0%; Pred. No. 1.4e-08;  
 RESULT 848  
 ID ADQ22371 standard; DNA; 4824 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.9%; Score 119.4; DB 12; Length 4824;  
 Best Local Similarity 92.0%; Pred. No. 1.4e-08;  
 RESULT 849  
 ID ABZ10104 standard; DNA; 35962 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #244.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.

PA (EP1G-) EPIGENOMICS AG.  
 Query Match 6.9%; Score 119.4; DB 8; Length 35962;  
 Best Local Similarity 79.7%; Pred. No. 1.4e-08;  
 RESULT 850  
 ID ADT97086 standard; cDNA; 196 BP.  
 DE Colon cancer associated human cDNA sequence #2593.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 6.9%; Score 119.2; DB 11; Length 196;  
 Best Local Similarity 80.8%; Pred. No. 1.4e-08;  
 RESULT 851  
 ID ACN56642 standard; cDNA; 598 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 6.9%; Score 119.2; DB 13; Length 598;  
 Best Local Similarity 90.7%; Pred. No. 1.4e-08;  
 RESULT 852  
 ID ADM47653 standard; DNA; 1708 BP.  
 DE Polynucleotide sequence #71 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D.  
 PA (CHOM/) CHOMET P S.  
 PA (LACC/) LACCETTI L B.  
 Query Match 6.9%; Score 119.2; DB 12; Length 1708;  
 Best Local Similarity 97.6%; Pred. No. 1.4e-08;  
 RESULT 853  
 ID AAV54587 standard; cDNA; 2447 BP.  
 DE Human secretory protein encoding cDNA clone CO1020-1.  
 PN WO98333916-A2.  
 PD 06-AUG-1998.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 6.9%; Score 119.2; DB 2; Length 2447;  
 Best Local Similarity 92.5%; Pred. No. 1.4e-08;  
 RESULT 854  
 ID AA225607 standard; cDNA; 2447 BP.  
 DE Human secreted protein clone CO1020\_1 nucleotide sequence.  
 PN US5965397-A.  
 PD 12-OCT-1999.  
 PA (GEMY) GENETICS INST INC.  
 Query Match 6.9%; Score 119.2; DB 2; Length 2447;  
 Best Local Similarity 92.5%; Pred. No. 1.4e-08;  
 RESULT 855  
 ID ABL33637 standard; DNA; 7306 BP.  
 DE Human immune system associated gene SEQ ID NO: 1610.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EP1G-) EPIGENOMICS AG.  
 Query Match 6.9%; Score 119.2; DB 6; Length 7306;  
 Best Local Similarity 82.9%; Pred. No. 1.5e-08;  
 RESULT 856  
 ID ADQ23662 standard; DNA; 15749 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6482.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.9%; Score 119.2; DB 12; Length 15749;  
 Best Local Similarity 97.6%; Pred. No. 1.5e-08;  
 RESULT 857  
 ID AAT13475 standard; RNA; 191 BP.  
 DE Capture probe for detection of target sequence by chimaeric probe.  
 PN EP707076-A1.  
 PD 17-APR-1996.  
 PA (STAD) AMOCO CORP.  
 Query Match 6.9%; Score 119; DB 2; Length 191;  
 Best Local Similarity 80.0%; Pred. No. 1.5e-08;  
 RESULT 858

ID ABY58763 standard; cDNA; 317 BP.  
 DE Human prostate expression marker cDNA 58754.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 6.9%; Score 119; DB 5; Length 317;  
 Best Local Similarity 92.6%; Pred. No. 1.5e-08;  
 RESULT 859  
 ID ACN50065 standard; cDNA; 555 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-034-Q6-N6-G11, SEQ:4846.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 6.9%; Score 119; DB 13; Length 555;  
 Best Local Similarity 89.5%; Pred. No. 1.5e-08;  
 RESULT 860  
 ID ADQ23651 standard; DNA; 3583 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6471.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.9%; Score 119; DB 12; Length 3583;  
 Best Local Similarity 89.5%; Pred. No. 1.6e-08;  
 RESULT 861  
 ID ADE15670 standard; DNA; 4288 BP.  
 DE Human structural and cytoskeleton-associated protein (SCAP) gene #18.  
 PN WO2003062391-A2.  
 PD 31-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 6.9%; Score 119; DB 10; Length 4288;  
 Best Local Similarity 89.5%; Pred. No. 1.6e-08;  
 RESULT 862  
 ID AA187975 standard; cDNA; 403 BP.  
 DE Human polynucleotide SEQ ID NO 8035.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 6.9%; Score 118.8; DB 4; Length 403;  
 Best Local Similarity 98.4%; Pred. No. 1.6e-08;  
 RESULT 863  
 ID AA183052 standard; cDNA; 452 BP.  
 DE Human polynucleotide SEQ ID NO 3112.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 6.9%; Score 118.8; DB 4; Length 452;  
 Best Local Similarity 98.4%; Pred. No. 1.6e-08;  
 RESULT 864  
 ID ACN50622 standard; cDNA; 508 BP.  
 DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-E9, SEQ:5403.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 6.9%; Score 118.8; DB 13; Length 508;  
 Best Local Similarity 77.4%; Pred. No. 1.6e-08;  
 RESULT 865  
 ID ACN46717 standard; cDNA; 522 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-N6-C8, SEQ:1498.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 6.9%; Score 118.8; DB 13; Length 522;  
 Best Local Similarity 77.4%; Pred. No. 1.6e-08;  
 RESULT 866

ID ACN51492 standard; cDNA; 546 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-K6-P3, SEQ:6273.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 6.9%; Score 118.8; DB 13; Length 546;  
Best Local Similarity 85.7%; Pred. No. 1.6e-08;  
RESULT 867  
ID ADI69621 standard; DNA; 805 BP.  
DE Human ovarian cancer DNA marker #2363.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.9%; Score 118.8; DB 5; Length 805;  
Best Local Similarity 76.3%; Pred. No. 1.6e-08;  
RESULT 868  
ID ADI75959 standard; DNA; 805 BP.  
DE Human ovarian cancer DNA marker #8701.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.9%; Score 118.8; DB 5; Length 805;  
Best Local Similarity 76.3%; Pred. No. 1.6e-08;  
RESULT 869  
ID ADR59280 standard; cDNA; 836 BP.  
DE Cotton cDNA sequence, SEQ ID 61.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 6.9%; Score 118.8; DB 13; Length 836;  
Best Local Similarity 85.7%; Pred. No. 1.6e-08;  
RESULT 870  
ID ADQ24551 standard; DNA; 1816 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7371.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.9%; Score 118.8; DB 12; Length 1816;  
Best Local Similarity 85.7%; Pred. No. 1.7e-08;  
RESULT 871  
ID AAV41257 standard; cDNA; 2082 BP.  
DE Mouse neuronal PAS domain protein NPAS1 cDNA.  
PN WO9831804-A1.  
PD 23-JUL-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 6.9%; Score 118.8; DB 2; Length 2082;  
Best Local Similarity 98.4%; Pred. No. 1.7e-08;  
RESULT 872  
ID AAZ43781 standard; cDNA; 2685 BP.  
DE Human fetal brain cDNA clone vb6\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 6.9%; Score 118.8; DB 3; Length 2685;  
Best Local Similarity 85.7%; Pred. No. 1.7e-08;  
RESULT 873  
ID ABL32279 standard; DNA; 5198 BP.  
DE Human immune system associated gene SEQ ID NO: 252.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 118.8; DB 6; Length 5198;  
Best Local Similarity 75.8%; Pred. No. 1.7e-08;  
RESULT 874  
ID ABL32788 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 761.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.9%; Score 118.8; DB 6; Length 6171;  
Best Local Similarity 79.2%; Pred. No. 1.7e-08;  
RESULT 875  
ID AAS60724 standard; cDNA; 237 BP.  
DE Human cancer agent-resistance marker #479.  
PN WO200179556-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.8%; Score 118.6; DB 4; Length 237;  
Best Local Similarity 92.5%; Pred. No. 1.7e-08;  
RESULT 876  
ID ADL35477 standard; DNA; 305 BP.  
DE Human filamin A alpha-related functional screen hit DNA 3.  
PN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.8%; Score 118.6; DB 12; Length 305;  
Best Local Similarity 84.7%; Pred. No. 1.7e-08;  
RESULT 877  
ID ABV13564 standard; cDNA; 394 BP.  
DE Human prostate expression marker cDNA 13555.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.8%; Score 118.6; DB 5; Length 394;  
Best Local Similarity 88.2%; Pred. No. 1.7e-08;  
RESULT 878  
ID ABV43535 standard; cDNA; 408 BP.  
DE Human prostate expression marker cDNA 43526.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.8%; Score 118.6; DB 5; Length 408;  
Best Local Similarity 88.2%; Pred. No. 1.7e-08;  
RESULT 879  
ID ABV34679 standard; cDNA; 408 BP.  
DE Human prostate expression marker cDNA 34670.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.8%; Score 118.6; DB 5; Length 408;  
Best Local Similarity 88.2%; Pred. No. 1.7e-08;  
RESULT 880  
ID ACN45362 standard; cDNA; 570 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 6.8%; Score 118.6; DB 13; Length 570;  
Best Local Similarity 82.4%; Pred. No. 1.7e-08;  
RESULT 881  
ID ACN51614 standard; cDNA; 584 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-C5, SEQ:6395.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 6.8%; Score 118.6; DB 13; Length 584;  
Best Local Similarity 96.8%; Pred. No. 1.7e-08;  
RESULT 882  
ID AAK88206 standard; cDNA; 698 BP.  
DE Human digestive system antigen coding sequence SEQ ID NO: 522.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.6; DB 4; Length 698;  
Best Local Similarity 81.4%; Pred. No. 1.8e-08;

RESULT 883  
ID AAS29150 standard; cDNA; 698 BP.  
DE cDNA encoding for human DNA-binding protein #121.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.6; DB 5; Length 698;  
Best Local Similarity 81.4%; Pred. No. 1.8e-08;  
RESULT 884  
ID AAD16659 standard; cDNA; 698 BP.  
DE Human novel protein-encoding cDNA clone HVAET61, SEQ ID NO:13.  
PN WO200155327-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.6; DB 5; Length 698;  
Best Local Similarity 81.4%; Pred. No. 1.8e-08;  
RESULT 885  
ID AB868290 standard; cDNA; 698 BP.  
DE cDNA encoding human DNA-binding protein #121.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 6.8%; Score 118.6; DB 6; Length 698;  
Best Local Similarity 81.4%; Pred. No. 1.8e-08;  
RESULT 886  
ID ADC25284 standard; cDNA; 698 BP.  
DE Human cDNA from extracellular matrix gene 121.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.6; DB 10; Length 698;  
Best Local Similarity 81.4%; Pred. No. 1.8e-08;  
RESULT 887  
ID ADP22613 standard; DNA; 1324 BP.  
DE Sea-squirt (Cliona intestinalis) zinc finger protein coding sequence #94.  
PN JP2004057126-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 6.8%; Score 118.6; DB 12; Length 1324;  
Best Local Similarity 90.1%; Pred. No. 1.8e-08;  
RESULT 888  
ID ADQ08635 standard; DNA; 1356 BP.  
DE Ciona intestinalis nervous system associated gene SeqID37.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 6.8%; Score 118.6; DB 12; Length 1356;  
Best Local Similarity 90.1%; Pred. No. 1.8e-08;  
RESULT 889  
ID ADQ24380 standard; DNA; 1781 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7200.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.8%; Score 118.6; DB 12; Length 1781;  
Best Local Similarity 75.1%; Pred. No. 1.8e-08;  
RESULT 890  
ID AAF91862 standard; cDNA; 2753 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HDPIE85, SEQ ID NO:15.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.6; DB 4; Length 2753;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 891  
ID ABL34033 standard; DNA; 4255 BP.  
DE Human immune system associated gene SEQ ID NO: 2006.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 6; Length 4255;

Best Local Similarity 80.3%; Pred. No. 1.8e-08;  
RESULT 892  
ID ADB54096 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 20.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 10; Length 4316;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 893  
ID ADS89248 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:264.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 13; Length 4316;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 894  
ID ABL32921 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 894.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 6; Length 5195;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 895  
ID ABK34027 standard; DNA; 6944 BP.  
DE Human DNA for staging of Astrocytomas, complement, #57.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 6; Length 6944;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 896  
ID ADA20447 standard; DNA; 6944 BP.  
DE Prostate tumour related genomic DNA complement sample #56.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 8; Length 6944;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 897  
ID ADA84254 standard; DNA; 6944 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 8; Length 6944;  
Best Local Similarity 84.7%; Pred. No. 1.8e-08;  
RESULT 898  
ID ADS89685 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:701.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 6.8%; Score 118.6; DB 13; Length 8900;  
Best Local Similarity 93.2%; Pred. No. 1.8e-08;  
RESULT 899  
ID AA185202 standard; cDNA; 390 BP.  
DE Human polynucleotide SEQ ID NO 5262.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.8%; Score 118.4; DB 4; Length 390;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 900  
ID ACN60479 standard; cDNA; 431 BP.  
DE Cotton gymnocium tissue EST Clone ID: L183829-023-Q6-K6-D10, SEQ:15260.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.

PA (ZIBG/) ZIEGLER T E.  
Query Match 6.8%; Score 118.4; DB 13; Length 431;  
Best Local Similarity 83.8%; Pred. No. 1.9e-08;  
RESULT 901  
ID ABV49907 standard; cDNA; 472 BP.  
DE Human prostate expression marker cDNA 49898.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 6.8%; Score 118.4; DB 5; Length 472;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 902  
ID AAS62239 standard; cDNA; 681 BP.  
DE cDNA sequence #26 encoding novel human secreted protein.  
PN WO200177291-A2.  
PD 18-OCT-2001.  
PA (GENY) GENETICS INST INC.  
Query Match 6.8%; Score 118.4; DB 6; Length 681;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 903  
ID ABZ82489 standard; cDNA; 805 BP.  
DE Human secreted protein cDNA #SEQ ID 36.  
PN WO200268628-A1.  
PD 06-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.4; DB 6; Length 805;  
Best Local Similarity 81.5%; Pred. No. 1.9e-08;  
RESULT 904  
ID ADF81828 standard; DNA; 873 BP.  
DE Leukemia-related DNA sequence #2384.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE-) HAFERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 6.8%; Score 118.4; DB 10; Length 873;  
Best Local Similarity 79.1%; Pred. No. 1.9e-08;  
RESULT 905  
ID AAX80668 standard; cDNA; 1132 BP.  
DE Clone am996\_12 encoding secreted protein-am996\_12.  
PN WO9928335-A1.  
PD 10-JUN-1999.  
PA (GENY) GENETICS INST INC.  
Query Match 6.8%; Score 118.4; DB 2; Length 1132;  
Best Local Similarity 91.2%; Pred. No. 1.9e-08;  
RESULT 906  
ID AAS59218 standard; cDNA; 1132 BP.  
DE Human cDNA encoding a secreted protein am996\_12.  
PN WO200175068-A2.  
PD 11-OCT-2001.  
PA (GENY) GENETICS INST INC.  
Query Match 6.8%; Score 118.4; DB 4; Length 1132;  
Best Local Similarity 91.2%; Pred. No. 1.9e-08;  
RESULT 907  
ID ABA50887 standard; cDNA; 1132 BP.  
DE Human polynucleotide SEQ ID NO 23.  
PN US2001039335-A1.  
PD 08-NOV-2001.  
PA (JACO/) JACOBS K.  
PA (MCCO/) MCCOY J M.  
PA (LAVA/) LAVALLIE E R.  
PA (COLL/) COLLINS-RACIE L A.  
PA (EVAN/) EVANS C.  
PA (MERB/) MERBERG D.  
PA (TREA/) TREACY M.  
PA (AGOS/) AGOSTINO M J.  
PA (STEI/) STEININGER R J.  
PA (SPAU/) SPAULDING V.  
PA (WONG/) WONG G G.  
PA (CLAR/) CLARK H.  
PA (FECH/) FECHTEL K.

Query Match 6.8%; Score 118.4; DB 6; Length 1132;  
Best Local Similarity 91.2%; Pred. No. 1.9e-08;  
RESULT 908  
ID ABK72084 standard; cDNA; 1225 BP.  
DE Human cDNA encoding ovarian antigen #43.  
PN WO200155329-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 118.4; DB 5; Length 1225;  
Best Local Similarity 76.0%; Pred. No. 1.9e-08;  
RESULT 909  
ID ABK91676 standard; cDNA; 1225 BP.  
DE cDNA encoding novel ovarian related polypeptide #43.  
PN US2002045230-A1.  
PD 18-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBI/) RUBIN S M.  
PA (BARA/) BARASH S C.  
Query Match 6.8%; Score 118.4; DB 6; Length 1225;  
Best Local Similarity 76.0%; Pred. No. 1.9e-08;  
RESULT 910  
ID ADR44025 standard; DNA; 1806 BP.  
DE Human colon tumour associated gene clone-36 SEQ ID NO:35.  
PN WO2004074506-A2.  
PD 02-SEP-2004.  
PA (MERG-) MERGEN LTD.  
Query Match 6.8%; Score 118.4; DB 13; Length 1806;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 911  
ID ADA00368 standard; cDNA; 2843 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2843;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 912  
ID AAZ65034 standard; cDNA; 2846 BP.  
DE Membrane-bound protein PRO1344 encoding cDNA.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 3; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 913  
ID AAS46009 standard; cDNA; 2846 BP.  
DE Human DNA encoding PRO polypeptide sequence #85.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 4; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 914  
ID AAF92076 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 4; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 915  
ID AAF44180 standard; cDNA; 2846 BP.  
DE Human PRO1344 (UNQ699) nucleotide sequence SEQ ID NO:230.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 5; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 916  
ID ABS74396 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2002119130-A1.  
PD 29-AUG-2002.

PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 6; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 917  
ID ACA99459 standard; cDNA; 2846 BP.  
DE CDNA encoding human PRO polypeptide #85.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 918  
ID ACA73469 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 919  
ID ACA05784 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 920  
ID ACA66618 standard; cDNA; 2846 BP.  
DE CDNA encoding human PRO protein #85.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 921  
ID ACA4316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 922  
ID ACA91182 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 923  
ID ACD81559 standard; cDNA; 2846 BP.  
DE Human CDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 924  
ID ACF20193 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 925  
ID ACF19579 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 926  
ID ACA70109 standard; cDNA; 2846 BP.

ID ACD21867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 927  
ID ACF13032 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 928  
ID ACD25135 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 929  
ID ACF00184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 930  
ID ACA60381 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 931  
ID ACA72241 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 932  
ID ACD04765 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 933  
ID ACD18226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 934  
ID ACD08233 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 935  
ID ACA86667 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 936  
ID ACA70109 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 937  
ID ACD12331 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 938  
ID ACC74246 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US200302725-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 939  
ID ACD15874 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 940  
ID ACD25442 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 941  
ID ACD17919 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 942  
ID ACC88206 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 943  
ID ACD21560 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 944  
ID ACD18627 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US200304916-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 945  
ID ACA58828 standard; cDNA; 2846 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 946  
ID ABX98237 standard; cDNA; 2846 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.

PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 947  
ID ACD13988 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 948  
ID ACD09768 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 949  
ID ACC88513 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 950  
ID ACD21253 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 951  
ID ABX75625 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 952  
ID ACA64004 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 953  
ID ABX97828 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 954  
ID AC397304 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 955  
ID ACA57767 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 956  
ID ACD14295 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032130-A1.



PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 957  
ID ACC91078 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 958  
ID ACC88820 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 959  
ID ACD07017 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 960  
ID ACA67468 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 961  
ID ACC81523 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 962  
ID ACA91268 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 963  
ID ACC89127 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 964  
ID ACC86483 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 965  
ID ACC89741 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 966  
ID ACC92920 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032135-A1.

PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 967  
ID ABX80775 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 968  
ID ACA72548 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 969  
ID ACA89066 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 970  
ID ACA69802 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 971  
ID ACA96945 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 972  
ID ACA90941 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 973  
ID ACA70723 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 974  
ID ACA95233 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 975  
ID ACD44284 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
RESULT 976  
ID ACC86176 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027263-A1.

PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA93715 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA8274 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ABX98739 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACC81216 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID AC95540 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACD0458 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACC87899 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACF12561 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACH66262 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ABX79455 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.

PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACD45167 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACC90048 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACD12656 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACF19886 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ABX76830 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA73162 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA68705 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA74549 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACA70416 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
ID ACD14602 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 997  
ID ACA96276 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 998  
ID ACA65050 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 999  
ID ACA73776 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1000  
ID ACA74188 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1001  
ID ACA96583 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1002  
ID ACDD10689 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1003  
ID ACC91385 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1004  
ID ACA93476 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1005  
ID ACD02720 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1006  
ID ACC87285 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;

RESULT 1007  
ID ACC85869 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1008  
ID ABX81158 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1009  
ID ACA65357 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1010  
ID ACA94174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1011  
ID ACA97918 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1012  
ID ACA91420 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1013  
ID ACA90634 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1014  
ID ACD16181 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1015  
ID ACD17342 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1016  
ID ACC91999 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1017  
ID ACD02316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1018  
ID ACA74856 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1019  
ID ACA91727 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1020  
ID ACA89307 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1021  
ID ACA71371 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1022  
ID ACC90771 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1023  
ID ACA65781 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1024  
ID ACA68944 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1025  
ID ACA92974 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1026  
ID ACA94926 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1027  
ID ACD16488 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1028  
ID ACD15567 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1029  
ID ACA98466 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1030  
ID ABX17058 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1031  
ID ABX16670 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 8; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1032  
ID ACA67913 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1033  
ID ACA63391 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1034  
ID ACA97611 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1035  
ID ACA99060 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1036  
ID ACC91692 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;

RESULT 1037  
ID ACD11103 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1038  
ID ACD14953 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1039  
ID ACA88362 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane polypeptide PRO1344 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1040  
ID ACD81869 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1041  
ID ACD11717 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1042  
ID ACC95846 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1043  
ID ACF16409 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1044  
ID ACF02527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1045  
ID ACF02834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1046  
ID ACF21421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049769-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1047  
ID ACF10105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1048  
ID ACF77998 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1049  
ID ACD46703 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1050  
ID ACD49466 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1051  
ID ACF28233 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1052  
ID ACD88923 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1053  
ID ACD84318 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1054  
ID ACD99092 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
Length 2846;  
RESULT 1055  
ID ADA77921 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1056  
ID ACF48834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1057  
ID ACD09154 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1058  
ID ACF11947 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1059  
ID ACF41181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1060  
ID ACF15795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1061  
ID ACF16102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1062  
ID ADB17094 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1063  
ID ACD31929 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1064  
ID ACF18737 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064452-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1065  
ID ACF09184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003068705-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1066  
ID ACF78305 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1067  
ID ACF51904 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1068  
ID ACF26391 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068704-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1069  
ID ACF24184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068722-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1070  
ID ACF63495 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073183-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1071  
ID ACF50369 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1072  
ID ACH07840 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1073  
ID ACF13646 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064462-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC. 91.9%; Pred. No. 1.9e-08;  
RESULT 1074  
ID ACD41572 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003065159-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1075  
ID ACD89844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1076  
ID ACF31985 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1077  
ID ACF23263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1078  
ID ACF39953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1079  
ID ACD45475 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1080  
ID ACF53132 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1081  
ID ACF27312 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1082  
ID ACF45150 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1083  
ID ACF29768 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1084  
ID ACD89844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1085  
ID ACD84625 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1086  
ID ACD98785 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1087  
ID ACF77077 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1088  
ID ACF76770 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1089  
ID ACF49755 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1090  
ID ACF50062 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1091  
ID ADA21427 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1092  
ID ACD09461 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1093  
ID ACD08540 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040061-A1.

PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1094  
ID ACH03594 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1095  
ID ACF12254 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1096  
ID ACC94762 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1097  
ID ACD22481 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1098  
ID ACF15181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1099  
ID ACC97276 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1100  
ID ACC92306 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1101  
ID ACF13953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1102  
ID ACF14260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1103

ID ADA10214 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1104  
ID ACF09491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1105  
ID ACD45782 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1106  
ID ACD47931 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1107  
ID ACD67662 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1108  
ID ACF25470 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1109  
ID ACF29154 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1110  
ID ACD84932 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1111  
ID ACD84011 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1112  
ID ACD88002 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.



Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1122  
ID ACF08570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1123  
ID ACF31371 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1124  
ID ACF52211 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1125  
ID ACD50080 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1126  
ID ACF38783 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1127  
ID ACF26698 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1128  
ID ACF24798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1129  
ID ACF46378 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;  
RESULT 1130  
ID ACF27926 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. NO. 1.9e-08;

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1131  
ID ACD9230 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US200308684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1132  
ID ACF63802 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1133  
ID ACF60442 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1134  
ID ACH12566 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1135  
ID ACH09989 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1136  
ID ACD03844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1137  
ID ACD10382 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1138  
ID ACD12024 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1139  
ID ACF42409 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1140  
ID ADA27866 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003054359-A1.

PD 20-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1141  
ID ACF18430 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1142  
ID ACF02220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1143  
ID ACF21728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1144  
ID ACF10412 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1145  
ID ACF33864 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1146  
ID ACF44826 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1147  
ID ACD90458 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1148  
ID ACD91071 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1149  
ID ACF30382 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1150  
ID ACD87081 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1151  
ID ACF60135 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1152  
ID ACF4685 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003083737-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1153  
ID ACF75542 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1154  
ID ADA79713 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1155  
ID ACF17202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1156  
ID ACF22956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1157  
ID ACF07956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1158  
ID ACF08263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1159  
ID ACF40567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064448-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1160  
ID ACF53746 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1161  
ID ACD47010 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1162  
ID ACF47913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1163  
ID ACF47299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1164  
ID ACF46071 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1165  
ID ACD86160 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1166  
ID ACF52518 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1167  
ID ACF52825 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1168  
ID ACF64818 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1169  
ID ACF76463 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1170  
ID ACF61363 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1171  
ID ACF61670 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1172  
ID ACD30701 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1173  
ID ACD31622 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1174  
ID ACD32543 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1175  
ID ADA20071 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1176  
ID ACD82108 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1177  
ID ACF17509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1178  
ID ADA94446 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1179  
ID ACF07342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1180  
ID ACP20500 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1181  
ID ACF20807 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1182  
ID ACF21114 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1183  
ID ACD47624 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1184  
ID ACF47606 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1185  
ID ACF53439 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1186  
ID ACD86774 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1187  
ID ACH05022 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1188  
ID ACF44519 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1189  
ID ADA81440 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1190  
ID ACD22174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1191  
ID ACD24521 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1192  
ID ACD39724 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1193  
ID ACD40031 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1194  
ID ACF13339 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1195  
ID ACF03141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1196  
ID ACF78612 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1197  
ID ACF11333 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169;  
ID US2003073171-A1.  
PD 17-APR-2003. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match 91.9%; Pred. No. 1.9e-08;  
Best Local Similarity  
RESULT 1198  
ID ACF50676 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169;  
ID US2003032121-A1.  
PD 13-FEB-2003. 6.8%; Score 118.4; DB 9; Length 2846;  
Query Match 91.9%; Pred. No. 1.9e-08;  
Best Local Similarity  
RESULT 1199  
ID ACF34171 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169;  
ID US2003064458-A1.  
PD 03-APR-2003. 6.8%; Score 118.4; DB 9; Length 2846;  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1200  
ID ACD46396 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
ID US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1201  
ID ACD48238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
ID US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1202  
ID ACF27619 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169;  
ID US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1203  
ID ACF24491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169;  
ID US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1204  
ID ACD85546 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
ID US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1205  
ID ACD90151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
ID US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1206  
ID ACD83704 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
ID US2003068738-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1207  
ID ACF49141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1208  
ID ACH07226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1209  
ID ACH07533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1210  
ID ACH08147 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1211  
ID ACH11338 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1212  
ID ACH11645 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1213  
ID ACH10296 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1214  
ID ACF01299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1215  
ID ACF40874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;

RESULT 1216  
ID ACD24214 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1217  
ID ACD31315 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1218  
ID ACF17816 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1219  
ID ADA38671 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1220  
ID ACF32599 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1221  
ID ACF40260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1222  
ID ACF48220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1223  
ID ACF38169 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1224  
ID ACF25105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1225  
ID ACF27005 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068730-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1226  
ID ACF29461 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1227  
ID ACD87695 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1228  
ID ACF76156 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1229  
ID ACF49448 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1230  
ID ACF43905 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1231  
ID ACH06250 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1232  
ID ACH06557 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1233  
ID ADA83238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1234  
ID ACC32613 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1235

ID ACC3227 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1236  
ID ACF19272 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1237  
ID ACD12963 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1238  
ID ACF06421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1239  
ID ACC94455 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1240  
ID ACC97883 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1241  
ID ACC94148 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1242  
ID ACF42102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1243  
ID ACD31008 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1244  
ID ACD3037 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1245

ID ACD43344 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1246  
ID ACF14874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1247  
ID ADA92792 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1248  
ID ACF01606 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1249  
ID ACF31678 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1250  
ID ACD57355 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1251  
ID ACD48545 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1252  
ID ACD48852 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1253  
ID ACF51290 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1254  
ID ACF54053 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068769-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1255  
ID ACF25777 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1256  
ID ACF39090 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1257  
ID ACF28847 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1258  
ID ACD90764 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1259  
ID ACD86467 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1260  
ID ACH05329 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1261  
ID ACF65125 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1262  
ID ADB20281 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1263  
ID ACF43598 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.



Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1264  
ID ACH09068 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1265  
ID ACH09375 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1266  
ID ADA78533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1267  
ID ACF09798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1268  
ID ACF50983 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1269  
ID ACF23877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1270  
ID ACD88309 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1271  
ID ACH09682 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1272  
ID ACH10603 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1273  
ID ACD11410 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1274  
ID ACC96460 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1275  
ID ACC98490 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1276  
ID ACP41795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1277  
ID ACF16716 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1278  
ID ACD32236 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1279  
ID ACD30394 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1280  
ID ACD41265 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1281  
ID ACF07649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1282  
ID ACF31064 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1283  
ID ACF77384 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1284  
ID ACF11026 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1285  
ID ACF32906 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1286  
ID ACF26084 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1287  
ID ACD83397 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1288  
ID ACF23570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003058764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1289  
ID ACF42984 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1290  
ID ACF43291 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1291  
ID ACH05943 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;

RESULT 1292  
ID ACH08761 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1293  
ID ACC90355 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1294  
ID ACF10719 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1295  
ID ACC93534 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1296  
ID ACC96153 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1297  
ID ACD24828 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1298  
ID ACF01913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1299  
ID ACF22035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1300  
ID ACF22649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;  
RESULT 1301  
ID ACF08877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068687-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1302  
ID ACF33213 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1303  
ID ACF54667 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1304  
ID ACF48527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1305  
ID ACD47317 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1306  
ID ACD49159 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1307  
ID ACF37862 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1308  
ID ACF30075 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1309  
ID ACD87388 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1310  
ID ACF61977 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1311  
ID ACHI0910 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1312  
ID ACD10075 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1313  
ID ACD16800 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1314  
ID ACH65430 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1315  
ID ACC99097 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1316  
ID ACF00491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1317  
ID ACD40958 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1318  
ID ACF14567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1319  
ID ACF22342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1320  
ID ACF78919 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049764-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1321  
ID ACF11640 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1322  
ID ADA22353 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1323  
ID ACF51597 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1324  
ID ACF33520 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1325  
ID ACD49773 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1326  
ID ACF37555 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1327  
ID ACF28540 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1328  
ID ACD88616 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1329  
ID ACF75235 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1330

ID ACF61056 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1331  
ID ACF44212 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1332  
ID ACH08454 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1333  
ID ACD39420 standard; DNA; 2846 BP.  
DE Human PRO 1344 PCR primer #1.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1334  
ID ACC93841 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1335  
ID ACD20946 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1336  
ID ACF06728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1337  
ID ACD20639 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US20030404919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1338  
ID ACD22788 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1339  
ID ACF41488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044528-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 9; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;

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RESULT 1340
ID ADA06519 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1341
ID ADA39212 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1342
ID ACF07035 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049746-A1.
PD 13-MAR-2003.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1343
ID ACF77691 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1344
ID ACF46089 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1345
ID ACF46992 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1346
ID ACF54360 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1347
ID ACF45764 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1348
ID ACF45457 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1349
ID ACF38476 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1350
ID ACD89537 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1351
ID ACD85239 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1352
ID ACD85853 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1353
ID ACF75849 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1354
ID ACF60749 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1355
ID ACH05636 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1356
ID ADA82604 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1357
ID ADB85610 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.8%; Score 118.4; DB 9; Length 2846;
Best Local Similarity 91.9%; Pred. No. 1.9e-08;
RESULT 1358
ID ADB96238 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003054403-A1.
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PD 20-MAR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;
RESULT 1359
ID ACF5895 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 9; Length 2846;
RESULT 1360
ID ACF5281 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1361
ID ADB85912 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1362
ID ACF56202 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1363
ID ACF56509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1364
ID ADB68289 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1365
ID ADB68096 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1366
ID ACF5588 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1367
ID ACF54974 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1368
ID ADB90913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1369
ID ADC57710 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1370
ID ADC55074 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1371
ID ADC11941 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1372
ID ADC06993 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1373
ID ADC56363 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1374
ID ADC17172 standard; cDNA; 2846 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 37).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1375
ID ADC07418 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1376
ID ADC11408 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 6.8%; Score 118.4; DB 10; Length 2846;
RESULT 1377
ID ADC14870 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1378  
 ID ADC52365 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US200313882-A1.  
 PD 24-JUL-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1379  
 ID ADC14530 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003082546-A1.  
 PD 01-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1380  
 ID ADD08062 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003068623-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1381  
 ID ADC81887 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #65.  
 PN US2003083461-A1.  
 PD 01-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1382  
 ID ADD07529 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2002193239-A1.  
 PD 19-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1383  
 ID ADC82420 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #65.  
 PN US2003059833-A1.  
 PD 27-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1384  
 ID ADD05642 standard; cDNA; 2846 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #85.  
 PN US2003087376-A1.  
 PD 08-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1385  
 ID ADD08600 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003073090-A1.  
 PD 17-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1386  
 ID ADD06849 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2002193300-A1.  
 PD 19-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1387  
 ID ADC83096 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #65.  
 PN US2003059783-A1.

PD 27-MAR-2003.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1388  
 ID ADD55203 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #85.  
 PN US2003077593-A1.  
 PD 24-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1389  
 ID ADD36041 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003105298-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1390  
 ID ADD56161 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #65.  
 PN US2003077594-A1.  
 PD 24-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1391  
 ID ADD34599 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #65.  
 PN US2002132253-A1.  
 PD 19-SEP-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1392  
 ID ADE26753 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003087304-A1.  
 PD 08-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1393  
 ID ADE26220 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003087305-A1.  
 PD 08-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1394  
 ID ADF67157 standard; cDNA; 2846 BP.  
 DE Human PRO1344 nucleotide sequence SEQ ID NO:230.  
 PN US2002198148-A1.  
 PD 26-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1395  
 ID ADG01042 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003078387-A1.  
 PD 24-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1396  
 ID ADG08595 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180793-A1.  
 PD 25-SEP-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
 Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
 RESULT 1397  
 ID ADG02637 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1398  
ID ADG01344 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1399  
ID ADP95519 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1400  
ID ADP95216 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1401  
ID ADG12334 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1402  
ID ADH24069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1403  
ID ADH34095 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1404  
ID ADH29928 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1405  
ID ADH23899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1406  
ID ADH08994 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003207395-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1407  
ID ADG85303 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1408  
ID ADH24579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1409  
ID ADH37435 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1410  
ID ADH02024 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1411  
ID ADH37605 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1412  
ID ADG85643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1413  
ID ADH24239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1414  
ID ADH38533 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1415  
ID ADG83654 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180794-A1.  
PD 25-SEP-2003.



Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1425  
ID ADI25385 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1426  
ID ADH90178 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1427  
ID ADI25555 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1428  
ID ADH97729 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1429  
ID ADI34411 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1430  
ID ADI03577 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1431  
ID ADI11934 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1432  
ID ADH90008 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1433  
ID ADH99903 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1434

ID ADH98409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.  
RESULT 1435  
ID ADI11084 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 25-SEP-2003.  
RESULT 1436  
ID ADI11594 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 25-SEP-2003.  
RESULT 1437  
ID ADH98239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 25-SEP-2003.  
RESULT 1438  
ID ADH98579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 25-SEP-2003.  
RESULT 1439  
ID ADH98069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 25-SEP-2003.  
RESULT 1440  
ID ABX78612 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 06-FEB-2003.  
RESULT 1441  
ID ACAY5584 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 13-FEB-2003.  
RESULT 1442  
ID ACA71064 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 13-FEB-2003.  
RESULT 1443  
ID ACC87592 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027278-A1.  
PD 06-FEB-2003.

Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.  
RESULT 1444  
ID ACC86978 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.  
RESULT 1445  
ID ACD04151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 27-FEB-2003.  
RESULT 1446  
ID ABX77859 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 06-FEB-2003.  
RESULT 1447  
ID ABX80271 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 13-FEB-2003.  
RESULT 1448  
ID ACA69177 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 13-FEB-2003.  
RESULT 1449  
ID ACA69482 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.  
RESULT 1450  
ID ACA90327 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.  
RESULT 1451  
ID ACC89434 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 06-FEB-2003.  
RESULT 1452  
ID ABX90248 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 31-OCT-2002.  
RESULT 1453  
ID ACA98225 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
PD 20-FEB-2003.

Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1454  
ID ACA93867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1455  
ID ACD15260 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1456  
ID ACD08847 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1457  
ID ACC96767 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1458  
ID ACF15488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1459  
ID ABX64094 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH) GENENTECH LTD.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1460  
ID ACA72855 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1461  
ID ACD03027 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1462  
ID ACD01842 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1463  
ID ACA92034 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1464  
ID ADI05057 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1465  
ID ADI03407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1466  
ID ADI04802 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1467  
ID ADH78256 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1468  
ID ADI19600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1469  
ID ADH90348 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1470  
ID ADI03067 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1471  
ID ADH7916 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1472  
ID ADH97899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1473  
ID ADH97899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;

ID ADI01284 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1474  
ID ADI01979 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1475  
ID ADI03237 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1476  
ID ADI11424 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1477  
ID ADI02326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1478  
ID ADI11764 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1479  
ID ADI05401 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1480  
ID ADH79473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1481  
ID ADI19430 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1482  
ID ADI05231 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1483  
ID ADH79643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1484  
ID ADI01469 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1485  
ID ADI01639 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1486  
ID ADI01809 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1487  
ID ADH79813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1488  
ID ADI04631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1489  
ID ADI02767 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1490  
ID ADH78086 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1491  
ID ADI25725 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 10; Length 2846;  
Query Match 6.8%; Score 118.4; DB 12; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1492  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 10; Length 2846;  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1493  
ID ADKG5407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 10; Length 2846;  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1494  
ID ADH98749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 10; Length 2846;  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1495  
ID ADH79990 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 10; Length 2846;  
Query Match 6.8%; Score 118.4; DB 10; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1496  
ID ADL32775 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 11; Length 2846;  
Query Match 6.8%; Score 118.4; DB 11; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1497  
ID ADM30309 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 11; Length 2846;  
Query Match 6.8%; Score 118.4; DB 11; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1498  
ID ADL93721 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 11; Length 2846;  
Query Match 6.8%; Score 118.4; DB 11; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1499  
ID ADC52175 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC. 6.8%; Score 118.4; DB 12; Length 2846;  
Query Match 6.8%; Score 118.4; DB 12; Length 2846;  
Best Local Similarity 91.9%; Pred. No. 1.9e-08;  
RESULT 1500  
ID ADE74306 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003211572-A1.

PD 13-NOV-2003.  
Query Match  
Best Local Similarity

6.8%; Score 118.4; DB 12; Length 2846;  
91.9%; Pred. No. 1.9e-08;



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OM protein - protein search, using sw model

Run on: May 15, 2005, 05:50:19 ; Search time 122 Seconds  
(without alignments)  
1846.843 Million cell updates/sec

Title: US-10-063-699-52

Perfect score: 2363

Sequence: 1 MKPQSLACLLALCLGSGE.....KLGFINWDINKDQRSSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2363	100.0	440	2	G6UXC7
2	1996	84.5	476	2	G6E0U4
3	1043	44.1	517	2	G6E0U6
4	1038.5	43.9	508	2	G6P253
5	1030	43.6	493	2	G6S239
6	546.5	23.1	407	2	G6C4L6
7	486	20.6	1553	2	G6FPR0
8	471	19.9	1274	2	G6CHN8
9	460.5	19.5	1938	2	G7TWC0
10	450.5	19.1	1079	2	G6MW7
11	439.5	18.6	1306	2	G7D9L6
12	439.5	18.6	1306	2	G6MX28
13	439.5	18.6	1306	2	G7UIQ7
14	433	18.3	725	2	G7SEB7
15	430	18.2	1391	2	G6C6W0
16	428	18.1	528	2	G63WJ8
17	426.5	18.0	1815	2	G6CP66
18	426	18.0	512	2	G62HK1
19	423	17.9	396	2	G65450
20	420.5	17.8	1384	2	G6VIZ1
21	415.5	17.6	1381	2	G6MW9
22	412.5	17.5	484	2	G6MWY1
23	412.5	17.5	1360	2	G7TWC4
24	406	17.2	1901	1	FG54_MYCTU
25	404.5	17.1	532	2	G7D7F8
26	403	17.1	1224	2	G6CN84
27	403	17.1	1489	2	G6MW6
28	400.5	16.9	992	2	G7TWB8
29	400.5	16.9	1538	2	G6MWY0
30	399.5	16.9	853	2	G79F55
31	399	16.9	786	2	O18740

32	398	16.8	850	2	Q7U0P1	Q7U0P1 mycobacteri
33	397.5	16.8	743	2	Q6RHW0	Q6RHW0 mus musculu
34	397.5	16.8	763	2	Q7U0R0	Q7U0R0 mycobacteri
35	397.5	16.8	1217	2	Q8VIY9	Q8VIY9 mycobacteri
36	397.5	16.8	1460	2	Q7TWC3	Q7TWC3 mycobacteri
37	397.5	16.8	1507	2	Q8VJ23	Q8VJ23 mycobacteri
38	397	16.8	897	2	Q6Q294	Q6Q294 agelenopis
39	396.5	16.8	1715	2	Q8VIZ0	Q8VIZ0 mycobacteri
40	395	16.7	714	2	Q6MMW8	Q6MMW8 mycobacteri
41	395	16.7	749	2	Q7TWK6	Q7TWK6 mycobacteri
42	395	16.7	1660	2	Q79FD4	Q79FD4 mycobacteri
43	395	16.7	1665	2	Q7D721	Q7D721 mycobacteri
44	393	16.6	626	2	Q7TWN2	Q7TWN2 mycobacteri
45	392.5	16.6	923	2	Q79F03	Q79F03 mycobacteri
46	392.5	16.6	923	2	Q7U0X8	Q7U0X8 mycobacteri
47	392	16.6	731	2	Q6MWX5	Q6MWX5 mycobacteri
48	392	16.6	775	2	Q8VJ15	Q8VJ15 mycobacteri
49	392	16.6	1329	2	Q79FP2	Q79FP2 mycobacteri
50	392	16.6	1408	2	Q8VK17	Q8VK17 mycobacteri
51	392	16.6	5263	1	FB0H_BOMMO	F05790 bombyx mori
52	391	16.5	2249	2	Q8NHW4	Q8NHW4 nephila cla
53	390.5	16.5	635	2	Q8VK71	Q8VK71 mycobacteri
54	389.5	16.5	1408	2	Q7U022	Q7U022 mycobacteri
55	388	16.4	1150	2	Q7TYG8	Q7TYG8 mycobacteri
56	387.5	16.4	619	2	Q91FQ9	Q91FQ9 cynomolgus
57	386	16.3	778	1	PG46_MYCTU	P71933 mycobacteri
58	385.5	16.3	518	2	Q67WR0	Q67WR0 oryza sativ
59	383.5	16.2	767	2	Q79FT0	Q79FT0 mycobacteri
60	383	16.2	641	1	EBN1_EBV	P03211 epstein-bar
61	383	16.2	641	2	Q777E1	Q777E1 human herpe
62	381.5	16.1	738	2	Q8VK15	Q8VK15 mycobacteri
63	381.5	16.1	741	2	Q79FP1	Q79FP1 mycobacteri
64	381.5	16.1	774	2	Q7U0P7	Q7U0P7 mycobacteri
65	381	16.1	390	2	Q9M3Y2	Q9M3Y2 triticum ae
66	380.5	16.1	749	2	Q7D974	Q7D974 mycobacteri
67	380.5	16.1	837	2	Q79FV9	Q79FV9 mycobacteri
68	380.5	16.1	2401	2	Q7RF52	Q7RF52 plasmodium
69	379.5	16.1	628	2	Q8VJ19	Q8VJ19 mycobacteri
70	379.5	16.1	1618	2	Q6FQ10	Q6FQ10 candida gla
71	379	16.0	465	1	GRP2_PHAVU	P10496 phaseolus v
72	378.5	16.0	490	2	Q7VBP6	Q7VBP6 mycobacteri
73	378	16.0	588	2	Q6MWX7	Q6MWX7 mycobacteri
74	378	16.0	617	2	Q46172	Q46172 nephila cla
75	376.5	15.9	749	2	Q79FV7	Q79FV7 mycobacteri
76	375	15.9	914	1	WA22_MYCTU	Q06794 mycobacteri
77	374	15.8	831	2	Q7U2D6	Q7U2D6 mycobacteri
78	373.5	15.8	584	2	Q7D580	Q7D580 mycobacteri
79	373.5	15.8	584	2	Q7TW48	Q7TW48 mycobacteri
80	373.5	15.8	667	2	Q7D8W7	Q7D8W7 mycobacteri
81	373.5	15.8	1382	2	Q79FT3	Q79FT3 mycobacteri
82	373.5	15.8	1382	2	Q6BN56	Q6BN56 debaryomyce
83	373	15.8	871	2	O44358	O44358 nephila cla
84	372	15.7	694	2	Q7D724	Q7D724 mycobacteri
85	372	15.7	909	2	Q7U1D3	Q7U1D3 mycobacteri
86	371.5	15.7	671	2	Q7U0R1	Q7U0R1 mycobacteri
87	371	15.7	400	2	Q8GTL0	Q8GTL0 oryza sativ
88	371	15.7	615	2	Q6MX26	Q6MX26 mycobacteri
89	371	15.7	615	2	Q7TXQ0	Q7TXQ0 mycobacteri
90	371	15.7	644	2	Q8WSM4	Q8WSM4 nephila cla
91	371	15.7	747	1	SPD1_NBPCL	P19837 mycobacteri
92	370.5	15.7	491	2	Q79FP3	Q79FP3 mycobacteri
93	369.5	15.6	491	2	Q7U027	Q7U027 mycobacteri
94	369.5	15.6	795	2	Q7U020	Q7U020 mycobacteri
95	369.5	15.6	1428	2	O44341	O44341 halotia ru
96	369	15.6	557	2	Q6BVD0	Q6BVD0 debaryomyce
97	369	15.6	622	2	Q8VKN3	Q8VKN3 mycobacteri
98	367.5	15.6	606	2	Q7U2C0	Q7U2C0 mycobacteri
99	367.5	15.6	608	2	Q7U125	Q7U125 mycobacteri
100	366.5	15.5	877	2	Q7U2D7	Q7U2D7 mycobacteri
101	366	15.5	408	2	Q43688	Q43688 vigna ungui
102	366	15.5	610	2	Q9V5V8	Q9V5V8 drosoephila
103	366	15.5	691	2	Q9BIJ3	Q9BIJ3 dolomedesa t
104	365.5	15.5	496	2	Q79G09	Q79G09 mycobacteri

105	365.5	15.5	496	2	Q7U2U5	Q7u2u5 mycobacteri	178	342	14.5	515	1	PG34 MYCTU	Q50594 mycobacteri
106	365.5	15.5	533	2	Q8VKR5	Q8vkr5 mycobacteri	179	341.5	14.5	1468	2	Q9GUB5	Q9gub5 galleria me
107	365	15.4	576	2	P71664	P71664 mycobacteri	180	341	14.4	674	2	Q681A9	Q681a9 arabidopsi
108	365	15.4	591	2	Q6MX50	Q6mx50 mycobacteri	181	340.5	14.4	452	2	Q7U049	Q7u049 mycobacteri
109	365	15.4	663	2	Q8VJC0	Q8vjc0 mycobacteri	182	339.5	14.4	487	2	Q79G08	Q79g08 mycobacteri
110	364.5	15.4	524	2	Q8VJC0	Q8vjc0 mycobacteri	183	339	14.3	614	2	Q9LH97	Q9lh97 arabidopsi
111	364.5	15.4	801	1	PG10 MYCTU	Q8i7u1 araneus ven	184	339	14.3	937	1	HYR1 CANAL	P46591 candida alb
112	364.5	15.4	907	2	Q44359	O53810 mycobactila	185	338	14.3	429	2	Q817T9	Q8i7t9 araneus ven
113	364	15.4	421	2	Q9DEY1	O44359 nephila cla	186	337	14.3	270	2	Q700C3	Q700c3 arabidopsi
114	364	15.4	606	2	Q9FV33	Q9dey1 cyprinus ca	187	337	14.3	290	2	Q7Y218	Q7y218 arabidopsi
115	364	15.4	609	2	Q8VKC5	Q8vkc5 mycobacteri	188	337	14.3	840	2	Q9SYF6	Q9syf6 patinopecte
116	364	15.4	626	2	Q9NHW1	Q8vkr1 mycobacteri	189	337	14.3	1002	2	Q9BIU8	Q9biu8 argiope tri
117	363.5	15.4	349	1	GRP ARATH	Q9nhw1 nephila ina	190	336.5	14.2	338	2	Q8VJ24	Q8vj24 mycobacteri
118	363	15.4	639	2	Q79E29	P27483 arabidopsi	191	335	14.2	581	2	Q7U1U2	Q7u1u2 mycobacteri
119	363	15.4	650	2	Q8VJW1	Q79fj9 mycobacteri	192	334.5	14.2	531	2	Q6BZJ0	Q6bzj0 debaryomyce
120	363	15.4	1114	2	Q6CCAI	Q8vjw1 mycobacteri	193	334	14.1	255	2	Q9SIH2	Q9sih2 arabidopsi
121	362.5	15.3	561	2	Q8VXR1	Q6ccai yarrowia li	194	334	14.1	284	1	Q73E49	Q73e49 bacillus ce
122	362.5	15.3	2850	1	HORN HUMAN	Q8vkr1 mycobacteri	195	334	14.1	498	1	PG33 MYCTU	Q50615 mycobacteri
123	362	15.3	486	1	LORI MOUSE	Q8vyz3 homo sapien	196	333.5	14.1	501	2	Q6GRZ1	Q6grz1 mycobacteri
124	361.5	15.3	422	2	Q6Z142	P18165 mus musculu	197	333	14.1	466	2	Q7TZG4	Q7tzg4 mycobacteri
125	361	15.3	540	2	Q7TZI3	O6z142 oryza sativ	198	332.5	14.1	342	2	Q9VKR8	Q9vkr8 drosophila
126	360.5	15.3	342	2	Q6HNMZ6	Q7tziz3 mycobacteri	199	332.5	14.1	356	2	Q6NNY8	Q6ny8 drosophila
127	360	15.2	562	2	Q79FQ7	Q6hnmz6 bacillus th	200	332.5	14.1	491	1	PG36 MYCTU	Q10707 mycobacteri
128	360	15.2	562	2	Q7U0B1	Q79fq7 mycobacteri	201	332.5	14.1	501	2	Q7TZH0	Q7tzh0 mycobacteri
129	360	15.2	586	2	Q7D8J2	Q7u0b1 mycobacteri	202	332.5	14.1	563	2	Q6J6N0	Q6j6n0 araneus ven
130	359.5	15.2	340	2	Q63G11	Q7d8j2 mycobacteri	203	331.5	14.0	622	2	Q8VKJ6	Q8vkj6 mycobacteri
131	359.5	15.2	773	2	Q7U160	O63g11 bacillus ce	204	330	14.0	447	2	Q9BIV1	Q9biv1 argiope aur
132	359.5	15.2	1011	2	Q7D877	Q7u160 mycobacteri	205	330	14.0	513	2	Q61067	Q61067 plasmodium
133	359.5	15.2	1011	2	Q79FL8	Q7d877 mycobacteri	206	329.5	13.9	504	2	Q7TXZ9	Q7txz9 mycobacteri
134	359.5	15.2	1018	2	Q7TZU3	Q79fl8 mycobacteri	207	329.5	13.9	2174	2	Q6CD35	Q6cd35 yarrowia li
135	359	15.2	463	1	PG20 MYCTU	Q7tzuz3 mycobacteri	208	329	13.8	549	2	Q19318	Q19318 caenorhabdi
136	359	15.2	854	2	Q9BIU4	O53416 mycobacteri	209	325.5	13.8	439	2	Q6MWV6	Q6mwv6 mycobacteri
137	358.5	15.2	486	2	Q9AR23	Q9biu4 dolomedes t	210	325.5	13.8	452	2	Q9LW52	Q9lw52 arabidopsi
138	358.5	15.2	988	2	Q6Z434	Q9ar23 oryza sativ	211	324.5	13.7	1458	2	Q910B9	Q910b9 oncorhynch
139	358	15.2	359	2	O6Z498	O17434 nephila cla	212	323.5	13.7	436	2	Q8VIX6	Q8vix6 mycobacteri
140	358	15.2	774	2	Q868B4	Q6z498 oryza sativ	213	323.5	13.7	1729	2	Q9U617	Q9u617 drosophila
141	357	15.1	760	2	Q6PY84	Q868b4 caenorhabdi	214	323	13.7	268	2	Q9FIQ2	Q9fiq2 arabidopsi
142	357	15.1	766	2	Q6CV63	Q6py84 kukulcania	215	322.5	13.6	355	2	Q7VEL2	Q7vel2 mycobacteri
143	357	15.1	1884	2	Q9NHW2	O6cv63 kluveromyce	216	322	13.6	1169	2	Q21535	Q21535 caenorhabdi
144	356	15.1	281	2	Q22843	Q9nhw2 nephila ina	217	321.5	13.6	431	2	Q6S2G4	Q6s2g4 nephila cla
145	356	15.1	603	2	Q6BTJ9	Q22843 caenorhabdi	218	320.5	13.6	756	2	Q8J1W4	Q8j1w4 claviiceps p
146	355.5	15.0	922	2	Q6BTJ9	Q7u079 mycobacteri	219	320.5	13.6	1071	2	Q7YU48	Q7yu48 drosophila
147	355	15.0	291	2	Q39337	O6btj9 debaryomyce	220	320.5	13.6	1713	2	Q9VTR6	Q9vtr6 drosophila
148	355	15.0	831	2	Q7U159	Q39337 brassica na	221	320	13.5	594	2	Q6MX30	Q6mx30 mycobacteri
149	355	15.0	868	2	Q7U2D8	Q7u159 mycobacteri	222	320	13.5	620	2	Q9V7U0	Q9v7u0 drosophila
150	354.5	15.0	340	2	Q81IE8	Q7u2d8 mycobacteri	223	320	13.5	1953	2	Q9B1T7	Q9b1t7 nephila ina
151	353	14.9	588	2	Q91PQ8	Q81ie8 bacillus ce	224	318	13.5	1464	2	Q6F9I2	Q6fp9i2 xenopus lae
152	353	14.9	624	2	Q7TZL0	Q91pq8 cynomolgus	225	317	13.4	2655	2	Q964F4	Q964f4 antheraea y
153	352.5	14.9	384	1	GRP1 PETHY	P09789 petunia hyb	226	316	13.4	546	2	Q7TY98	Q7ty98 mycobacteri
154	352	14.9	603	1	PG24 MYCTU	Q10637 mycobacteri	227	316	13.4	1036	2	Q6FX21	Q6fx21 candida gla
155	351.5	14.9	895	2	Q6P9W8	O6fpm8 candida gla	228	315	13.3	302	2	Q9SL09	Q9sl09 arabidopsi
156	351	14.9	316	2	Q6FHY3	Q6fhy3 homo sapien	229	315	13.3	462	2	Q9NHW3	Q9nhw3 nephila cla
157	351	14.9	957	1	PG03 MYCTU	P56879 mycobacteri	230	314.5	13.3	543	1	PG44 MYCTU	Q50330 mycobacteri
158	350.5	14.8	461	2	Q79FC3	Q79fc3 mycobacteri	231	314	13.3	304	2	Q7XJ17	Q7xj17 lycopersico
159	350.5	14.8	476	2	Q7D6W4	Q7d6w4 mycobacteri	232	314	13.3	367	2	Q7PXP6	Q7pxp6 anopheles g
160	350.5	14.8	879	2	Q8VKD2	Q8vkd2 mycobacteri	233	314	13.3	387	2	Q692G3	Q692g3 nephila cla
161	350	14.8	316	1	LORI HUMAN	P23490 homo sapien	234	314	13.3	521	2	Q6V5C3	Q6v5c3 arabidopsi
162	349	14.8	618	2	Q79FK9	Q79fk9 mycobacteri	235	313.5	13.3	3659	2	Q98LN6	Q98ln6 rhizobium l
163	349	14.8	882	2	Q79FV6	Q79fv6 mycobacteri	236	313	13.2	1449	2	Q910C0	Q910c0 oncorhynch
164	347.5	14.7	464	2	Q7TY83	Q7ty83 mycobacteri	237	312.5	13.2	252	1	GRP1 PHAVU	P10495 phaseolus v
165	347.5	14.7	544	2	Q46171	O46171 nephila cla	238	310.5	13.1	775	2	Q6BGP1	Q6bgp1 debaryomyce
166	346	14.6	648	2	Q9BIU7	Q9biu7 argiope tri	239	310	13.1	321	2	Q69XV3	Q69xv3 oryza sativ
167	346	14.6	974	1	GLH2 CAEL	Q96619 caenorhabdi	240	309.5	13.1	265	2	Q69K59	Q69k59 oryza sativ
168	345	14.6	672	1	PHX3_MOUSE	P08399 mus musculu	241	309.5	13.1	509	2	Q7TYG7	Q7tyg7 mycobacteri
169	345	14.6	966	1	FIB1_PETMA	P02674 petromyzon	242	309	13.1	454	2	Q8VUD7	Q8vud7 mycobacteri
170	344.5	14.6	797	2	Q7UID4	P02674 petromyzon	243	308.5	13.1	251	2	Q9UVE7	Q9uve7 yarrowia li
171	344	14.6	525	2	Q79FB3	Q79fb3 mycobacteri	244	308.5	13.1	2639	2	Q76786	Q76786 antheraea p
172	344	14.6	651	2	Q9BIU9	Q9biu9 argiope tri	245	308	13.0	271	2	Q08529	Q08529 nicotiana t
173	344	14.6	783	2	Q7D9C6	Q7d9c6 mycobacteri	246	308	13.0	2496	1	HORN MOUSE	Q8vhd8 mus musculu
174	344	14.6	783	2	Q79FW8	Q79fw8 mycobacteri	247	307	13.0	426	2	Q6WEQ9	Q6weq9 arabidopsi
175	343	14.5	538	2	Q7U2T0	Q7u2t0 mycobacteri	248	306.5	13.0	419	1	CSP_FLACM	P08676 plasmodium
176	342.5	14.5	575	2	Q86P83	Q86p83 drosophila	249	306.5	13.0	904	2	Q76271	Q76271 mytilus edu
177	342.5	14.5	636	2	Q16987	Q16987 araneus dia	250	306	12.9	284	2	Q21073	Q21073 caenorhabdi



251	306	12.9	1034	2	Q6FX23	Q6fx23 candida gla	324	286	12.1	563	2	Q9BIT5	Q9bit5 nephila ina
252	305.5	12.9	267	2	Q6I417	Q6i417 bacillus an	325	286	12.1	2112	2	Q9VEL9	Q9vel9 drosophila
253	305.5	12.9	343	2	Q9FJ53	Q9fj53 arabidopsis	326	285.5	12.1	1370	2	Q6C3B8	Q6c3b8 yarrowia li
254	305.5	12.9	511	2	Q9L132	Q9l132 cercopitheci	327	285	12.1	227	2	Q6Z8R3	Q6z8r3 cryza sativ
255	305.5	12.9	902	2	Q16161	Q16161 mytilus edu	328	285	12.1	250	2	Q92P84	Q92p84 rhizobium m
256	305.5	12.9	905	2	Q8MM55	Q8mw55 mytilus gal	329	284	12.0	233	2	Q9DEX9	Q9dex9 cyprinus ca
257	305.5	12.9	922	2	Q8MM55	Q8mw55 mytilus gal	330	284	12.0	236	2	Q6Z4Y5	Q6z4y5 cryza sativ
258	305	12.9	404	2	Q6C7Y4	Q6c7y4 yarrowia li	331	284	12.0	543	2	Q94FQ0	Q94fq0 arabidopsis
259	303.5	12.8	1884	2	Q7S737	Q7s737 neurospora	332	283.5	12.0	379	2	Q692G2	Q692g2 nephila cla
260	302.5	12.8	678	2	Q93486	Q93486 oncorhynch	333	283	12.0	464	2	Q7XD15	Q7xd15 cryza sativ
261	302	12.8	426	2	Q8Y293	Q8y293 ralestonia s	334	283	12.0	464	2	Q9FWK8	Q9fwk8 cryza sativ
262	302	12.8	582	2	Q9PF60	Q9pf60 xylella fas	335	283	12.0	689	2	Q8BSK0	Q8bsk0 mus musculu
263	301.5	12.8	285	2	Q69TW7	Q69tw7 cryza sativ	336	283	12.0	1051	2	Q26055	Q26055 paracentrot
264	301	12.7	388	2	Q7SXQ3	Q7sxx3 brachydanio	337	283	12.0	1160	2	Q8R564	Q8r564 mus musculu
265	301	12.7	393	1	CSP_PLABR	PL4593 plasmodium	338	283	12.0	1160	2	Q9WUN1	Q9wun1 mus musculu
266	301	12.7	1666	2	Q7PT93	Q7pt93 anopheles g	339	283	12.0	1198	2	Q924G8	Q924g8 mus musculu
267	300.5	12.7	622	1	K1CI_HUMAN	P35527 homo sapien	340	283	12.0	1198	2	Q99PM6	Q99pm6 mus musculu
268	300	12.7	738	2	Q02402	Q02402 pintada fu	341	283	12.0	1260	2	Q7T5J9	Q7t5j9 mus musculu
269	300	12.7	1346	2	Q8UUJ3	Q8uuJ3 oncorhynch	342	283	12.0	1346	2	Q801M5	Q801m5 xenopus lae
270	299.5	12.7	490	2	Q6V5D8	Q6v5d8 olinarabido	343	283	12.0	1736	2	Q80TJ5	Q80tj5 mus musculu
271	299.5	12.7	618	2	Q8CIS9	Q8ci89 rattus norv	344	283	12.0	1987	2	Q99PB3	Q99pb3 mus musculu
272	299.5	12.7	3198	2	Q26639	Q26639 strongyloce	345	283	12.0	2087	2	Q6DIC6	Q6dic6 mus musculu
273	299	12.7	280	2	Q7XDU0	Q7xd00 cryza sativ	346	282.5	12.0	1447	2	Q9IB91	Q9ib91 xenopus lae
274	299	12.7	373	2	Q9BIT9	Q9bit9 latrodectus	347	282	11.9	338	2	Q60354	Q60354 homo sapien
275	298.5	12.6	210	2	Q41187	Q41187 arabidopsis	348	282	11.9	394	2	Q7SHJ4	Q7shj4 neurospora
276	298.5	12.6	262	2	Q8MYJ1	Q8myj1 dictyosteli	349	282	11.9	400	1	RTOA_DICDI	P54681 dictyosteli
277	298.5	12.6	284	2	Q94CI8	Q94ci8 lycopersico	350	282	11.9	543	2	Q9LY09	Q9ly09 arabidopsis
278	298.5	12.6	922	2	Q44367	Q44367 mytilus edu	351	281.5	11.9	185	2	Q7XDV1	Q7xdv1 cryza sativ
279	298.5	12.6	2174	2	Q92UJ8	Q92uu8 rhizobium m	352	281.5	11.9	1147	2	Q733C1	Q733c1 bacillus ce
280	298	12.6	214	2	Q6PY82	Q6py82 kukulcania	353	281	11.9	827	2	Q7PZ88	Q7pz88 anopheles g
281	298	12.6	2359	2	Q81519	Q8i519 plasmodium	354	281	11.9	1150	1	APMU_FIG	P12021 sus scrofa
282	297.5	12.6	270	2	Q7XDT4	Q7xdt4 cryza sativ	355	281	11.9	1439	2	Q97406	Q97406 hallotis di
283	296.5	12.5	429	2	Q87ZY8	Q87zy8 neurospora	356	280.5	11.9	476	2	Q80890	Q80890 herpesvirus
284	296.5	12.5	480	2	Q8T215	Q8t215 dictyosteli	357	280.5	11.9	1449	2	Q6NZ15	Q6nz15 brachydanio
285	296.5	12.5	1047	2	Q7UN71	Q7un71 rhodopirell	358	280	11.8	444	2	Q9BIU6	Q9biu6 arglope tri
286	296	12.5	486	2	Q9SPA6	Q9spa6 hordeum vul	359	280	11.8	1380	1	DXH3_MOUSE	Q70133 mus musculu
287	296	12.5	627	1	SPD2_NEPCL	P46804 nephila cla	360	280	11.8	1466	1	CA13_HUMAN	P02461 homo sapien
288	296	12.5	1124	2	Q6C7C1	Q6c7c1 yarrowia li	361	279.5	11.8	1449	2	Q640B2	Q640b2 xenopus tro
289	296	12.5	1450	2	Q9Y1B4	Q9y1b4 cynops pyr	362	278.5	11.8	526	1	FUS_HUMAN	P35637 homo sapien
290	295.5	12.5	894	2	Q8MW54	Q8mw54 mytilus gal	363	278.5	11.8	526	2	Q8TBR3	Q8tbr3 homo sapien
291	295	12.5	1352	2	Q8UJ14	Q8uj14 oncorhynch	364	278.5	11.8	929	2	Q9NBL3	Q9nbl3 drosophila
292	294.5	12.5	614	2	Q87AH4	Q87ah4 xylella fas	365	278.5	11.8	929	2	Q9NEM0	Q9nbw0 drosophila
293	294	12.4	273	2	Q7Y215	Q7y215 arabidopsis	366	278.5	11.8	939	2	Q9KX9	Q9kxh9 drosophila
294	294	12.4	1356	1	CA21_ONCMY	Q93484 oncorhynch	367	278.5	11.8	939	2	Q9NHQ0	Q9nhq0 drosophila
295	293.5	12.4	222	2	Q9VGH5	Q7xdv2 cryza sativ	368	278.5	11.8	978	2	Q6BLF5	Q6blf5 debaryomyce
296	293.5	12.4	586	2	Q9VGH5	Q9vgh5 drosophila	369	278.5	11.8	2280	2	Q9V8E6	Q9v8e6 drosophila
297	293.5	12.4	794	2	P93560	P93560 sagittaria	370	278.5	11.8	2302	2	Q9NG93	Q9ng93 drosophila
298	293	12.4	256	2	Q79FH2	Q79fh2 mycobacteri	371	278	11.8	220	2	Q93367	Q93367 brassica ol
299	293	12.4	257	2	Q81Z75	Q81z75 bacillus an	372	278	11.8	270	2	Q61764	Q61764 mus musculu
300	292.5	12.4	707	2	Q61869	Q61869 mus musculu	373	278	11.8	1447	2	Q6P4U1	Q6p4u1 brachydanio
301	292	12.4	912	2	Q9BIT2	Q9bit2 plectreureys	374	277.5	11.7	230	2	Q7XDU2	Q7xd2 cryza sativ
302	291.5	12.3	367	2	Q86KL5	Q86kl5 dictyosteli	375	277.5	11.7	621	2	Q8VJK6	Q8vjx6 mycobacteri
303	291.5	12.3	502	2	Q9ZTR5	Q9ztr5 hordeum vul	376	277.5	11.7	1198	2	Q7PKP4	Q7pkp4 anopheles g
304	291	12.3	821	2	Q8VPM9	Q8vpm9 micrococci	377	277.5	11.7	1378	2	Q97405	Q97405 hallotis di
305	290.5	12.3	406	2	Q82524	Q82524 streptomyce	378	277.5	11.7	1449	2	Q6PEI9	Q6pei9 brachydanio
306	290.5	12.3	1387	1	TROP_HUMAN	Q12816 homo sapien	379	277.5	11.7	1449	2	Q802B5	Q802b5 xenopus lae
307	290	12.3	543	2	Q43302	Q43302 arabidopsis	380	277	11.7	256	2	Q24568	Q24568 zea mays (m
308	290	12.3	751	2	Q7M3U9	Q7m3u9 riftia pach	381	277	11.7	335	2	Q6IH99	Q6ih99 drosophila
309	289.5	12.3	543	2	Q94FQ4	Q94fq4 arabidopsis	382	277	11.7	1355	1	CA21_RANCA	Q42350 rana catesb
310	289	12.2	1414	2	Q26634	Q26634 strongyloce	383	277	11.7	1447	2	Q6UIJ5	Q6uij5 brachydanio
311	288.5	12.2	499	2	Q6C268	Q6c268 yarrowia li	384	276.5	11.7	682	2	Q22537	Q22537 caenorhabdi
312	288.5	12.2	528	2	Q13344	Q13344 homo sapien	385	276.5	11.7	748	2	Q636W5	Q636w5 bacillus ce
313	288.5	12.2	543	2	Q94FR0	Q94fr0 arabidopsis	386	276.5	11.7	1372	1	CA21_RAT	P02466 rattus norv
314	288	12.2	535	2	Q94202	Q94202 cryza sativ	387	276.5	11.7	2332	2	Q6ALH4	Q6alh4 desulfotale
315	288	12.2	1051	2	Q6MJ51	Q6mj51 bdellovibri	388	276	11.7	1366	2	Q15177	Q15177 homo sapien
316	288	12.2	1962	2	Q873R2	Q873r2 emeritella	389	276	11.7	1366	2	Q7Z5S6	Q7z5s6 homo sapien
317	287.5	12.2	185	2	Q6PY83	Q6py83 kukulcania	390	275	11.6	193	2	Q7YWK8	Q7ywk8 caenorhabdi
318	287.5	12.2	2363	2	Q6ALH2	Q6alh2 desulfotale	391	275	11.6	950	2	Q9VK59	Q9vk59 drosophila
319	287	12.1	2795	2	Q18758	Q18758 paracentrot	392	275	11.6	1156	1	GLH4_CAEEL	Q76743 caenorhabdi
320	287	12.1	13288	2	Q18758	Q18758 sus scrofa	393	274.5	11.6	929	2	Q9NGW5	Q9ngw5 drosophila
321	286.5	12.1	857	2	Q6RH33	Q6rh33 dinocampus	394	274.5	11.6	1376	2	Q7S5H8	Q7s5h8 neurospora
322	286	12.1	399	2	Q7ZX33	Q7zx33 xenopus lae	395	274	11.6	460	2	Q6C0R1	Q6c0r1 yarrowia li
323	286	12.1	543	2	Q94FP9	Q94fp9 arabidopsis	396	274	11.6	593	1	K1CJ_HUMAN	P13645 homo sapien

397	274	11.6	730	2	Q9ZU23	Q9zu23 arabidopsis	470	263.5	11.2	2147	2	Q98MG8	Q98mg8 rhizobium l
398	274	11.6	889	2	Q7Q5L2	Q7q5l2 anopheles g	471	263	11.1	435	2	Q721S2	Q721s2 caenorhabdi
399	274	11.6	3016	2	P73590	P73590 synchocyst	472	263	11.1	907	2	Q26312	Q26312 strongyloce
400	273	11.6	970	2	Q7Q6V4	Q7q6v4 anopheles g	473	263	11.1	1097	2	Q6C029	Q6c029 yarrowia li
401	273	11.6	1168	2	Q6HF99	Q6hf99 bacillus th	474	263	11.1	1752	2	Q07265	Q07265 strongyloce
402	273	11.6	1491	2	Q91718	Q91718 xenopus lae	475	262.5	11.1	410	2	Q72UE3	Q72ue3 brachydanio
403	273	11.6	1491	2	Q7ZTM4	Q7ztm4 xenopus lae	476	262.5	11.1	645	2	Q79FW4	Q79fw4 mycobacteri
404	272.5	11.5	604	2	Q9L252	Q9l252 streptomyc	477	262.5	11.1	645	2	Q79U1C5	Q79u1c5 mycobacteri
405	272.5	11.5	1372	1	CA21_MOUSE	Q01149 mus musculu	478	262.5	11.1	646	2	Q7D9B9	Q7d9b9 mycobacteri
406	272.5	11.5	1445	2	Q93Z51	Q93z51 rana catesb	479	262.5	11.1	685	2	Q6IG02	Q6ig02 rattus norv
407	272.5	11.5	2104	2	Q81KG1	Q81kg1 plasmodium	480	262.5	11.1	1049	1	CA13_BOVIN	P04258 bos taurus
408	272.5	11.5	2310	2	Q9GRA9	Q9gra9 drosophila	481	262.5	11.1	2038	1	FSH_DROME	P13709 drosophila
409	272	11.5	375	1	SANT_PLAFV	P09593 plasmodium	482	262	11.1	245	2	Q6BYG2	Q6byg2 debaryomyce
410	271.5	11.5	370	2	Q79PE0	Q79fp0 mycobacteri	483	262	11.1	1549	2	Q60444	Q60444 cricetus
411	271.5	11.5	370	2	Q7U007	Q7u007 mycobacteri	484	261.5	11.1	815	2	Q632M4	Q632m4 bacillus ce
412	271.5	11.5	375	2	Q7D8B3	Q7d8b3 mycobacteri	485	261.5	11.1	1110	2	Q81RN6	Q81rn6 drosophila
413	271	11.5	681	2	Q8YTC9	Q8ytc9 anabaena sp	486	261.5	11.1	2038	2	Q9W3L3	Q9w3l3 drosophila
414	271	11.5	1364	1	CA21_BOVIN	P02465 bos taurus	487	261	11.0	1226	2	Q7UL12	Q7ul12 rhodopirell
415	270.5	11.4	360	2	Q7TVP1	Q7tvp1 mycobacteri	488	260.5	11.0	1321	2	Q72202	Q72202 bacillus ce
416	270.5	11.4	1027	1	CAFF_RIPPA	P30754 riftingia pach	489	260	11.0	359	2	Q81G99	Q81g99 drosophila
417	270.5	11.4	1226	2	Q7Q3B9	Q7q3b9 anopheles g	490	260	11.0	722	2	Q76B22	Q76b22 bombyx mori
418	270.5	11.4	1366	1	CA21_HUMAN	P08123 homo sapien	491	260	11.0	730	2	Q26052	Q26052 paracentrot
419	270	11.4	779	2	Q76B23	Q76b23 bombyx mori	492	260	11.0	1366	1	CA21_CANFA	Q46392 canis fami
420	270	11.4	854	2	Q09238	C09238 pseudocorti	493	260	11.0	1486	2	Q91717	Q91717 xenopus lae
421	270	11.4	1035	2	Q76C74	Q76c74 saccharomyc	494	260	11.0	1486	2	Q7ZTI6	Q7zt16 xenopus lae
422	270	11.4	1366	2	Q6N964	Q6n964 rhodopseudo	495	259.5	11.0	261	2	Q92WM2	Q92wm2 cucumis sat
423	270	11.4	1713	2	Q8TGE1	Q8tge1 saccharomyc	496	259.5	11.0	399	2	Q9BIT8	Q9bit8 latrodectus
424	270	11.4	1844	2	Q7SGQ1	Q7sgq1 neurospora	497	259.5	11.0	1186	2	Q76B21	Q76b21 bombyx mori
425	269.5	11.4	360	2	Q9BIU0	Q9biu0 latrodectus	498	259.5	11.0	1222	2	Q8K173	Q8k173 mus musculu
426	269.5	11.4	443	2	Q9GUB4	Q9gub4 gallieria me	499	259.5	11.0	1464	1	CA13_MOUSE	P08121 mus musculu
427	269	11.4	361	2	Q79PE6	Q79fe6 mycobacteri	500	259.5	11.0	1464	2	Q7TT32	Q7tt32 mus musculu
428	269	11.4	382	2	Q7D777	Q7d777 mycobacteri	501	259.5	11.0	1464	2	Q8BKY2	Q8bky2 mus musculu
429	269	11.4	410	2	Q16988	Q16988 araneus dia	502	259.5	11.0	1464	2	Q8BLM4	Q8blm4 mus musculu
430	269	11.4	422	2	Q803K3	Q803k3 brachydanio	503	259	11.0	263	2	Q6ZL79	Q6zl79 oryza sativ
431	269	11.4	1025	2	Q7WIW0	Q7wiw0 bordetella	504	259	11.0	441	2	Q26062	Q26062 plasmodium
432	268.5	11.4	259	2	Q02049	C02049 caenorhabdi	505	259	11.0	517	2	Q8CFQ9	Q8cfq9 mus musculu
433	268.5	11.4	323	2	Q6BC34	Q6bc34 patinopecte	506	259	11.0	684	2	P90679	P90679 arenicola m
434	268.5	11.4	557	2	Q8B046	Q8b046 mus musculu	507	259	11.0	886	2	Q9VKR7	Q9vkr7 drosophila
435	268.5	11.4	584	2	Q6CASA	Q6cas0 yarrowia li	508	259	11.0	3145	2	Q98MG7	Q98mg7 rhizobium l
436	268	11.3	183	1	GRP2_ORYSA	P29834 oryza sativ	509	258.5	10.9	1309	2	Q812N4	Q812n4 bacillus ce
437	268	11.3	241	2	Q61IW5	Q61iw5 drosophila	510	258	10.9	138	2	Q964C4	Q964c4 cephalito
438	268	11.3	647	2	Q6HS19	Q6hel19 bacillus an	511	258	10.9	208	2	Q9ZRV2	Q9zrv2 cicor ariet
439	268	11.3	870	2	Q6FPN0	Q6fpn0 candida gla	512	258	10.9	394	1	THYD_CLAFA	Q9uv14 clavicaps f
440	268	11.3	1055	2	Q6HCF4	Q6hcf4 bacillus th	513	258	10.9	604	2	Q6BQ06	Q6bq06 debaryomyce
441	267.5	11.3	429	2	Q76966	Q76966 podocoryne	514	257.5	10.9	386	1	RB87_DROME	P48810 drosophila
442	267.5	11.3	1207	2	Q9PVP5	Q9pvp5 brachydanio	515	257.5	10.9	503	2	Q734G5	Q734g5 bacillus ce
443	266.5	11.3	561	2	Q7TPC1	Q7tpc1 mus musculu	516	257.5	10.9	518	1	FUS_MOUSE	P56959 mus musculu
444	266.5	11.3	987	2	Q89CB5	Q89cb5 bradyrhizob	517	257.5	10.9	584	2	Q8N175	Q8n175 homo sapien
445	266	11.3	243	2	Q98DS7	Q98ds7 rhizobium l	518	257.5	10.9	735	2	Q7Z009	Q7z009 anagasta ku
446	266	11.3	342	2	Q8SX59	Q8sx59 drosophila	519	257	10.9	385	2	Q9VFT2	Q9vft2 drosophila
447	266	11.3	586	2	Q8EXJ2	Q8exj2 leptospira	520	257	10.9	433	2	Q61152	Q61152 plasmodium
448	266	11.3	683	2	Q9PDW2	Q9pdw2 xylella fas	521	257	10.9	632	2	Q7TX52	Q7tx52 mycobacteri
449	266	11.3	1088	2	Q69UP6	Q69up6 oryza sativ	522	257	10.9	686	2	Q8VJ65	Q8vj65 mycobacteri
450	265.5	11.2	175	2	Q9LSN6	Q9len6 arabidopsis	523	257	10.9	998	2	Q8CFM4	Q8cfm4 mus musculu
451	265.5	11.2	265	2	Q69PC6	Q69pc6 oryza sativ	524	257	10.9	1160	2	Q14046	Q14046 homo sapien
452	265.5	11.2	461	2	Q6V5F7	Q6v5f7 capsella ru	525	257	10.9	1352	2	Q90VJ0	Q90vj0 brachydanio
453	265.5	11.2	568	2	Q9NL38	Q9nl38 pinetada ma	526	256.5	10.9	508	2	Q7KHL0	Q7khl0 drosophila
454	265.5	11.2	614	2	Q7TYR8	Q7tyr8 mycobacteri	527	256.5	10.9	809	2	Q93485	Q93485 oncorhynch
455	265.5	11.2	615	2	Q7D7A1	Q7d7a1 mycobacteri	528	256.5	10.9	1352	2	Q61QX2	Q61qx2 brachydanio
456	265	11.2	331	2	Q692G6	Q692g6 nephila cla	529	256	10.8	421	2	Q93119	Q93119 antheraea p
457	265	11.2	717	2	Q75FL0	Q75fl0 leptospira	530	256	10.8	429	2	Q61150	Q61150 plasmodium
458	265	11.2	1119	2	Q75DC8	Q75dc8 ashbya goss	531	256	10.8	436	2	Q967T8	Q967t8 antheraea p
459	264.5	11.2	297	2	Q7XDU7	Q7xd7 mycobacteri	532	256	10.8	743	2	Q6R6B2	Q6r6b2 vibriophag
460	264.5	11.2	536	1	FAEB_PIREQ	Q9y871 piromyces e	533	256	10.8	1487	2	Q77753	Q77753 canis fami
461	264.5	11.2	1820	2	Q91907	Q91907 pagrus majo	534	255.5	10.8	501	2	Q86X94	Q86x94 homo sapien
462	264	11.2	227	2	Q84W21	Q84w21 arabidopsis	535	255.5	10.8	592	1	RB56_HUMAN	Q92804 homo sapien
463	264	11.2	741	2	Q6RCF4	Q6rcf4 vibriophag	536	255.5	10.8	1269	2	Q6V5D4	Q6v5d4 olinarabido
464	264	11.2	818	2	Q812Y5	Q812y5 bacillus ce	537	255	10.8	357	2	Q6V5F6	Q6v5f6 capsella ru
465	264	11.2	1163	2	Q8N6U4	Q8n6u4 homo sapien	538	255	10.8	632	2	Q9N2N7	Q9n2n7 hemiceotrop
466	263.5	11.2	581	2	Q7W7Z1	Q7w7z1 bordetella	539	255	10.8	1052	2	Q7YZ84	Q7yz84 plasmodium
467	263.5	11.2	763	1	GLH1_CAEEL	P34689 caenorhabdi	540	254.5	10.8	413	2	Q81ME3	Q81me3 drosophila
468	263.5	11.2	1412	2	Q8MUF5	Q8muf5 hydra atten	541	254.5	10.8	496	2	Q7KRL6	Q7krl6 drosophila
469	263.5	11.2	1418	2	Q9W7R9	Q9w7r9 cynops pyrr	542	254.5	10.8	502	2	Q7KRL7	Q7krl7 drosophila

543	254.5	10.8	700	2	Q8C1T9	Q8C1T9 mus musculus	616	247.5	10.5	1419	2	Q80X38	Q80X38 mus musculus
544	254	10.7	1419	2	Q63123	Q63123 rattus norv	617	247.5	10.5	1487	2	Q641K3	Q641K3 mus musculus
545	254	10.7	1487	2	Q14047	Q14047 homo sapien	618	247.5	10.5	1739	2	Q9JLI2	Q9JLI2 mus musculus
546	254	10.7	1745	1	CA35 HUMAN	P25940 homo sapien	619	247.5	10.5	3275	2	Q8VVM3	Q8VVM3 mycobacteri
547	254	10.7	1747	2	Q26640	Q26640 strongyloce	620	247.5	10.5	3300	2	Q6MX44	Q6MX44 mycobacteri
548	253.5	10.7	336	2	Q03136	Q03136 plasmodium	621	247.5	10.5	3507	2	Q7U270	Q7U270 mycobacteri
549	253.5	10.7	401	1	CSP_PLACG	P08674 plasmodium	622	247	10.5	425	2	Q61146	Q61146 plasmodium
550	253.5	10.7	509	2	Q875B1	Q875B1 podospora a	623	246.5	10.4	1225	2	Q6PCL3	Q6PCL3 mus musculus
551	253.5	10.7	539	2	Q8MQG9	Q8MQG9 caenorhabdi	624	246.5	10.4	1453	1	CA11 MOUSE	P11087 mus musculus
552	253.5	10.7	660	2	Q86D04	Q86D04 caenorhabdi	625	246.5	10.4	1453	1	CA11 MOUSE	Q81079 mus musculus
553	253.5	10.7	1492	2	Q6P422	Q6P422 xenopus tro	626	246.5	10.4	1460	1	CA11 CANFA	Q9XJ17 canis famil
554	253	10.7	818	2	Q9N1P0	Q9N1P0 bos taurus	627	246.5	10.4	1958	2	Q69340	Q69340 suid herpes
555	253	10.7	1217	2	Q17240	Q17240 bombyx mori	628	246	10.4	182	2	Q9CR91	Q9CR91 m mus muscu
556	252.5	10.7	1418	1	CA12 HUMAN	P02458 homo sapien	629	246	10.4	250	2	Q9VVB7	Q9VVB7 drosophila
557	252.5	10.7	386	2	Q24486	Q24486 drosophila	630	246	10.4	886	2	Q8CEP7	Q8CEP7 mus musculus
558	252.5	10.7	496	2	Q7KA80	Q7KA80 drosophila	631	246	10.4	1262	1	CA13 CHICK	P12105 gallus gall
559	252	10.7	582	2	Q7D5C5	Q7D5C5 mycobacteri	632	245.5	10.4	185	2	Q7XDT5	Q7XDT5 oryza sativ
560	252	10.7	582	2	Q7TW98	Q7TW98 mycobacteri	633	245.5	10.4	354	2	Q79FP3	Q79FP3 mycobacteri
561	252	10.7	1497	2	Q61431	Q61431 mus musculus	634	245.5	10.4	636	1	CA13 RAT	P13941 rattus norv
562	252	10.7	1583	2	Q6C398	Q6C398 yarrowia li	635	245	10.4	373	2	Q23062	Q23062 caenorhabdi
563	251.5	10.6	343	2	Q01914	Q01914 phytophthor	636	245	10.4	894	1	ILF3 HUMAN	Q12906 h interleuk
564	251.5	10.6	490	2	Q9SUW9	Q9SUW9 arabidopsis	637	245	10.4	1349	2	Q8AWI7	Q8AWI7 brachydanio
565	251.5	10.6	810	2	Q9ESZ9	Q9ESZ9 mus musculus	638	245	10.4	1684	2	Q80815	Q80815 arabidopsis
566	251.5	10.6	860	1	ELS_MOUSE	P54320 mus musculus	639	245	10.4	1759	1	CA14 CAEBL	P17139 caenorhabdi
567	251.5	10.6	860	2	Q8C9L8	Q8C9L8 mus musculus	640	245	10.4	1804	1	CA1B MOUSE	P12145 mus musculus
568	251.5	10.6	1723	2	Q9GQB1	Q9GQB1 hydra atten	641	244.5	10.3	1453	1	CA11 CHICK	P02457 gallus gall
569	251	10.6	125	2	Q964C1	Q964C1 encphalito	642	244.5	10.3	1461	2	Q76045	Q76045 homo sapien
570	251	10.6	232	2	Q7S4R3	Q7S4R3 neurospora	643	244.5	10.3	1464	1	CA11 HUMAN	P02452 homo sapien
571	251	10.6	315	2	Q8IGP8	Q8IGP8 drosophila	644	244.5	10.3	1464	2	Q8N473	Q8N473 homo sapien
572	251	10.6	425	2	Q61151	Q61151 plasmodium	645	244.5	10.3	1737	2	Q9J104	Q9J104 rattus norv
573	251	10.6	429	1	CSP_PLAWA	P13815 plasmodium	646	243.5	10.3	413	2	Q89UQ1	Q89UQ1 bradyrhizob
574	251	10.6	429	2	Q61144	Q61144 plasmodium	647	243.5	10.3	418	2	Q7PGN6	Q7PGN6 anopheles g
575	251	10.6	429	2	Q61148	Q61148 plasmodium	648	243.5	10.3	615	2	Q8MS22	Q8MS22 drosophila
576	251	10.6	429	2	Q62597	Q62597 plasmodium	649	243.5	10.3	1046	1	IF2 STRAW	Q82K53 streptomyce
577	251	10.6	671	1	CA11 RAT	P02454 rattus norv	650	243	10.3	237	2	Q7TW10	Q7TW10 mycobacteri
578	251	10.6	1420	2	Q6FW44	Q6FW44 candida gla	651	243	10.3	424	2	Q42626	Q42626 brassica na
579	251	10.6	1453	2	Q63079	Q63079 rattus norv	652	243	10.3	555	2	Q8SX80	Q8SX80 drosophila
580	250.5	10.6	360	2	Q16985	Q16985 araneus dia	653	243	10.3	712	2	Q6HL98	Q6HL98 bacillus th
581	250.5	10.6	540	2	Q7NL21	Q7NL21 gloebacter	654	243	10.3	1069	2	Q6LAN8	Q6LAN8 homo sapien
582	250.5	10.6	585	2	Q8NN98	Q8NN98 corynebacte	655	243	10.3	1092	2	Q964R2	Q964R2 theileria t
583	250	10.6	315	2	Q7K3L5	Q7K3L5 drosophila	656	243	10.3	1160	2	Q7YXC8	Q7YXC8 caenorhabdi
584	250	10.6	366	2	Q854M0	Q854M0 mycobacteri	657	243	10.3	1357	2	Q9W4M4	Q9W4M4 drosophila
585	250	10.6	603	2	Q8VJ66	Q8VJ66 mycobacteri	658	242.5	10.3	205	2	Q22432	Q22432 pinus taeda
586	250	10.6	813	2	Q636W4	Q636W4 bacillus ce	659	242.5	10.3	207	2	Q03797	Q03797 schistosoma
587	250	10.6	1497	2	Q7TMS0	Q7TMS0 mus musculus	660	242.5	10.3	243	2	Q67WQ9	Q67WQ9 oryza sativ
588	250	10.6	1570	2	Q6INP8	Q6INP8 xenopus lae	661	242.5	10.3	423	2	Q9FM47	Q9FM47 arabidopsis
589	249.5	10.6	395	2	Q7M3X0	Q7M3X0 plasmodium	662	242.5	10.3	803	2	Q7XJ36	Q7XJ36 chlamydomon
590	249.5	10.6	589	2	Q7TX53	Q7TX53 mycobacteri	663	242.5	10.3	940	2	Q96QC0	Q96QC0 homo sapien
591	249.5	10.6	940	2	Q00405	Q00405 homo sapien	664	242.5	10.3	1496	1	CA25 HUMAN	P05997 homo sapien
592	249.5	10.6	1033	1	IF2_STRCO	Q8CJQ8 streptomyce	665	242.5	10.3	1562	2	Q6GQS7	Q6GQS7 mus musculus
593	249	10.5	516	2	Q9XEJ0	Q9XEJ0 zea mays (m	666	242.5	10.3	1775	1	CA14 DROME	P08120 drosophila
594	249	10.5	590	2	Q6MX04	Q6MX04 mycobacteri	667	242.5	10.3	1779	2	Q9VMV4	Q9VMV4 drosophila
595	249	10.5	773	2	Q95TR3	Q95TR3 drosophila	668	242	10.2	193	2	Q7XDR9	Q7XDR9 oryza sativ
596	249	10.5	1215	2	Q9W2K4	Q9W2K4 drosophila	669	242	10.2	347	2	Q9GZC7	Q9GZC7 trypanosoma
597	249	10.5	2465	2	Q8CB66	Q8CB66 yarrowia li	670	242	10.2	385	2	Q93424	Q93424 caenorhabdi
598	248.5	10.5	507	2	Q8ISB3	Q8ISB3 antheraea m	671	242	10.2	421	2	Q61145	Q61145 plasmodium
599	248.5	10.5	710	2	Q8VWD1	Q8VWD1 streptomyce	672	242	10.2	779	1	CA11 BOVIN	P02453 bos taurus
600	248.5	10.5	1011	2	Q7VXS7	Q7VXS7 bordetella	673	242	10.2	1804	2	Q80WR4	Q80WR4 mus musculus
601	248.5	10.5	1016	2	Q9XTX5	Q9XTX5 caenorhabdi	674	241.5	10.2	185	2	Q7XDT7	Q7XDT7 oryza sativ
602	248.5	10.5	1442	2	Q62031	Q62031 mus musculus	675	241.5	10.2	608	2	Q9SUX1	Q9SUX1 arabidopsis
603	248.5	10.5	1442	2	Q62033	Q62033 mus musculus	676	241.5	10.2	685	2	Q6CE66	Q6CE66 yarrowia li
604	248.5	10.5	1459	1	CA12 MOUSE	P28481 mus musculus	677	241.5	10.2	1258	2	Q8AW11	Q8AW11 brachydanio
605	248.5	10.5	1459	2	Q62032	Q62032 mus musculus	678	241.5	10.2	1347	2	Q96QB3	Q96QB3 homo sapien
606	248	10.5	117	2	Q964C2	Q964C2 encphalito	679	241	10.2	342	2	Q9BITU1	Q9BITU1 gasteracant
607	248	10.5	343	2	Q81761	Q81761 arabidopsis	680	241	10.2	380	2	Q07138	Q07138 microciona
608	248	10.5	385	1	RO32 XENLA	P51992 xenopus iae	681	241	10.2	678	2	Q7TXZ3	Q7TXZ3 mycobacteri
609	248	10.5	425	2	Q61147	Q61147 plasmodium	682	241	10.2	730	2	Q7Q3C5	Q7Q3C5 anopheles g
610	247.5	10.5	279	2	Q57148	Q57148 human herpe	683	241	10.2	1928	2	Q8T9H1	Q8T9H1 drosophila
611	247.5	10.5	347	2	Q01916	Q01916 phytophthor	684	240	10.2	170	2	Q43539	Q43539 lilium long
612	247.5	10.5	399	1	CAZ_DROME	Q27294 drosophila	685	240	10.2	421	2	Q61149	Q61149 plasmodium
613	247.5	10.5	481	2	Q97641	Q97641 equus cabal	686	240	10.2	512	1	FUS_BOVIN	Q28009 bos taurus
614	247.5	10.5	1418	2	Q28396	Q28396 equus cabal	687	240	10.2	678	1	PP21_MCTU	Q10778 mycobacteri
615	247.5	10.5	1419	2	Q80VY3	Q80VY3 mus musculus	688	240	10.2	1015	2	Q7XZU9	Q7XZU9 hordeum vul

689	240	10.2	1348	2	Q7PXX1	O7pxk1 anopheles g	762	234	9.9	237	2	Q6DXX9	Q6dxx9 plasmodium
690	239.5	10.1	469	2	Q81KL9	Q81kl9 bacillus an	763	234	9.9	301	2	Q01927	Q01927 phytophthor
691	239.5	10.1	538	2	Q8NOR6	Q8nor6 turbo marmo	764	234	9.9	309	2	Q8V6M8	Q8v6m8 halovirus h
692	239.5	10.1	663	2	Q812T6	Q812t6 streptomyc	765	234	9.9	339	2	Q941H8	Q941h8 solanum tub
693	239.5	10.1	706	2	Q41972	Q41972 murid herpe	766	234	9.9	1626	2	Q8NFW1	Q8nfw1 homo sapien
694	239.5	10.1	727	2	Q41973	Q41973 murid herpe	767	234	9.9	1655	2	Q24754	Q24754 drosophila
695	239.5	10.1	774	2	Q41971	Q41971 murid herpe	768	233.5	9.9	165	1	GRP1_ORYSA	P25074 oryza sativ
696	239.5	10.1	812	2	Q06452	Q06452 ephydatia m	769	233.5	9.9	171	2	Q04339	P25074 oryza sativ
697	239.5	10.1	1669	1	CA14_MOUSE	P02463 mus musculu	770	233.5	9.9	180	2	P91207	P91207 caenorhabdi
698	239	10.1	584	2	Q62BE4	Q62ee4 burkholderi	771	233.5	9.9	811	2	Q9AD50	Q9ad50 streptomyc
699	239	10.1	826	2	Q8KON6	Q8kon6 mus musculu	772	233.5	9.9	966	2	Q01385	Q01385 neurospora
700	239	10.1	1041	2	Q66851	Q66851 oikopleura	773	233.5	9.9	1617	2	Q6MGB2	Q6mgb2 rattus norv
701	239	10.1	2165	2	Q8NPD5	Q8nfd5 homo sapien	774	233.5	9.9	2936	2	Q7YRK8	Q7yrk8 canis fami
702	238.5	10.1	121	2	Q964C5	Q964c5 encephalito	775	233	9.9	237	2	Q6DXZ7	Q6dxz7 plasmodium
703	238.5	10.1	212	1	EGG1_SCHJA	P19470 schistosoma	776	233	9.9	296	2	Q8RUS0	Q8rus0 aradidopsis
704	238.5	10.1	267	2	Q9B088	Q9b088 mycobacteri	777	233	9.9	373	1	RO31_XENLA	P51968 xenopus lae
705	238.5	10.1	387	2	Q7M3W8	Q7m3w8 plasmodium	778	233	9.9	536	2	Q6DKB4	Q6dkb4 xenopus lae
706	238.5	10.1	387	2	Q7M3W9	Q7m3w9 plasmodium	779	233	9.9	658	2	Q6FRG1	Q6frg1 candida gla
707	238.5	10.1	450	1	SWP1_ENCCU	Q9xv17 encephalito	780	233	9.9	783	2	Q9XAI1	Q9xai1 streptomyc
708	238.5	10.1	615	2	Q9VVL7	Q9xv17 drosophila	781	233	9.9	864	1	ELS_RAT	Q99372 rattus norv
709	238.5	10.1	689	2	Q75EH4	Q75eh4 ashbya gos	782	232.5	9.8	253	2	Q7XDR2	Q7xdr2 oryza sativ
710	238.5	10.1	1420	2	Q90W37	Q90w37 gallus gall	783	232.5	9.8	290	2	Q21294	Q21294 caenorhabdi
711	238	10.1	963	2	Q90UW12	Q90u12 neurospora	784	232.5	9.8	342	1	CU36_MANSE	Q8muc5 manduca sex
712	238	10.1	1011	2	Q6CF27	Q6cf27 yarrowia li	785	232.5	9.8	388	2	Q86NR7	Q86nr7 drosophila
713	238	10.1	1736	1	CA2B_HUMAN	P13942 homo sapien	786	232.5	9.8	652	2	Q86NR7	Q86nr7 drosophila
714	238	10.1	1806	1	CA1B_HUMAN	P12107 homo sapien	787	232.5	9.8	2109	2	P79787	P79787 gallus gall
715	238	10.1	1991	2	Q7RFD0	Q7rfd0 plasmodium	788	232	9.8	329	2	Q9DEY0	Q9dey0 cypripus ca
716	238	10.1	2037	2	Q9PVZ2	Q9pvz2 xenopus lae	789	232	9.8	460	1	CY87_DICDI	Q94504 dictyosteli
717	237.5	10.1	185	2	Q7XDT6	Q7xdt6 oryza sativ	790	232	9.8	463	2	Q97640	Q97640 felis silve
718	237.5	10.1	247	2	Q6DY38	Q6dy38 plasmodium	791	232	9.8	797	2	Q9GV13	Q9gv13 hydra magni
719	237.5	10.1	349	2	Q9BIV0	Q9biv0 argiope aur	792	232	9.8	913	2	Q6C979	Q6c979 yarrowia li
720	237.5	10.1	495	2	Q918P0	Q918p0 ovine herpe	793	231.5	9.8	239	2	Q9BMN2	Q9bm2 plasmodium
721	237.5	10.1	940	2	Q7YR38	Q7yr38 pan troglod	794	231.5	9.8	244	2	Q9LY08	Q9ly08 aradidopsis
722	237.5	10.1	1362	1	CA21_CHICK	P02467 gallus gall	795	231.5	9.8	487	2	Q9ZB39	Q9zb39 ureaplasma
723	237.5	10.1	1831	2	Q7Q1Y4	Q7q1y4 anopheles g	796	231.5	9.8	544	2	Q6BU19	Q6bu19 streptomyc
724	237.5	10.1	2944	2	Q63870	Q63870 mus musculu	797	231.5	9.8	925	2	Q767K9	Q767k9 sus scrofa
725	237	10.0	309	2	Q9FNR1	Q9fnr1 aradidopsis	798	231.5	9.8	1475	2	Q9XEP3	Q9xep3 sorghum bic
726	237	10.0	365	2	Q61P29	Q61p29 xenopus lae	799	231	9.8	185	2	Q948R3	Q948r3 oryza sativ
727	237	10.0	490	2	Q9V948	Q9v948 drosophila	800	231	9.8	221	2	Q65514	Q65514 aradidopsis
728	237	10.0	535	2	Q7WLD1	Q7wld1 bordetella	801	231	9.8	237	2	Q6DXZ8	Q6dxz8 plasmodium
729	237	10.0	642	2	Q6G364	Q6g364 bartonella	802	231	9.8	237	2	Q6DXZ9	Q6dxz9 plasmodium
730	237	10.0	854	2	Q8IVT9	Q8ivt9 homo sapien	803	231	9.8	237	2	Q6DY01	Q6dy01 plasmodium
731	237	10.0	1024	2	Q6FLA5	Q6fla5 candida gla	804	231	9.8	237	2	Q7XLA1	Q7xla1 oryza sativ
732	237	10.0	3409	2	Q6SSE6	Q6sse6 chlamydomon	805	231	9.8	350	2	Q8C2H8	Q8c2h8 mus musculu
733	236.5	10.0	247	2	Q6DY44	Q6dy44 plasmodium	806	231	9.8	373	2	Q9P639	Q9p639 neurospora
734	236.5	10.0	717	2	Q6MI66	Q6mi66 bdellovibri	807	231	9.8	413	2	Q7D7A7	Q7d7a7 mycobacteri
735	236.5	10.0	747	1	CA12_BOVIN	P02459 bos taurus	808	231	9.8	413	2	Q7TYS4	Q7ty54 mycobacteri
736	236.5	10.0	961	2	Q7RW88	Q7rw88 neurospora	809	231	9.8	422	2	Q94KD0	Q94kd0 aradidopsis
737	236.5	10.0	977	2	Q8X005	Q8x005 neurospora	810	231	9.8	501	2	Q6GLD1	Q6gld1 xenopus tro
738	236.5	10.0	1733	1	VNUA_PRVKA	P33485 pseudorabie	811	231	9.8	536	2	Q7ZXQ2	Q7zxq2 xenopus lae
739	236.5	10.0	1736	1	CA2B_MOUSE	Q64739 mus musculu	812	231	9.8	898	2	Q8K588	Q8k588 mus musculu
740	236	10.0	504	2	Q6FL65	Q6fl65 candida gla	813	231	9.8	911	2	Q812A1	Q812a1 mus musculu
741	236	10.0	518	2	Q8MQG8	Q8mqg8 caenorhabdi	814	231	9.8	1758	1	CA24_CAEEL	P17140 caenorhabdi
742	236	10.0	524	2	Q02123	Q02123 caenorhabdi	815	230.5	9.8	284	2	Q6EEZ3	Q6eez3 euprostheno
743	236	10.0	888	2	Q90796	Q90796 gallus gall	816	230.5	9.8	485	2	Q9UV68	Q9uv68 neocallimas
744	236	10.0	1827	2	Q8UUM5	Q8uum5 oryzias lat	817	230.5	9.8	643	2	Q87E00	Q87e00 xylella fas
745	235.5	10.0	228	2	Q6DY00	Q6dy00 plasmodium	818	230.5	9.8	859	2	Q81RV3	Q81rv3 drosophila
746	235.5	10.0	643	1	KZC1_HUMAN	P04264 homo sapien	819	230.5	9.8	887	2	Q9W4V1	Q9w4v1 drosophila
747	235.5	10.0	682	2	Q9VRM2	Q9vrm2 drosophila	820	230.5	9.8	1300	2	Q36421	Q36421 alciaphine
748	235.5	10.0	1714	2	Q7Z5L5	Q7z5l5 homo sapien	821	230.5	9.8	2096	2	Q7TWN7	Q7twn7 mycobacteri
749	235	9.9	448	2	Q18265	Q18265 caenorhabdi	822	230.5	9.8	3157	2	Q6MWN9	Q6mwn9 mycobacteri
750	235	9.9	568	2	Q6E1Z0	Q6e1z0 canis fami	823	230	9.7	115	1	SER1_GALME	Q96614 gallieria me
751	235	9.9	839	2	Q9RX57	Q9rx57 deinococcus	824	230	9.7	1023	2	Q7Q3C0	Q7q3c0 anopheles g
752	235	9.9	891	2	Q8OV58	Q8ov58 mus musculu	825	230	9.7	1778	1	N189_SCHPO	Q9uk4 schizosacch
753	235	9.9	1269	2	Q7T227	Q7t227 gallus gall	826	229.5	9.7	160	2	Q94669	Q94669 plasmodium
754	234.5	9.9	207	1	EGG2_SCHJA	P19469 schistosoma	827	229.5	9.7	167	2	Q7QIN7	Q7qin7 anopheles g
755	234.5	9.9	419	2	Q42638	Q42638 brassica ol	828	229.5	9.7	175	2	Q7XDT1	Q7xdt1 oryza sativ
756	234.5	9.9	438	2	Q7M3U7	Q7m3u7 paralvinell	829	229.5	9.7	294	2	Q16986	Q16986 araneus dia
757	234.5	9.9	455	2	Q28495	Q28495 macaca mula	830	229.5	9.7	398	2	Q7Q1A7	Q7q1a7 anopheles g
758	234.5	9.9	2109	1	EGC3_CHICK	P07898 gallus gall	831	229.5	9.7	539	2	Q7TWN9	Q7twn9 mycobacteri
759	234.5	9.9	2585	2	Q23587	Q23587 caenorhabdi	832	229.5	9.7	569	1	K1CU_MOUSE	P02535 mus musculu
760	234.5	9.9	2944	1	CA17_HUMAN	Q02388 homo sapien	833	229.5	9.7	585	2	Q7QB99	Q7qby9 anopheles g
761	234	9.9	237	2	Q26166	Q26166 plasmodium	834	229.5	9.7	708	2	Q7ZWN8	Q7zwn8 xenopus lae

835	229.5	9.7	740	2	Q73J82	Q73J82 treponema d	908	225	9.5	767	2	Q7PM40	Q7pm40 anopheles g
836	229.5	9.7	824	2	Q81B45	Q81b45 bacillus ce	909	225	9.5	1196	1	ICEV_PSEX	Q33479 pseudomonas
837	229.5	9.7	853	2	Q8VQ20	Q8vq20 myxococcus	910	225	9.5	1746	2	Q7PVR9	Q7pvr9 anopheles g
838	229.5	9.7	857	2	Q85783	Q85783 myxococcus	911	224.5	9.5	174	2	Q9LTP5	Q9ltp5 aradidopsis
839	229	9.7	162	2	Q9M0B4	Q9m0b4 aradidopsis	912	224.5	9.5	235	2	Q9LIZ2	Q9liz2 oryza sativ
840	229	9.7	192	2	Q7XDT3	Q7xd3 oryza sativ	913	224.5	9.5	442	2	Q7PUK2	Q7puk2 anopheles g
841	229	9.7	391	2	Q6S216	Q6s216 triticum ae	914	224.5	9.5	561	2	Q8BVU3	Q8bv3 mus musculus
842	229	9.7	570	2	Q8RS16	Q8rs16 uncultured	915	224.5	9.5	775	2	Q9F342	Q9f342 streptomyce
843	228.5	9.7	197	2	Q6ATP3	Q6atp3 pennisetum	916	224.5	9.5	801	2	Q8T5G4	Q8t5g4 anopheles g
844	228.5	9.7	228	2	Q6DXV0	Q6dxv0 plasmodium	917	224.5	9.5	830	2	Q7PVR8	Q7pvr8 anopheles g
845	228.5	9.7	429	1	DR48_YEAST	P18899 saccharomyc	918	224.5	9.5	910	1	ILF3_RAT	Q9j13 rattus norv
846	228.5	9.7	560	2	Q50275	Q50275 mycoplasma	919	224	9.5	167	2	Q63115	Q63115 rattus norv
847	228.5	9.7	561	2	Q14664	Q14664 homo sapien	920	224	9.5	387	2	Q6S7B1	Q6s7b1 aradidopsis
848	228.5	9.7	800	2	Q6NU13	Q6nul3 xenopus lae	921	224	9.5	404	2	Q22791	Q22791 aradidopsis
849	228.5	9.7	2523	2	Q8TJ58	Q8tj58 methanosarc	922	224	9.5	447	2	Q9VTJ3	Q9vtj3 ateline her
850	228.5	9.7	5146	2	Q9VXR3	Q9vxr3 drosophila	923	224	9.5	544	2	Q816C4	Q816c4 drosophila
851	228	9.6	189	2	Q7XDS0	Q7xd0 oryza sativ	924	224	9.5	625	2	Q61MF3	Q61mf3 rattus norv
852	228	9.6	196	2	Q22638	Q22638 zea mays (m	925	224	9.5	681	2	Q6AZQ8	Q6azq8 xenopus lae
853	228	9.6	238	2	Q6TQ07	Q6tq07 plasmodium	926	224	9.5	1115	2	Q6PFB1	Q6pfb1 mus musculus
854	228	9.6	690	2	Q73T97	Q73t97 mycobacteri	927	224	9.5	1497	1	CA1G_HUMAN	Q9und9 homo sapien
855	228	9.6	738	2	Q82YD4	Q82yd4 streptomyce	928	224	9.5	1691	2	Q9ESQ1	Q9esq1 mus musculus
856	228	9.6	738	2	Q90779	Q90779 gallus gall	929	224	9.5	2310	2	Q9W2U7	Q9w2u7 drosophila
857	228	9.6	1684	2	Q8JNB6	Q8jnb6 white spot	930	223.5	9.5	339	2	Q6CA18	Q6ca18 yarrowia li
858	228	9.6	1684	2	Q8VAA1	Q8vaa1 white spot	931	223.5	9.5	572	2	P71187	P71187 enterobacte
859	228	9.6	1684	2	Q911LK9	Q91lk9 white spot	932	223.5	9.5	572	2	Q936Y6	Q936y6 pseudomonas
860	227.5	9.6	116	2	Q9NI04	Q9ni04 plasmodium	933	223.5	9.5	572	2	Q6UP53	Q6up53 alcaligenes
861	227.5	9.6	228	2	Q6TQ08	Q6tq08 plasmodium	934	223.5	9.5	572	2	Q76M30	Q76m30 comamonas a
862	227.5	9.6	237	2	Q6DY02	Q6dy02 plasmodium	935	223.5	9.5	572	2	Q7X3E2	Q7x3e2 uncultured
863	227.5	9.6	277	2	Q7PWP8	Q7pwp8 anopheles g	936	223.5	9.5	631	2	Q9N1P1	Q9n1p1 bos taurus
864	227.5	9.6	372	2	Q7Z008	Q7z008 anagasta ku	937	223.5	9.5	659	2	Q8MT98	Q8mt98 drosophila
865	227.5	9.6	431	2	Q7QC69	Q7qc69 anopheles g	938	223.5	9.5	824	2	Q69YT0	Q69yt0 homo sapien
866	227.5	9.6	726	2	Q812X1	Q812x1 streptomyce	939	223.5	9.5	974	2	Q9UVL3	Q9uyl3 neurospora
867	227.5	9.6	1130	2	Q6CJH1	Q6cjh1 kluyveromyc	940	223.5	9.5	978	2	P91777	P91777 pacifastacu
868	227.5	9.6	1297	2	Q6VB19	Q6vb19 candida gla	941	223.5	9.5	1075	2	Q86X41	Q86x41 homo sapien
869	227.5	9.6	1997	2	Q7RXD0	Q7rxd0 neurospora	942	223.5	9.5	1427	2	Q8GIZ2	Q8giz2 mycoplasma
870	227	9.6	236	2	Q94FQ5	Q94fq5 aradidopsis	943	223.5	9.5	1855	2	Q8QZF0	Q8qzf0 rattus norv
871	227	9.6	371	2	Q45114	Q45114 caenorhabdi	944	223	9.4	192	2	Q9ZWM7	Q9zwm7 zea mays (m
872	227	9.6	536	2	Q816B9	Q816b9 drosophila	945	223	9.4	441	2	Q6G4M7	Q6g4m7 bartonella
873	227	9.6	544	2	Q816C5	Q816c5 drosophila	946	223	9.4	544	2	Q816C3	Q816c3 drosophila
874	227	9.6	645	2	Q63P58	Q63p58 burkholderi	947	223	9.4	911	1	ILF3_MOUSE	Q9z1x4 mus musculus
875	227	9.6	703	1	CA28_HUMAN	P25067 homo sapien	948	223	9.4	1001	2	Q05154	Q05154 saccharomyc
876	227	9.6	1148	1	ICEK_PSEX	O30611 pseudomonas	949	223	9.4	1200	1	ICEN_PSESY	P06620 pseudomonas
877	227	9.6	1210	1	ICEN_PSEFL	P09815 pseudomonas	950	222.5	9.4	228	2	Q6TOR2	Q6tor2 plasmodium
878	227	9.6	1622	2	Q7GFG9	Q7gfg9 vibrio para	951	222.5	9.4	655	2	Q8IRV2	Q8irv2 drosophila
879	226.5	9.6	228	2	Q6V4E19	Q6v4e19 plasmodium	952	222.5	9.4	739	2	Q70575	Q70575 mus musculus
880	226.5	9.6	252	2	Q7VEJ9	Q7vej9 prochloroco	953	222.5	9.4	1063	2	Q9CH86	Q9ch86 lactococcus
881	226.5	9.6	469	1	CS65_WHEAT	P45526 triticum ae	954	222.5	9.4	1260	2	Q9UGY9	Q9ugy9 homo sapien
882	226.5	9.6	637	2	Q9D2K8	Q9d2k8 mus musculus	955	222.5	9.4	1761	2	O18407	O18407 drosophila
883	226.5	9.6	641	2	Q17740	Q17740 caenorhabdi	956	222.5	9.4	2523	2	Q6MWY2	Q6mw2 mycobacteri
884	226.5	9.6	1022	1	CA26_CHICK	P15988 gallus gall	957	222	9.4	363	2	Q9FGH5	Q9fgh5 aradidopsis
885	226.5	9.6	1709	2	Q86L43	Q86l43 dictyosteli	958	222	9.4	365	1	ROA1_XENLA	P17130 xenopus lae
886	226	9.6	189	2	Q7XDS8	Q7xd8 oryza sativ	959	222	9.4	504	2	Q7QDT6	Q7qdt6 anopheles g
887	226	9.6	199	2	Q94476	Q94476 dictyosteli	960	222	9.4	544	2	Q81081	Q81081 drosophila
888	226	9.6	251	2	Q853E6	Q853e6 mycobacteri	961	222	9.4	552	2	Q6MWW0	Q6mww0 mycobacteri
889	226	9.6	544	2	Q81072	Q81072 drosophila	962	222	9.4	552	2	Q7TW76	Q7tw76 mycobacteri
890	226	9.6	544	2	Q816C7	Q816c7 drosophila	963	222	9.4	623	2	Q8VIY0	Q8viy0 mycobacteri
891	226	9.6	834	2	Q8W056	Q8w056 oryza sativ	964	222	9.4	676	2	Q6DE50	Q6de50 xenopus lae
892	226	9.6	1600	2	Q9URH6	Q9ueh6 homo sapien	965	222	9.4	946	2	Q857Y4	Q857y4 mycobacteri
893	226	9.6	1621	2	Q9H4R9	Q9h4r9 homo sapien	966	222	9.4	1519	2	Q7Z3C4	Q7z3c4 homo sapien
894	226	9.6	1669	1	CA14_HUMAN	P02462 homo sapien	967	221.5	9.4	100	2	Q964C3	Q964c3 encophalito
895	226	9.6	1691	1	CA64_HUMAN	Q14031 homo sapien	968	221.5	9.4	173	2	Q41191	Q41191 aradidopsis
896	226	9.6	2189	2	Q9BI05	Q9bi05 eimeria ten	969	221.5	9.4	193	2	Q9VWM4	Q9vwm4 drosophila
897	225.5	9.5	265	2	Q6DDA7	Q6dda7 xenopus tro	970	221.5	9.4	228	2	Q6TOR0	Q6tor0 plasmodium
898	225.5	9.5	751	2	Q9RLN9	Q9rln9 mus musculus	971	221.5	9.4	249	2	Q6TOR5	Q6tor5 plasmodium
899	225.5	9.5	770	2	Q6BIY3	Q6biy3 debaryomyce	972	221.5	9.4	249	2	Q6C605	Q6c605 yarrowia li
900	225.5	9.5	809	2	Q76869	Q76869 drosophila	973	221.5	9.4	503	2	Q9HEH4	Q9heh4 neurospora
901	225.5	9.5	1113	1	N116_YEAST	Q02630 saccharomyc	974	--221	9.4	273	2	Q65X75	Q65x75 oryza sativ
902	225.5	9.5	1338	2	Q7TW60	Q7tw60 mycobacteri	975	221	9.4	310	2	Q90612	Q90612 gallus gall
903	225.5	9.5	1474	2	Q86G87	Q86g87 pseudoplusi	976	221	9.4	544	2	Q816C0	Q816c0 drosophila
904	225	9.5	325	2	Q8INH0	Q8inh0 drosophila	977	221	9.4	544	2	Q816C1	Q816c1 drosophila
905	225	9.5	544	2	Q816C8	Q816c8 drosophila	978	221	9.4	544	2	Q816C6	Q816c6 drosophila
906	225	9.5	572	2	Q63IU2	Q63iu2 burkholderi	979	221	9.4	561	2	Q9CXH6	Q9cxh6 mus musculus
907	225	9.5	624	2	Q8NIV1	Q8niv1 neurospora	980	221	9.4	575	2	Q9SBI7	Q9sb17 hordeum vul

981	981	221	9.4	594	2	Q67Q95	Q67q95 symbiobacte	1054	217	9.2	718	2	Q91TR1	Q91tr1 tupalid her
982	982	221	9.4	758	2	Q6TBC0	Q6tec0 crassostrea	1055	217	9.2	1045	2	Q801S8	Q801s8 xenopus lae
983	983	220.5	9.3	141	2	Q9BJP8	Q9bjp8 plasmodium	1056	216.5	9.2	212	2	Q949F9	Q949f9 oryza sativ
984	984	220.5	9.3	316	2	Q19111	Q19111 caenorhabdi	1057	216.5	9.2	244	2	Q6V5C2	Q6v5c2 arabidopsis
985	985	220.5	9.3	618	2	Q79F80	Q79f80 mycobacteri	1058	216.5	9.2	290	2	Q260S4	Q260s4 paracentroc
986	986	220.5	9.3	618	2	Q79F80	Q79f80 mycobacteri	1059	216.5	9.2	419	2	Q6F222	Q6f222 candida gla
987	987	220.5	9.3	636	2	Q8VK65	Q8vk65 mycobacteri	1060	216.5	9.2	674	1	CA1A_BOVIN	P23206 bos taurus
988	988	220.5	9.3	645	1	K22E_HUMAN	P35908 homo sapien	1061	216.5	9.2	837	2	Q81B46	Q81b46 bacillus ce
989	989	220	9.3	192	2	Q7XD52	Q7xde2 oryza sativ	1062	216.5	9.2	1019	1	CA26_HUMAN	P12110 homo sapien
990	990	220	9.3	202	2	Q8WML4	Q8wml4 dictyosteli	1063	216.5	9.2	1019	1	Q6PQ01	Q6pq01 homo sapien
991	991	220	9.3	332	2	Q6CLZ7	Q6clz7 yarrowia li	1064	216.5	9.2	2090	1	N214_HUMAN	P35858 homo sapien
992	992	220	9.3	413	2	Q9HEJ0	Q9hej0 neurospora	1065	216.5	9.2	2091	2	Q75R47	Q75r47 homo sapien
993	993	220	9.3	568	2	Q8CD80	Q8cd80 mus musculu	1066	216	9.1	191	2	Q7XDR5	Q7xdr5 oryza sativ
994	994	220	9.3	572	2	Q9AHG8	Q9ahg8 comamonas t	1067	216	9.1	405	2	Q6WMT4	Q6wmt4 bdellovibri
995	995	220	9.3	595	2	Q7XJ24	Q7xj24 oryza sativ	1068	216	9.1	409	2	Q19414	Q19414 caenorhabdi
996	996	220	9.3	954	2	Q8WXV8	Q8wxv8 homo sapien	1069	216	9.1	569	2	Q6CH78	Q6ch78 yarrowia li
997	997	220	9.3	957	2	Q96P44	Q96p44 homo sapien	1070	216	9.1	1838	1	CA15_HUMAN	P20308 homo sapien
998	998	220	9.3	957	2	Q9H0V3	Q9hov3 homo sapien	1071	216	9.1	1838	1	Q88207	Q88207 mus musculu
999	999	220	9.3	1206	2	Q869X8	Q869x8 dictyosteli	1072	216	9.1	2090	2	Q9W2T1	Q9w2t1 drosophila
1000	1000	220	9.3	1333	2	Q8PD38	Q8pd38 xanthomonas	1073	216	9.1	2093	2	Q15010	Q15010 homo sapien
1001	1001	220	9.3	1740	2	Q9HCJ0	Q9hcj0 homo sapien	1074	215.5	9.1	102	2	Q964C0	Q964c0 encephalito
1002	1002	219.5	9.3	207	2	Q43522	Q43522 lycopersico	1075	215.5	9.1	424	2	Q6H9M8	Q6h9m8 erwinia pyr
1003	1003	219.5	9.3	214	2	Q6H3Y0	Q6h3y0 oryza sativ	1076	215.5	9.1	520	1	MRCO_HUMAN	Q9uew3 homo sapien
1004	1004	219.5	9.3	262	2	Q6CBL5	Q6cbl5 yarrowia li	1077	215.5	9.1	1034	2	Q8K229	Q8k229 mus musculu
1005	1005	219.5	9.3	311	2	Q8V6M2	Q8v6m2 halovirus h	1078	215.5	9.1	2132	1	PGCA_MOUSE	Q61282 mus musculu
1006	1006	219.5	9.3	539	2	Q81097	Q81097 drosophila	1079	215	9.1	200	1	GRP_HORVU	P17816 hordeum vul
1007	1007	219.5	9.3	684	1	CA39_HUMAN	Q14050 homo sapien	1080	215	9.1	232	2	Q94FR1	Q94fr1 arabidopsis
1008	1008	219.5	9.3	1191	2	Q6PCK7	Q6pck7 xenopus lae	1081	215	9.1	250	2	Q9VX64	Q9vx64 drosophila
1009	1009	219	9.3	191	2	Q7XDR3	Q7xdr3 oryza sativ	1082	215	9.1	340	2	Q6WEQ0	Q6weq0 boechea dr
1010	1010	219	9.3	193	2	Q70592	Q70592 rattus norv	1083	215	9.1	448	2	Q7XDS3	Q7xds3 oryza sativ
1011	1011	219	9.3	294	2	Q6MG73	Q6mgt3 bdellovibri	1084	215	9.1	479	2	Q06292	Q06292 mycobacteri
1012	1012	219	9.3	342	2	Q9LH90	Q9lh90 arabidopsis	1085	215	9.1	479	2	Q7U280	Q7u280 mycobacteri
1013	1013	219	9.3	345	2	Q7TDH1	Q7tdh1 halovirus h	1086	215	9.1	541	2	Q9MA97	Q9ma97 arabidopsis
1014	1014	219	9.3	368	2	Q8MPJ9	Q8mpj9 plasmodium	1087	215	9.1	566	2	Q91VL4	Q91vl4 mus musculu
1015	1015	219	9.3	379	1	ROA3_MOUSE	Q8bg05 mus musculu	1088	215	9.1	575	2	Q9SPA7	Q9spa7 hordeum vul
1016	1016	219	9.3	379	1	ROA3_RAT	Q6urk4 rattus norv	1089	215	9.1	594	2	Q7WKH2	Q7wkh2 bordetella
1017	1017	219	9.3	413	2	Q64939	Q64939 lophopyrum	1090	215	9.1	635	2	Q6UD62	Q6ud62 uncultured
1018	1018	219	9.3	473	2	Q84WQ1	Q84wq1 arabidopsis	1091	215	9.1	669	2	Q7UE67	Q7ue67 rhodopirell
1019	1019	219	9.3	544	2	Q816B7	Q816b7 drosophila	1092	215	9.1	1029	1	CA26_MOUSE	Q02788 mus musculu
1020	1020	219	9.3	544	2	Q816B8	Q816b8 drosophila	1093	215	9.1	1119	1	MN1_HUMAN	Q10571 homo sapien
1021	1021	219	9.3	544	2	Q816C2	Q816c2 drosophila	1094	215	9.1	1405	2	Q8KMK1	Q8kmk1 mycoplasma
1022	1022	219	9.3	716	2	Q825D6	Q825d6 streptomyce	1095	215	9.1	1567	1	ICEN_XANCT	P18127 xanthomonas
1023	1023	219	9.3	734	2	Q61VJ4	Q61vj4 ciona intes	1096	215	9.1	1690	1	CA44_HUMAN	P53420 homo sapien
1024	1024	219	9.3	775	2	Q82CQ3	Q82cq3 streptomyce	1097	215	9.1	1838	2	Q15094	Q15094 homo sapien
1025	1025	219	9.3	1053	2	Q920S4	Q920s4 mus musculu	1098	215	9.1	3848	2	P94772	P94772 erwinia chr
1026	1026	219	9.3	1112	2	Q80U93	Q80u93 mus musculu	1099	214.5	9.1	191	2	Q7XDR8	Q7xdr8 oryza sativ
1027	1027	219	9.3	2303	2	Q7QCA2	Q7qca2 anopheles g	1100	214.5	9.1	241	2	Q6V5D7	Q6v5d7 olimarabido
1028	1028	218.5	9.2	237	2	Q86HE5	Q86he5 dictyosteli	1101	214.5	9.1	373	2	Q9U2I7	Q9u2i7 caenorhabdi
1029	1029	218.5	9.2	370	2	Q95TX4	Q95tx4 drosophila	1102	214.5	9.1	465	2	Q9RXC3	Q9rx3 deinococcus
1030	1030	218.5	9.2	378	1	ROA3_HUMAN	P51991 homo sapien	1103	214.5	9.1	558	2	Q6BT51	Q6bti51 debaryomyce
1031	1031	218.5	9.2	487	2	Q7K536	Q7k536 drosophila	1104	214.5	9.1	589	2	Q99LL6	Q99ll6 mus musculu
1032	1032	218.5	9.2	589	2	Q66043	Q66043 cercopitheci	1105	214.5	9.1	678	2	Q6P467	Q6p467 homo sapien
1033	1033	218.5	9.2	612	2	Q7X678	Q7x678 chlamydomon	1106	214.5	9.1	778	2	Q86BH1	Q86bh1 drosophila
1034	1034	218.5	9.2	705	2	Q04310	Q04310 arabidopsis	1107	214.5	9.1	792	2	Q8MT89	Q8mt89 drosophila
1035	1035	218.5	9.2	1218	2	Q6VB74	Q6vb74 candida gla	1108	214.5	9.1	970	2	Q8VBY1	Q8vby1 rattus norv
1036	1036	218.5	9.2	1416	2	Q6VB73	Q6vb73 candida gla	1109	214.5	9.1	1018	2	Q9HWU6	Q9hwu6 pseudomonas
1037	1037	218.5	9.2	1535	2	Q62D27	Q62d27 burkholderi	1110	214	9.1	301	2	Q8WSZ3	Q8wsz3 nephila cla
1038	1038	218.5	9.2	1580	2	Q8BLX7	Q8blx7 mus musculu	1111	214	9.1	399	2	Q9MS4	Q9ms4 rhizobium l
1039	1039	218.5	9.2	1940	2	Q9VMV5	Q9vmv5 drosophila	1112	214	9.1	594	2	Q7W927	Q7w927 bordetella
1040	1040	218	9.2	284	2	Q9BIS8	Q9bis8 tetragmatha	1113	214	9.1	627	1	K2C1_MOUSE	P04104 mus musculu
1041	1041	218	9.2	481	2	Q8VRM5	Q8vrm5 mycobacteri	1114	214	9.1	699	2	Q6P1C4	Q6pic4 mus musculu
1042	1042	218	9.2	763	2	Q7Q1W5	Q7q1w5 anopheles g	1115	214	9.1	911	1	CA1B_BOVIN	Q28083 bos taurus
1043	1043	218	9.2	2119	2	Q86XD3	Q86xd3 homo sapien	1116	214	9.1	1275	2	Q76602	Q76602 caenorhabdi
1044	1044	217.5	9.2	218	2	Q8SV22	Q8sv22 drosophila	1117	214	9.1	1332	2	Q8SZ27	Q8sz27 drosophila
1045	1045	217.5	9.2	355	2	Q9L8W2	Q9l8w2 mycoplasma	1118	214	9.1	1332	2	Q86S06	Q86s06 drosophila
1046	1046	217.5	9.2	384	2	Q9L8V9	Q9l8v9 mycoplasma	1119	214	9.1	1375	2	Q86S05	Q86s05 drosophila
1047	1047	217.5	9.2	1521	2	Q8CHS9	Q8chs9 mus musculu	1120	214	9.1	1461	2	Q8MKQ2	Q8mkq2 drosophila
1048	1048	217.5	9.2	1666	2	Q8LP68	Q8lp68 chlamydomon	1121	214	9.1	1472	2	Q9V358	Q9v358 drosophila
1049	1049	217.5	9.2	1752	2	Q7QBX5	Q7qb5 anopheles g	1122	214	9.1	1756	2	Q7PWG9	Q7pwg9 anopheles g
1050	1050	217.5	9.2	1880	2	Q18465	Q18465 hirudo medi	1123	214	9.1	1840	2	Q60467	Q60467 cricetus
1051	1051	217	9.2	351	2	Q8GX10	Q8gx10 arabidopsis	1124	214	9.1	2447	2	Q6SF13	Q6sf13 uncultured
1052	1052	217	9.2	575	2	Q40042	Q40042 hordeum vul	1125	213.5	9.0	195	2	Q6MWV0	Q6mwv0 mycobacteri
1053	1053	217	9.2	632	2	Q6C5E6	Q6c5e6 yarrowia li	1126	213.5	9.0	575	2	Q8C1F9	Q8c1f9 mus musculu

1127	213.5	9.0	687	1	DSPP RAT	662598 rattus norv	1200	209.5	8.9	2333	1	PGCA CANFA	Q28343 canis famil
1128	213.5	9.0	695	1	Q9XUQ0	Q9xuq0 caenorhabdi	1201	209.5	8.9	3080	2	Q9V602	Q9v602 drosophila
1129	213.5	9.0	959	1	N100 YEAST	Q26229 saccharomyc	1202	209.5	8.9	3109	2	Q9BMQ0	Q9bmq0 drosophila
1130	213.5	9.0	1653	1	Q3M66	Q63m66 burkholderi	1203	209.5	8.9	3276	2	Q9W321	Q9w321 drosophila
1131	213.5	9.0	1670	1	CA34 HUMAN	Q01955 homo sapien	1204	209	8.8	288	2	Q6L8H1	Q6l8h1 homo sapien
1132	213.5	9.0	1840	2	Q9J703	Q9ji03 rattus norv	1205	209	8.8	457	2	Q7U0X5	Q7u0x5 mycobacteri
1133	213.5	9.0	2415	1	PGCA HUMAN	F61l12 homo sapien	1206	209	8.8	554	2	Q8S7B5	Q8s7b5 oryza sativ
1134	213	9.0	193	2	Q7XDT0	Q7xdt0 oryza sativ	1207	209	8.8	554	2	Q7XFL8	Q7xfl8 oryza sativ
1135	213	9.0	218	2	Q6K5T4	Q6k5t4 oryza sativ	1208	209	8.8	610	2	Q6F0U0	Q6f0u0 candida gla
1136	213	9.0	368	2	Q8MPK1	Q8mpk1 plasmodium	1209	209	8.8	799	2	Q8BNS7	Q8bns7 mus musculu
1137	213	9.0	457	2	Q9VC90	Q9vc90 drosophila	1210	209	8.8	847	2	Q69T67	Q69t67 oryza sativ
1138	213	9.0	529	2	Q43509	Q43509 homo sapien	1211	209	8.8	934	2	Q9GMD3	Q9gmd3 bos taurus
1139	213	9.0	529	2	Q81ZU4	Q81zu4 homo sapien	1212	209	8.8	1707	1	CA24_MOUSE	Q81z22 mus musculu
1140	212.5	9.0	189	2	Q66K53	Q66k53 homo sapien	1213	209	8.8	2573	2	Q7SAE9	Q7sae9 neuropeptora
1141	212.5	9.0	220	1	SER2 GALME	Q96615 gallieria me	1214	209	8.8	3137	1	CA36 CHICK	P15989 gallus gall
1142	212.5	9.0	829	2	Q94C88	Q94c88 arabisdopsis	1215	208.5	8.8	194	2	Q96853	Q96853 schistosoma
1143	212.5	9.0	857	2	Q69Z83	Q69z83 mus musculu	1216	208.5	8.8	353	2	Q7QPF4	Q7qff4 anopheles g
1144	212.5	9.0	882	2	Q80VW9	Q80vw9 mus musculu	1217	208.5	8.8	377	2	Q42627	Q42627 brassica na
1145	212.5	9.0	950	2	Q68SC8	Q68sc8 ciona intes	1218	208.5	8.8	442	1	C184_DICTDI	P54639 dictyostell
1146	212.5	9.0	1035	2	Q6F0U6	Q6f0u6 candida gla	1219	208.5	8.8	491	2	Q6EI03	Q6ei03 streptococc
1147	212.5	9.0	1804	2	Q9ZVV0	Q9zvv0 arabisdopsis	1220	208.5	8.8	809	2	P90534	P90534 dictyostell
1148	212.5	9.0	1835	2	Q9IAU4	Q9iau4 gallus gall	1221	208	8.8	201	2	Q48848	Q48848 arabisdopsis
1149	212.5	9.0	1845	2	Q80UA8	Q80ua8 mus musculu	1222	208	8.8	370	2	Q9BPK6	Q9bpk6 plasmodium
1150	212.5	9.0	2285	2	Q9HBJ5	Q9hbj5 homo sapien	1223	208	8.8	370	2	Q9BPK8	Q9bpk8 plasmodium
1151	212.5	9.0	2551	2	Q8CYI8	Q8cyi8 streptococc	1224	208	8.8	377	2	Q26116	Q26116 plasmodium
1152	212.5	9.0	2572	2	Q7PRV6	Q7prv6 anopheles g	1225	208	8.8	394	2	Q6FX84	Q6fx84 candida gla
1153	212	9.0	347	2	Q9XT25	Q9xt25 bos taurus	1226	208	8.8	436	2	Q7QDL5	Q7qdl5 anopheles g
1154	212	9.0	390	1	CS12 WHEAT	P46525 triticum ae	1227	208	8.8	457	2	Q79FU0	Q79fu0 mycobacteri
1155	212	9.0	568	2	Q6NUV1	Q6nuv1 brachydanio	1228	208	8.8	529	2	Q79R44	Q79r44 pan troglod
1156	212	9.0	619	2	Q7PQ47	Q7pq47 anopheles g	1229	208	8.8	588	2	Q9QEK6	Q9qek6 cynomolgus
1157	212	9.0	633	2	Q6E1Z1	Q6e1z1 canis famil	1230	208	8.8	680	1	CA1A_MOUSE	Q05306 mus musculu
1158	212	9.0	645	2	Q9KXB9	Q9kxb9 escherichia	1231	208	8.8	689	1	CA29_HUMAN	Q14055 homo sapien
1159	212	9.0	907	2	Q26675	Q26675 theileria a	1232	208	8.8	1691	2	Q9ESQ2	Q9esq2 mus musculu
1160	212	9.0	975	2	Q6FWU3	Q6fwu3 candida gla	1233	208	8.8	1691	2	Q63ZW6	Q63zw6 mus musculu
1161	212	9.0	1023	2	Q7RT42	Q7rt42 plasmodium	1234	207.5	8.8	186	2	Q9DEX8	Q9dex8 cyprinus ca
1162	212	9.0	1046	2	Q8K388	Q8k388 mus musculu	1235	207.5	8.8	236	2	Q6V5H3	Q6v5h3 arabisdopsis
1163	212	9.0	3056	2	Q7USQ0	Q7usq0 rhodopirell	1236	207.5	8.8	332	2	Q69ZG1	Q69zg1 nephila cla
1164	211.5	9.0	193	2	Q9D6J0	Q9dj0 mus musculu	1237	207.5	8.8	334	2	Q9JKB4	Q9jkb4 mus musculu
1165	211.5	9.0	226	2	Q7QCJ2	Q7qcj2 anopheles g	1238	207.5	8.8	365	1	ROA1_DROME	P07909 drosophila
1166	211.5	9.0	248	2	Q8VIW6	Q8viw6 mycobacteri	1239	207.5	8.8	389	1	SERI_BOMMO	P07856 bombyx mori
1167	211.5	9.0	286	2	Q9UIG9	Q9uig9 drosophila	1240	207.5	8.8	428	2	Q8H9M9	Q8h9m9 erwinia sp.
1168	211.5	9.0	394	2	Q9VVC3	Q9vvc3 drosophila	1241	207.5	8.8	476	2	Q8VKA5	Q8vka5 mycobacteri
1169	211.5	9.0	431	2	Q7N1B7	Q7n1b7 photorhabdu	1242	207.5	8.8	522	2	Q9P9G7	Q9p9g7 methanococc
1170	211.5	9.0	457	2	Q7TYR9	Q7tyr9 mycobacteri	1243	207.5	8.8	603	2	Q6FLA7	Q6fla7 candida gla
1171	211.5	9.0	480	2	Q8IGI0	Q8igi0 drosophila	1244	207.5	8.8	632	2	Q8CJT6	Q8cjt6 streptomyc
1172	211.5	9.0	957	2	Q641F3	Q641f3 xenopus lae	1245	207.5	8.8	662	2	Q8VHY3	Q8vhy3 mus musculu
1173	211	8.9	253	2	Q9BIT4	Q9bit4 nephila sen	1246	207.5	8.8	981	2	Q8MQ11	Q8mq11 drosophila
1174	211	8.9	286	2	Q9VB86	Q9vb86 drosophila	1247	207	8.8	208	2	Q25949	Q25949 plasmodium
1175	211	8.9	367	2	Q7QEF9	Q7qef9 anopheles g	1248	207	8.8	303	2	Q828N1	Q828n1 streptomyc
1176	211	8.9	371	1	ROA1_HUMAN	P09651 homo sapien	1249	207	8.8	313	2	Q9SYZ5	Q9syz5 arabisdopsis
1177	211	8.9	643	2	Q68ED0	Q68ed0 mus musculu	1250	207	8.8	314	2	Q9FGY2	Q9fgy2 arabisdopsis
1178	211	8.9	890	2	Q77087	Q77087 alvinella p	1251	207	8.8	405	2	Q23057	Q23057 caenorhabdi
1179	211	8.9	967	2	Q08294	Q08294 saccharomyc	1252	207	8.8	448	2	Q716P3	Q716p3 mycobacteri
1180	210.5	8.9	255	2	Q69ZG5	Q69z95 nephila cla	1253	207	8.8	529	2	Q63TR5	Q63tr5 burkholderi
1181	210.5	8.9	428	2	Q6XDB9	Q6xdb9 erwinia pyr	1254	207	8.8	645	2	Q776P1	Q776p1 bacterioph
1182	210.5	8.9	471	2	Q9UAY0	Q9uay0 caenorhabdi	1255	207	8.8	645	2	Q7X2W1	Q7x2w1 stx2 conver
1183	210.5	8.9	509	2	Q7Z010	Q7z010 plodia inte	1256	207	8.8	645	2	Q9X3C2	Q9x3c2 stx1 conver
1184	210.5	8.9	623	2	Q7SZR6	Q7szr6 brachydanio	1257	207	8.8	645	2	Q9XJK8	Q9xjk8 bacterioph
1185	210.5	8.9	624	2	Q6NUX1	Q6nux1 brachydanio	1258	207	8.8	645	2	Q8XAX7	Q8xax7 escherichia
1186	210.5	8.9	941	2	Q85ST8	Q85st8 mycobacteri	1259	207	8.8	680	1	CA1A_HUMAN	Q03692 homo sapien
1187	210.5	8.9	1488	2	Q8NPK0	Q8npk0 corynebacte	1260	207	8.8	824	2	Q7QUH6	Q7quh6 anopheles g
1188	210.5	8.9	3190	2	Q01368	Q01368 drosophila	1261	207	8.8	1306	2	Q93N36	Q93n36 pantocoe ana
1189	210	8.9	192	2	Q7XDR7	Q7xdr7 oryza sativ	1262	207	8.8	1336	2	Q6R241	Q6r241 homo sapien
1190	210	8.9	430	2	Q95RR2	Q95rr2 drosophila	1263	207	8.8	1516	2	Q6R239	Q6r239 homo sapien
1191	210	8.9	459	2	Q6FB76	Q6fb76 acinetobact	1264	207	8.8	1751	2	Q6R240	Q6r240 homo sapien
1192	210	8.9	1315	2	Q8QHL9	Q8qhl9 xenopus lae	1265	206.5	8.7	2124	1	PGCA RAT	P07897 rattus norv
1193	209.5	8.9	302	2	Q84Q60	Q84q60 arabisdopsis	1266	206.5	8.7	322	2	Q8G4E5	Q8g4e5 bifidobact
1194	209.5	8.9	319	2	Q6C4B0	Q6c4b0 yarrowia li	1267	206.5	8.7	342	1	ROA1_SCHAM	P21522 schistocerc
1195	209.5	8.9	595	2	Q82K69	Q82k69 streptomyc	1268	206.5	8.7	434	2	Q7N1B8	Q7n1b8 photorhabdu
1196	209.5	8.9	597	2	Q640K4	Q640k4 xenopus lae	1269	206.5	8.7	456	2	Q6CAZ4	Q6caz4 yarrowia li
1197	209.5	8.9	688	1	CA29_MOUSE	Q07643 mus musculu	1270	206.5	8.7	504	2	Q6JAY8	Q6jay8 gallus gall
1198	209.5	8.9	688	2	Q8K2W0	Q8k2w0 mus musculu	1271	206.5	8.7	528	2	Q81ZU5	Q81zu5 homo sapien
1199	209.5	8.9	920	2	Q78EC6	Q78ec6 mus sp. typ	1272	206.5	8.7	528	2	Q81ZU6	Q81zu6 homo sapien

1273	206.5	8.7	528	2	Q8NSP3	Q8n5p3 homo sapien	1346	203.5	8.6	456	2	Q638E4	Q638e4 bacillus ce
1274	206.5	8.7	573	2	Q8K7M7	Q8k7m7 streptococ	1347	203.5	8.6	476	1	Q9VA86	Q9va86 drosophila
1275	206.5	8.7	597	2	Q7PS59	Q7pts59 anopheles g	1348	203.5	8.6	486	2	CDSN_HUMAN	Q15517 homo sapien
1276	206.5	8.7	647	2	Q9PT10	Q9pt10 oncornynchu	1349	203.5	8.6	500	2	Q9NP52	Q9np52 homo sapien
1277	206.5	8.7	691	2	Q66L59	Q66l59 brachydanio	1350	203.5	8.6	513	2	Q9SIF9	Q9sif9 homo sapien
1278	206.5	8.7	1025	1	CA16_MOUSE	Q04857 mus musculus	1351	203.5	8.6	943	2	Q8BK12	Q8bk12 mus musculus
1279	206	8.7	202	2	Q8M5K2	Q25952 plasmodium	1352	203.5	8.6	1124	2	Q63UH1	Q63uh1 burkholderi
1280	206	8.7	370	2	Q8MPK2	Q8mpk2 plasmodium	1353	203.5	8.6	1535	2	Q6NVE4	Q6nve4 mus musculus
1281	206	8.7	374	2	Q75JC9	Q75jc9 dictyosteli	1354	203.5	8.6	1953	2	Q98HJ2	Q98hj2 rhizobium l
1282	206	8.7	447	2	Q9SIA8	Q9sia8 aradidopsis	1355	203	8.6	196	2	Q8P2F2	Q8p2f2 methanosaar
1283	206	8.7	713	2	Q9GV24	Q9gv24 sarcophaga	1356	203	8.6	223	2	Q9C6I9	Q9c6i9 aradidopsis
1284	206	8.7	770	2	Q7WHU6	Q7whu6 bordetella	1357	203	8.6	260	2	Q8ISA8	Q8isa8 plasmodium
1285	206	8.7	1257	2	Q14654	Q14654 homo sapien	1358	203	8.6	277	2	Q9GQP0	Q9gqp0 plasmodium
1286	206	8.7	1322	1	ICEA_PANAN	P20469 pantoea ana	1359	203	8.6	439	2	Q8S7B4	Q8s7b4 oryza sativ
1287	205.5	8.7	406	2	Q23J28	Q23j28 aradidopsis	1360	203	8.6	439	2	Q7XFL9	Q7xfl9 oryza sativ
1288	205.5	8.7	411	2	Q8W034	Q8w034 aradidopsis	1361	203	8.6	499	2	Q9NRH4	Q9nrh4 homo sapien
1289	205.5	8.7	424	2	Q6H9M6	Q6h9m6 erwinia pyr	1362	203	8.6	526	2	Q6IFW6	Q6ifw6 rattus norv
1290	205.5	8.7	428	2	Q82FT8	Q82ft8 streptomyce	1363	203	8.6	637	2	Q7Q5C7	Q7q5c7 anopheles g
1291	205.5	8.7	518	1	MTCO_MOUSE	Q60754 mus musculus	1364	203	8.6	680	2	P93658	P93658 brassica na
1292	205.5	8.7	561	2	Q961F4	Q961f4 homo sapien	1365	203	8.6	690	2	Q6K2M1	Q6k2m1 oryza sativ
1293	205.5	8.7	582	2	Q90W75	Q90w75 oncorhynch	1366	203	8.6	813	2	Q8GFF3	Q8gff3 streptomyce
1294	205.5	8.7	680	2	Q8BSX1	Q8bsx1 mus musculus	1367	203	8.6	825	1	SE5_RAT	Q63003 rattus norv
1295	205.5	8.7	1028	2	Q7Z645	Q7z645 homo sapien	1368	203	8.6	1034	1	ICEN_PANAN	Q47879 pantoea ana
1296	205.5	8.7	1112	2	Q7RM90	Q7rm90 plasmodium	1369	203	8.6	1253	1	DSPP_HUMAN	Q9nzw4 homo sapien
1297	205	8.7	164	2	Q7XDT8	Q7xdt8 oryza sativ	1370	203	8.6	2149	2	Q6XL68	P13608 bos taurus
1298	205	8.7	177	2	Q26577	Q26577 schistosoma	1371	203	8.6	2364	1	PGCA_BOVIN	Q63167 bos taurus
1299	205	8.7	187	2	Q8L3S8	Q8l3s8 zea mays (m	1372	203	8.6	2365	2	Q6XL67	Q6xl67 bos taurus
1300	205	8.7	207	2	Q25701	Q25701 plasmodium	1373	202.5	8.6	425	2	Q8WSL2	Q8wsl2 plasmodium
1301	205	8.7	224	2	Q94FP7	Q94fp7 aradidopsis	1374	202.5	8.6	431	2	Q8GLD8	Q8gld8 bacillus th
1302	205	8.7	224	2	Q94FP8	Q94fp8 aradidopsis	1375	202.5	8.6	456	2	Q7UJ76	Q7uj76 rhodospirell
1303	205	8.7	368	2	Q8MPK0	Q8mpk0 plasmodium	1376	202.5	8.6	667	2	Q8XRM8	Q8xrm8 ralatonia s
1304	205	8.7	393	2	Q8MPK3	Q8mpk3 plasmodium	1377	202.5	8.6	677	1	CA29_CHICK	P12108 gallus gall
1305	205	8.7	640	2	Q6KAQ4	Q6kaq4 mus musculus	1378	202.5	8.6	771	2	Q63LV4	Q63lv4 burkholderi
1306	205	8.7	775	2	Q7MX25	Q7mx25 oryctolagus	1379	202.5	8.6	831	2	Q62BI8	Q62bi8 burkholderi
1307	205	8.7	1012	2	Q62KN5	Q62kn5 burkholderi	1380	202.5	8.6	1028	1	CA16_HUMAN	P12109 homo sapien
1308	205	8.7	1036	2	Q6CWM9	Q6cwm9 kluyveromyc	1381	202.5	8.6	1456	2	Q6C4S5	Q6c4s5 yarrowia li
1309	205	8.7	1603	1	CA1F_HUMAN	Q01212 homo sapien	1382	202.5	8.6	3176	1	CA36_HUMAN	P12111 homo sapien
1310	205	8.7	1131	2	Q75DJ5	Q75dj5 ashbya goss	1383	202	8.5	324	2	Q7SDB1	Q7sdb1 neurospora
1311	205	8.7	1301	2	Q6P3M9	Q6p3m9 xenopus tro	1384	202	8.5	348	2	Q75CJ3	Q75cj3 ashbya goss
1312	205	8.7	1417	2	Q9HVN6	Q9hvn6 pseudomonas	1385	202	8.5	430	1	NU42_YEAST	P49686 saccharomyc
1313	205	8.7	1516	1	CA1H_HUMAN	P39060 homo sapien	1386	202	8.5	464	2	Q8WSL4	Q8wsl4 plasmodium
1314	205	8.7	1603	1	CA1F_HUMAN	Q7092 homo sapien	1387	202	8.5	488	2	Q6RBZ1	Q6rbz1 chlamydomon
1315	205	8.7	1610	2	Q92KQ8	Q92kq8 rhizobium m	1388	202	8.5	571	2	Q6H086	Q6h086 fremyella d
1316	205	8.7	2189	2	Q8IKV6	Q8ikv6 plasmodium	1389	202	8.5	692	2	Q8XT20	Q8xt20 ralatonia s
1317	205	8.7	2351	2	Q8PCQ5	Q8pcq5 xanthomonas	1390	202	8.5	700	2	Q9VXH1	Q9vxl1 drosophila
1318	204.5	8.7	279	2	Q6C3L2	Q6c3l2 yarrowia li	1391	202	8.5	733	2	Q9ADN4	Q9adn4 streptomyce
1319	204.5	8.7	280	2	Q91VQ2	Q91vq2 mus musculus	1392	202	8.5	742	2	Q8IR16	Q8ir16 drosophila
1320	204.5	8.7	443	2	Q28243	Q28243 canis famil	1393	202	8.5	749	2	Q82FQ7	Q82fq7 streptomyce
1321	204.5	8.7	483	1	MRCO_MESAU	Q9wub9 mesocricetu	1394	202	8.5	1432	2	Q9FPR8	Q9fpr8 chlamydomon
1322	204.5	8.7	611	2	Q624M4	Q624m4 oryza sativ	1395	201.5	8.5	231	2	Q75QN8	Q75qn8 triticum ae
1323	204.5	8.7	654	2	Q9BXS0	Q9bxa0 homo sapien	1396	201.5	8.5	233	2	Q9BIT6	Q9bit6 nephila ina
1324	204.5	8.7	1019	1	CA16_CHICK	P20785 gallus gall	1397	201.5	8.5	393	2	Q18880	Q18880 caenorhabdi
1325	204.5	8.7	1310	2	Q6DFR4	Q6dfr4 xenopus tro	1398	201.5	8.5	425	2	Q6MWT5	Q6mwt5 bdellovibri
1326	204	8.6	177	1	EGG2_SCHMA	P12796 schistosoma	1399	201.5	8.5	433	2	Q9VEF5	Q9vet5 drosophila
1327	204	8.6	177	1	EGG3_SCHMA	P13396 schistosoma	1400	201.5	8.5	531	2	Q8SXP8	Q8sxp8 drosophila
1328	204	8.6	191	2	Q7XDR4	Q7xdr4 oryza sativ	1401	201.5	8.5	531	2	Q8XQ8	Q8xq8 drosophila
1329	204	8.6	228	2	Q43308	Q43308 aradidopsis	1402	201.5	8.5	555	2	Q6ZQR0	Q6zqr0 homo sapien
1330	204	8.6	247	2	Q95254	Q95254 plasmodium	1403	201.5	8.5	623	2	Q8K2U8	Q8k2u8 mus musculus
1331	204	8.6	364	2	Q7Q5C0	Q7q5c0 anopheles g	1404	201.5	8.5	888	2	Q80W00	Q80w00 mus musculus
1332	204	8.6	476	2	Q18453	P18853 heterodera	1405	201.5	8.5	1344	2	Q934I9	Q934i9 gallus gall
1333	204	8.6	547	1	CAFI_EPHMU	P18455 ephydatia m	1406	201.5	8.5	1671	2	Q78E26	Q78e26 neurospora
1334	204	8.6	717	2	Q9LOI2	Q9loi2 streptomyce	1407	201.5	8.5	1711	1	N214_DROME	Q9wix4 drosophila
1335	204	8.6	798	2	Q9H4U3	Q9h4u3 homo sapien	1408	201	8.5	233	2	Q6WEQ8	Q6weq8 aradidopsis
1336	204	8.6	832	2	Q96JF7	Q96jf7 homo sapien	1409	201	8.5	302	2	Q9QLL8	Q9ql18 plasmodium
1337	204	8.6	866	2	Q6FPD8	Q6fpd8 candida gla	1410	201	8.5	302	2	Q9QLL9	Q9ql19 plasmodium
1338	204	8.6	953	2	Q67QD7	Q67qd7 symbiobacte	1411	201	8.5	317	2	Q9BH54	Q9bh54 plasmodium
1339	204	8.6	1146	1	CA1G_CHICK	Q90584 gallus gall	1412	201	8.5	381	2	Q76450	Q76450 strongyloce
1340	204	8.6	1802	2	Q17163	Q17163 brugia mala	1413	201	8.5	422	2	Q6H9N0	Q6h9n0 erwinia sp.
1341	204	8.6	1860	2	Q812C6	Q81zc6 homo sapien	1414	201	8.5	433	2	Q69TP6	Q69tp6 oryza sativ
1342	203.5	8.6	262	2	Q767M8	Q767m8 sus scrofa	1415	201	8.5	445	2	Q9VEB9	Q9veb9 drosophila
1343	203.5	8.6	280	1	C36A_MANSE	Q8t634 manduca sex	1416	201	8.5	690	2	Q8JGL8	Q8jgl8 brachydanio
1344	203.5	8.6	341	2	Q912R9	Q912r9 mus musculus	1417	201	8.5	798	2	Q8SK18	Q8sk18 drosophila
1345	203.5	8.6	353	2	Q8CJ71	Q8cj71 mus musculus	1418	201	8.5	798	2	Q9VHP0	Q9vhp0 drosophila





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QY 361 MREISKEGNLLGGSDNYRGQSSWGSGGDAVGGVNTVNSSETSGMNFDTFWKNEKS 420
DB 361 MREISKEGNLLGGSDNYRGQSSWGSGGDAVGGVNTVNSSETSGMNFDTFWKNEKS 420
QY 421 KLGFINWDAINKDQSSRIP 440
DB 421 KLGFINWDAINKDQSSRIP 440

RESULT 2
Q6E0U4 PRELIMINARY; PRT; 476 AA.
AC Q6E0U4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Dermokine-beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Inai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RL Genomics 84:384-397(2004).
DR EMBL; AY622965; AAT68269.1; -.
SQ SEQUENCE 476 AA; 47010 MW; E2206CCE64AC4992 CRC64;

Query Match 84.5%; Score 1996; DB 2; Length 476;
Best Local Similarity 87.1%; Pred. No. 2.8e-86;
Matches 378; Conservative 2; Mismatches 0; Indels 54; Gaps 2;

QY 1 MKPQGPLACLLALCLGSGEAGPLQSGESTGTNIGEAHLGDLSEGVGKAIKEAG 60
DB 1 MKPQGPLACLLALCLGSGEAGPLQSGESTGTNIGEAHLGDLSEGVGKAIKEAG 60
QY 61 GAAGSKVSEALGQGTREAVGTGVQVPGFAGADALGNRVGEAAHALGNTGHEIGROAEDV 120
DB 61 GAAGSKVSEALGQGTREAVGTGVQVPGFAGADALGNRVGEAAHALGNTGHEIGROAEDV 120
QY 121 IRGADAVRGSWQGVPHSGAWETSGHGI FGSGGLGGQGNPGLGTPWVHGYPGNS 180
DB 121 IRGADAVRGSWQGVPHSGAWETSGHGI FGSGGLGGQGNPGLGTPWVHGYPGNS 180
QY 181 AGSFGMNPQAGPWQGGNGGPPNFGTNTQGAVAQPGYGVRSNQNQEGCTNPPPSGGG 240
DB 181 AGSFGMNPQAGPWQGGNGGPPNFGTNTQGAVAQPGYGVRSNQNQEGCTNPPPSGGG 240
QY 241 SSSNGSGSGSQSGSGSGSGNDNNGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSG 300
DB 241 SSSNGSGSGSQSGSGSGSGSGNDNNGSSSGSGSGSGSGSGSGSGSGSGSGSGSG 296
QY 301 RGDGSESSWGSGTSGSSNGHGGGGGKHGPKCEKPGNEARGSGSGIQGFRGQGVSSN 360
DB 297 RGDGSESSWGSGTSGSSNGHGGGGGKHGPKCEKPGNEARGSGSGIQGFRGQGVSSN 346
QY 361 MREISKEGNLLGGSDNYRGQSSWGSGGDAVGGVNTVNSSETSGMNFDTFWKNEKS 420
DB 347 -----NSETSGMNFDTFWKNEKS 366
QY 421 KLGFINWDAINKDQ 434
DB 367 KLGFINWDAINKDQ 380

RESULT 3
Q6E0U6 PRELIMINARY; PRT; 517 AA.
AC Q6E0U6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Dermokine-beta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15234001; DOI=10.1016/j.ygeno.2004.03.010;
RA Matsui T., Hayashi-Kisumi F., Kinoshita Y., Katahira S., Morita K.,
RA Miyachi Y., Ono Y., Inai T., Tanigawa Y., Komiya T., Tsukita S.;
RT "Identification of novel keratinocyte-secreted peptides dermokine-
RT alpha/-beta and a new stratified epithelium-secreted protein gene
RL Genomics 84:384-397(2004).
DR EMBL; AY622963; AAT68267.1; -.
SQ SEQUENCE 517 AA; 51660 MW; 61E2974EEB36650B CRC64;

Query Match 44.1%; Score 1043; DB 2; Length 517;
Best Local Similarity 48.9%; Pred. No. 1.3e-41;
Matches 231; Conservative 41; Mismatches 102; Indels 98; Gaps 13;

QY 1 MKPQGPLACLLALCLGSGEAGPLQSGESTGTNIGEAHLGDLSEGVGKAIKEAG 60
DB 1 MKLQGSGLACLLALCLGSGAANPLHSGEGTGA----SAAHGAGDAISHGIGEAVGQGA 56
QY 61 GAAGSKVSEALGQGTREAVGTGVQVPGFAGADALGNRVGEAAHALGNTGHEIGROAEDV 120
DB 57 EAASSGIQNALQGGHGEESTLMSRG-----DVFHRLGEAARSIGNAGNELGROAEDI 112
QY 121 IRGADAVRGSWQGVPHSGAWETSGHGI FGSGGLGGQGNPGLGTPWVHGYPGNS 180
DB 113 IRQGVDAVH-----NAGSMTSGHGAYSQGGAG--VQGNPGQGTPTMASG----- 157
QY 181 AGSFGMNPQAGPWQGGNGGPPNFGTNTQGAVAQPGYGVRSNQNQEGCTNPPPSGS 237
DB 158 -GNYGTNLSGGVGGGNGGGLNYETNAQGAQPGYGTVRGNQNSGCTNPPPSGSHS 216
QY 238 ---GGSSGSSNGG-GSGSQSGSGSGSGNG-----DNNNGSSGSGSGSGSGSGSGSS 286
DB 217 FNSGSGSSNDGSGSGSGSHSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGNS 274
QY 287 GSGSGSGSSNGG-----GSRGDSGSESSWGSGSGSGSGSGSGSGSGSGSGSGSG 325
DB 275 GNSNSGNSGNSGSGSRDIETSNFDEGYSVSRGTGSRGSGG-----GSGGSGSGSGSG 329
QY 326 GGNHGPCKEKPNEARGSGESGIQGRGQGVSSNWEISKEGNLLGSGSDNYRGQSS 385
DB 330 GGN--KPECNPNQNDVRMAGSGSQ-----GSGSGSGSGSGSGSGSGSGSGSGSG 357
QY 386 WSGSGGDAVGGVNTVNSSETSGMNFDTFWKFKSLGFINWDAINKDQSS 437
DB 358 GGNIQKEAVNGLTWNDSASTLPFNIDNFWNLKSKTRFINWDAINKHAPS 409

RESULT 4
Q6P253 PRELIMINARY; PRT; 508 AA.
AC Q6P253;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 1110014F24Rik protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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[1]
RN  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Embryo;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA  Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Small U., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RL  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Embryo;
RX  Strausberg R.;
RL  Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC064724; AAH64724.1; -.
DR  GO; GO:0005615; C:extracellular space; TAS.
SQ  SEQUENCE 508 AA; 51057 MW; 1B7913E7275A1926 CRC64;

Query Match 43.9%; Score 1038.5; DB 2; Length 508;
Best Local Similarity 50.0%; Pred. No. 2.1e-41;
Matches 229; Conservative 44; Mismatches 106; Indels 79; Gaps 13;

QY  1 MKPQGPLACLLALCLGSGAGPLQSGEESTGTNIGEGALGHGDLSEGVGKAIGKEAG 60
DB  1 MKLQGSLLACLLALCLGGAANPLHSGGEGTGA----SAAHGAGDAISHGIGAVGQAK 56

QY  61 GAAGSKVSEALGQGTREAVGTGVRVPGFAADALGNRVEAAHALGNTGHEIGRAQEDV 120
DB  57 EAASSGIQNALGQGHGEGSTLMGSRG----DVFEHRLGEAAARSILGNAGNEIGKQAEI 112

QY  121 IRHGADAVRGSGVQVPGHSGAWETSGHGIFGSGQGLGQGGQGNPGGLGTPFWHGYPGNS 180
DB  113 IRQGVDAVH-----NAGSWGTSGGHGYGSGGAG--VQGNPQGTPTWASG----- 157

QY  181 AGSFGMNPQAGPQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGS 237
DB  158 -GNYGTNSLGGSVGQGGNGGGLDYETNAQGAQPGYGTGVRGNQNSGCTNPPPSGSHS 216

QY  238 ---GGSSNSGG--GSGSQSGSSGSGNG-----DNNNGSSGSSGSSGSSGSSGSS 286
DB  217 FNSNGSSNDGSRGSGSHGSGNGQSGRGGGQGNNDNGSSS--SSSGNSGNSGNS 274

QY  287 GSGSGSSGSGNSG--GSRGDSGSEBSWGSSTGSSSGNHGSGGGNGHKGPCCKPGNEARGSG 345
DB  275 GNSNSGNSGNSGSGSRG-----TGSRGSGSGSGSGGSGGNGKPECNPNPGNDRMAG 323

QY  346 ESGIQGPRGQGVSSNMREISKEGNRLGGSDNYRGQSGSGSGGDAVGVVNTVNSETS 405
DB  324 GSGSQ-----GHGNSGNGNIQKEAVNGLNTMSDAS 353

QY  406 PGMFNEDTFFWKNFKSLGFINWDINKDQSS 437
DB  354 TLPFNIDNFWENLKSRTFINWDINKHAPS 385

RESULT 6
Q6SZJ9 ID Q8C4L6 PRELIMINARY; PRT; 407 AA.
OS  Q8C4L6 ID Q8C4L6 PRELIMINARY; PRT; 407 AA.
DT  01-MAR-2003 (TREMBlrel. 23, Created)
DT  01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE  library, clone:Cl30074A08 product:inferred:RIKEN cDNA
DE  1110014F24.
GN  Name=1110014F24Rik;
OS  Mus musculus (Mouse).
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Q6SZJ9;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Epidermis-specific secreted protein SK89 precursor.
OS  Mus musculus (Mouse)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RC  SEQUENCE FROM N.A.
RP  STRAIN=CD1;
RA  Moffatt P., Salois P., St-Amant N., Gaumont M.-H., Lanctot C.;
RT  "Identification of a conserved cluster of skin-specific genes encoding
RT  secreted proteins.";
RL  Gene 334:123-131(2004).
DR  EMBL; AY444557; AAR20796.1; -.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  InterPro; IPR02952; Eggshell.
DR  PRINTS; PR01228; EGGSHELL.
KW  Signal.
FT  SIGNAL 1 22 Potential.
SQ  SEQUENCE 493 AA; 49338 MW; 59A94D74FALC5978 CRC64;

Query Match 43.8%; Score 1030; DB 2; Length 493;
Best Local Similarity 49.6%; Pred. No. 5.1e-41;
Matches 224; Conservative 45; Mismatches 101; Indels 82; Gaps 12;

QY  1 MKPQGPLACLLALCLGSGAGPLQSGEESTGTNIGEGALGHGDLSEGVGKAIGKEAG 60
DB  1 MKLQGSLLACLLALCLGGAANPLHSGGEGTGA----SAAHGAGDAISHGIGAVGQAK 56

QY  61 GAAGSKVSEALGQGTREAVGTGVRVPGFAADALGNRVEAAHALGNTGHEIGRAQEDV 120
DB  57 EAASSGIQNALGQGHGEGSTLMGSRG----DVFEHRLGEAAARSILGNAGNEIGKQAEI 112

QY  121 IRHGADAVRGSGVQVPGHSGAWETSGHGIFGSGQGLGQGGQGNPGGLGTPFWHGYPGNS 180
DB  113 IRQGVDAVH-----NAGSWGTSGGHGYGSGGAG--VQGNPQGTPTWASG----- 157

QY  181 AGSFGMNPQAGPQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGS 237
DB  158 -GNYGTNSLGGSVGQGGNGGGLDYETNAQGAQPGYGTGVRGNQNSGCTNPPPSGSHS 216

QY  238 ---GGSSNSGG--GSGSQSGSSGSGNG-----DNNNGSSGSSGSSGSSGSSGSS 286
DB  217 FNSNGSSNDGSRGSGSHGSGNGQSGRGGGQGNNDNGSSS--SSSGNSGNSGNS 274

QY  287 GSGSGSSGSGNSG--GSRGDSGSEBSWGSSTGSSSGNHGSGGGNGHKGPCCKPGNEARGSG 345
DB  275 GNSNSGNSGNSGSGSRG-----TGSRGSGSGSGSGGSGGNGKPECNPNPGNDRMAG 323

QY  346 ESGIQGPRGQGVSSNMREISKEGNRLGGSDNYRGQSGSGSGGDAVGVVNTVNSETS 405
DB  324 GSGSQ-----GHGNSGNGNIQKEAVNGLNTMSDAS 353

QY  406 PGMFNEDTFFWKNFKSLGFINWDINKDQSS 437
DB  354 TLPFNIDNFWENLKSRTFINWDINKHAPS 385

RESULT 6
Q6SZJ9 ID Q8C4L6 PRELIMINARY; PRT; 407 AA.
OS  Q8C4L6 ID Q8C4L6 PRELIMINARY; PRT; 407 AA.
DT  01-MAR-2003 (TREMBlrel. 23, Created)
DT  01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE  library, clone:Cl30074A08 product:inferred:RIKEN cDNA
DE  1110014F24.
GN  Name=1110014F24Rik;
OS  Mus musculus (Mouse).
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Db 675 ---GLDGGTGGGAGGSGGAWAGNGGTGGAGGTGGVGGTGGSGSDGVNGSSAGADGHPG 731
Qy 167 GLGTPWVHGYPGNSAGSFGMNPQ-----APWGGGNGGPPNFCTN-----TOG 210
Db 732 GTGGVGTGGKGGDGGGAAPNGVAGSQCPGAGGDDGTGGVGGNGRIGDADGATAG 791
Qy 211 AVAQPVGVSRAVNQNEGCTNPP-----PSGS-----CGSSNSGGSGSGSGSGSGSGND 262
Db 792 ARGQDGGAGGAGGKGRGGTGGPGAGPAGTTGSGAGGNGSGGCTGGDPDGGGNGANGS 851
Qy 263 ---NNNGSSSGSGSGSGSGSGSGSG-----GSS-----CGSSNSG----- 298
Db 852 VFTNNGTGGNGGNGAGPSGAGSGGAGSTFGATGSSSIHVNGGNGGNGDHALSG 911
Qy 299 -GSRGDSGSSSGSGSGSGSGSGSG-----CGNGHKPGCEKPGNEARGSGSGSI 349
Db 912 NGAAGGNGGNGGSLRSGSGAGGNGGNGASRCMGDDGTGGAGGNAQIINGGAGGN 971
Qy 350 QGFRGQGVSNMREISKEGNR-----LLGSGDNYRGSGSGSGSGSGSGDAVGGV---NTVNS 402
Db 972 GGDGGTGSNPGAITGSGGRGDDGGVGGGSGSVAGDAGDGRGAGGTGGTGLRGTGA 1031
Qy 403 ETSFGMFN 410
Db 1032 TGATGTFD 1039

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## RESULT 12

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Q6MX28 ID Q6MX28 PRELIMINARY; PRT; 1306 AA.
AC Q6MX28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS7; OrderedLocustNames=Rv0578c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Tekaita F., Badcock K., Banham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL; BX842573; CAB55300.1; -.
DR TuberculList; Rv0578c; -.
DR InterPro; IPR002952; Eggehell.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR000084; PE_region_N.
DR InterPro; IPR002173; PfkB.
DR Pfam; PF00934; PE; 1.
DR PRINTS; PR01228; EGGSHELL.
DR ProDom; PD001223; PE_region_N; 1.
DR PROSITE; PS00583; PFKB_KINASES; UNKNOWN_2.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1306 AA; 105964 MW; 843A30955FFA56B6 CRC64;

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Query Match 18.6%; Score 439.5; DB 2; Length 1306;  
 Best Local Similarity 30.9%; Pred. No. 5.1e-13;  
 Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

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Qy 17 GSGEAGPELOSGBESTGTN---IGBALGHGLDALSEGVGKAIGK-----EACGAAGSKV 67
Db 567 GHCAAGAL-----GVNGVGAGGCHG-GD---PGVGGAGGCGSGSTPCANGAPCNTP 615
Qy 68 SEA--LGGTREAIVGTQVQVPGFADALCNRVGE-AAHALGNTGHE-----TGRQAEV 120
Db 616 TSCGNGNGNGRGADATGFGQTGASGGRGDDGLVNGGAGGAGNGSKGLPGLRGLGNP- 674
Qy 121 IRRHADAVRGSWMGVPHSGAWETSGHGIFGSGGGLGGQ-----CGNPG 166
Db 675 ---GLDGGTGGNGAGSGSGAWAGNGGTGGAGGTGGVGGTGGSGSDGVNGSSAGADGHPG 731
Qy 167 GLGTPWVHGYPGNSAGSFGMNPQ-----APWGGGNGGPPNFCTN-----TOG 210
Db 732 GTGGVGTGGKGGDGGGAAPNGVAGSQCPGAGGDDGTGGVGGNGRIGDADGATAG 791
Qy 211 AVAQPVGVSRAVNQNEGCTNPP-----PSGS-----CGSSNSGGSGSGSGSGSGND 262
Db 792 ARGQDGGAGGAGKGRGGTGGPGAGPAGTTGSGAGGNGSGGCTGGDPDGGGNGANGS 851
Qy 263 ---NNNGSSSGSGSGSGSGSGSGSG-----GSS-----CGSSNSG----- 298
Db 852 VFTNNGTGGNGGNGAGPSGAGSGGAGSTFGATGSSSIHVNGGNGGNGDHALSG 911
Qy 299 -GSRGDSGSSSGSGSGSGSGSGSG-----CGNGHKPGCEKPGNEARGSGSGSI 349
Db 912 NGAAGGNGGNGGSLRSGSGAGGNGGNGASRCMGDDGTGGAGGNAQIINGGAGGN 971
Qy 350 QGFRGQGVSNMREISKEGNR-----LLGSGDNYRGSGSGSGSGSGDAVGGV---NTVNS 402
Db 972 GGDGGTGSNPGAITGSGGRGDDGGVGGGSGSVAGDAGDGRGAGGTGGTGLRGTGA 1031
Qy 403 ETSFGMFN 410
Db 1032 TGATGTFD 1039

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## RESULT 13

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Q7UIQ7 ID Q7UIQ7 PRELIMINARY; PRT; 1306 AA.
AC Q7UIQ7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS7; OrderedLocustNames=Mb0593c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248336; CAD93455.1; -.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR000084; PE_region_N.
DR InterPro; IPR002173; PfkB.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region_N; 1.
DR PROSITE; PS00583; PFKB_KINASES; UNKNOWN_2.
DR PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1306 AA; 105994 MW; 65628FB401F4AD42 CRC64;

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Query Match 18.6%; Score 439.5; DB 2; Length 1306;

Best Local Similarity 30.9%; Pred. No. 5.le-13;  
Matches 151; Conservative 34; Mismatches 194; Indels 109; Gaps 22;

QY 17 GSCEAGPLOSGBESTGTN--IGALGHGLDALSGBGVKAIGK-----EAGGAGSKV 67  
DB 17 GSCEAGPLOSGBESTGTN--IGALGHGLDALSGBGVKAIGK-----EAGGAGSKV 67  
QY 567 GHGAAGAL-----GVNGGVGAGHG-GD---PGVGGAGGGSGSTPGANGAPNTP 615  
DB 567 GHGAAGAL-----GVNGGVGAGHG-GD---PGVGGAGGGSGSTPGANGAPNTP 615  
QY 68 SEA--LQOGTREAIVGTGVRVPGFMAADALGNRVE-AAHALGNTGHE----IGRQAEV 120  
DB 68 SEA--LQOGTREAIVGTGVRVPGFMAADALGNRVE-AAHALGNTGHE----IGRQAEV 120  
QY 616 TSGNGNGNGRGADATGFGQTGASGGRGGGLVNGGAGGAGGNSKGLPLGLRLGNP- 674  
DB 616 TSGNGNGNGRGADATGFGQTGASGGRGGGLVNGGAGGAGGNSKGLPLGLRLGNP- 674  
QY 121 IRHGADAVRSGWQVPGHSGAWETSGGHGIFGSGGLGGQ-----QGNPG 166  
DB 121 IRHGADAVRSGWQVPGHSGAWETSGGHGIFGSGGLGGQ-----QGNPG 166  
QY 675 --GLDGGTGGNGGAGSGGAWAGNGGTGAGGTGGVGTGGSGSDGVNGSSAGADHPG 731  
DB 675 --GLDGGTGGNGGAGSGGAWAGNGGTGAGGTGGVGTGGSGSDGVNGSSAGADHPG 731  
QY 167 GLGTTPWHVHGPNSAGSFGMNPQ-----APWCGGNGGPPNPTN-----TQG 210  
DB 167 GLGTTPWHVHGPNSAGSFGMNPQ-----APWCGGNGGPPNPTN-----TQG 210  
QY 732 GTGGVGTGGKGGDGGDGAAPNGVAGSQGPGAGGDDGTGGVGGNGGRGIDGADGATAG 791  
DB 732 GTGGVGTGGKGGDGGDGAAPNGVAGSQGPGAGGDDGTGGVGGNGGRGIDGADGATAG 791  
QY 211 AVAQPVGVSVRASNQNEGCTNPP-----PSGS-----GGSSNSGGSGSQSGSGSNGD 262  
DB 211 AVAQPVGVSVRASNQNEGCTNPP-----PSGS-----GGSSNSGGSGSQSGSGSNGD 262  
QY 792 ARQDGGAGAGAGKGRGTGGFGGAGPAGTTTSGAGGNGSGSGGTGGDPDGGNGANGS 851  
DB 792 ARQDGGAGAGAGKGRGTGGFGGAGPAGTTTSGAGGNGSGSGGTGGDPDGGNGANGS 851  
QY 263 --NNNGSSSGSGSSSGSSSGSSG-----GSS-----GGSSNSG----- 298  
DB 263 --NNNGSSSGSGSSSGSSSGSSG-----GSS-----GGSSNSG----- 298  
QY 852 VFTNNGIGGNGGNGAGPSGAGSGGAGSTFGATGSSSIHVNGGNGGNGDHALSG 911  
DB 852 VFTNNGIGGNGGNGAGPSGAGSGGAGSTFGATGSSSIHVNGGNGGNGDHALSG 911  
QY 299 -GSRGDSGSSWSSTGS--SSNHGSG-----GNGHKFGCEKPGNEARGSGSGI 349  
DB 299 -GSRGDSGSSWSSTGS--SSNHGSG-----GNGHKFGCEKPGNEARGSGSGI 349  
QY 912 NGAAGNGGNGGNGSLRSGGAGGAGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 971  
DB 912 NGAAGNGGNGGNGSLRSGGAGGAGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 971  
QY 350 QGPRGQGVSSNMRISKEGNNR-----LLGGSGDNVRGQSGSWGSGGDAVGGV---NTVNS 402  
DB 350 QGPRGQGVSSNMRISKEGNNR-----LLGGSGDNVRGQSGSWGSGGDAVGGV---NTVNS 402  
QY 972 GGGGTGSDGNPCAITGSGGRGGDGGVGGGCGSVAGDAGCGGAGGTGGTGLRTTGA 1031  
DB 972 GGGGTGSDGNPCAITGSGGRGGDGGVGGGCGSVAGDAGCGGAGGTGGTGLRTTGA 1031  
QY 403 ETSPGMFN 410  
DB 1032 TGATGTFD 1039

RESULT 14  
Q7SEP7  
ID Q7SEP7 PRELIMINARY; PRT; 725 AA.  
AC Q7SEP7  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Predicted protein.  
GN Names=NCU02170.1;  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OR74A;  
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,  
Kryzofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,  
Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,  
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
Nativig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
RL Nature 0:0-0(2003).

-!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AABX01000029; EAA35293.1; -.  
DR InterPro: IPR002086; Aldehyd dehydrog.  
DR InterPro: IPR002952; Eggshell.  
DR PRINTS: PRO1228; EGGSHLL.  
DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN 1.  
SQ SEQUENCE 725 AA; 63929 MW; 60F0003860219B9C CRC64;

Query Match 18.3%; Score 433; DB 2; Length 725;  
Best Local Similarity 29.8%; Pred. No. 6.4e-13;  
Matches 137; Conservative 46; Mismatches 173; Indels 104; Gaps 20;

QY 17 GSCEAGPLOSGBESTGTNIGALGHGLDALSGBGVKAIGKAGGAGSKVSEALQOGTR 76  
DB 185 GSG-LGFPAGAGAGYNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAG 243  
QY 77 EAVGTGVRVPGFQ-----AADALGNRVGAAHALGNTGHEIGRQAEVIRHGADAV 128  
DB 244 N--GLGVNGIGLGNSSAGSLGDSGAYGNGAG-AGNGAGNGG--LG----- 284  
QY 129 RGSWQGV-PHSGAWETSGHG-IFGSGGLGGGOGNPGGLGTPWHVHGPNSAGSFGM 186  
DB 285 NGSNGGLNGGSGCANNGMGMDGCSGMGGAGGPG--GGAGGLNG--ASGPGNGVGG 341  
QY 187 NPQGAPWGGGNGGPPNFTGNTQGAQVAPQGYSVRASNQNEGCTN-----PPPSGSG 238  
DB 342 GAGGLGYSGGPGCGGTGNGNGNIGASNNNGNSAGNGNNNGSGNGAGSGAPCPDNG 401  
QY 239 GGSNSGGSG 276  
DB 402 NNGN--GNGGNGNGAGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 460  
QY 277 -----SSGSSSG 519  
DB 461 IGTPSPAIVPGSGAGNGGNGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 367  
QY 326 GGNHKGPKCEKPGNEARGSGSGIQG-----FRGQGVSSNM-----REISKE---- 367  
DB 520 NNGN-----GNDG-AGNGGAPAPTCPGTGSGPSSFLVLTITVTPQARVVEKKQYWN 571  
QY 368 GNRLLGGSGDNVRGQSGSWGSGGDAVGGVNTVNSGTPG 407  
DB 572 ANVMAYGGPDD--GAGAAPGSGSGVAPGNGGNGSGSAPG 609

RESULT 15  
Q6C6W0  
ID Q6C6W0 PRELIMINARY; PRT; 1391 AA.  
AC Q6C6W0;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|P08640|Saccharomyces cerevisiae YIR019c STAI  
DE extracellular alpha-1.  
GN ORFNames=YALIOE05819g;  
OS Yarrowia lipolytica CLIB99.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodascaceae; Yarrowia.  
OX NCBI\_TaxID=284591;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,  
Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,  
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,







GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 15, 2005, 06:06:39 ; Search time 4843 Seconds  
(without alignments)  
4402.291 Million cell updates/sec

Title: US-10-063-699-52

Perfect score: 2363

Sequence: 1 MKPQGLACLLALCLSGE.....KLGFINDAINKDQRSRIP 440

Scoring table: BLOSUM62

Gapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-O=/cgn2.1/USPTO spool\_p/US10063699/runat\_12052005\_103528\_15798/app.query.fasta\_1.583  
-DB=GenEmbl -QFMT=fastap -SURFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2363	100.0	1734	6	AX0923320 Sequence
2	2363	100.0	1734	6	AX358902 Sequence
3	2363	100.0	1734	6	AX362395 Sequence
4	2363	100.0	1734	6	AX376134 Sequence

5	2363	100.0	1734	6	AX403750	AX403750 Sequence
6	2363	100.0	1734	6	AX454564	AX454564 Sequence
7	2363	100.0	1734	6	AX491042	AX491042 Sequence
8	2363	100.0	1734	6	AX696983	AX696983 Sequence
9	2363	100.0	1734	6	AX358412	AX358412 Homo sapi
10	2030	85.9	1441	6	BD275935	BD275935 62 Human
11	1996	84.5	1431	9	AY622965	AY622965 Homo sapi
12	1396	84.5	1982	9	BC035311	BC035311 Homo sapi
13	1330.5	56.3	11311	9	AC138125	AC138125 Homo sapi
14	1330.5	56.3	46275	9	AC002389	AC002389 Human DNA
15	1043	44.1	1554	10	AY622963	AY622963 Mus muscu
16	1038.5	43.9	2044	10	BC064724	BC064724 Mus muscu
17	1030	43.6	1947	10	AY444557	AY444557 Mus muscu
18	997.5	42.2	888	6	CQ721208	CQ721208 Sequence
19	669	28.3	914	6	BD206280	BD206280 Human nuc
20	669	28.3	914	6	AR400595	AR400595 Sequence
21	669	28.3	914	6	AX013099	AX013099 Sequence
22	613	25.9	154673	2	AC079472	AC079472 Mus muscu
23	591.5	25.0	253523	2	AC126062	AC126062 Rattus no
24	494.5	20.9	110000	8	CR380958_00	CR380958 Candida g
25	486	20.6	110000	8	CR380956_01	Continuation (2 of
26	471	19.9	940	9	BC004493	BC004493 Homo sapi
27	471	19.9	110000	8	CR382127_06	Continuation (7 of
28	468	19.8	163553	5	BX640403	BX640403 Zebrafish
29	468	19.8	170632	2	BX927206	BX927206 Danio rer
30	468	19.8	212555	2	BX640460	BX640460 Danio rer
31	461.5	19.5	161474	2	AC144356	AC144356 Danio rer
32	460.5	19.5	175348	5	BX548049	BX548049 Zebrafish
33	460.5	19.5	316050	1	BX248346	BX248346 Mycobacte
34	460	19.5	170509	2	AL928714	AL928714 Zebrafish
35	456	19.3	152340	2	CR396595	CR396595 Danio rer
36	456	19.3	157585	5	BX322664	BX322664 Zebrafish
37	451.5	19.1	214693	2	CR846093	CR846093 Danio rer
38	451	19.1	186499	2	CR382373	CR382373 Danio rer
39	450.5	19.1	110000	1	AE000516_39	Continuation (40 o
40	450.5	19.1	349606	1	BX842583	BX842583 Mycobacte
41	450	19.0	169572	2	BX957333	BX957333 Danio rer
42	448.5	19.0	158667	2	AX465851	AX465851 Danio rer
43	448	19.0	41185	9	HGB1LIC6	AL049849 Homo sapi
44	447	18.9	187101	9	AL589862	AL589862 Human DNA
45	445.5	18.9	277991	2	BX950222	BX950222 Danio rer
46	445.5	18.9	278040	5	AL954847	AL954847 Zebrafish
47	444	18.8	185549	2	BX927317	BX927317 Danio rer
48	442.5	18.7	186246	5	BX548008	BX548008 Zebrafish
49	442.5	18.7	215607	5	BX569798	BX569798 Zebrafish
50	442.5	18.7	225024	2	CR394539	CR394539 Danio rer
51	442.5	18.7	276484	1	CR762405	CR762405 Danio rer
52	442	18.7	349563	1	BX842582	BX842582 Mycobacte
53	441.5	18.7	161099	5	BX322608	BX322608 Zebrafish
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57	440	18.6	186979	2	CR631129_06	Continuation (7 of
58	439.5	18.6	110000	1	AE000516_06	Continuation (7 of
59	439.5	18.6	159007	5	AL935180	AL935180 Zebrafish
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63	437.5	18.5	232621	2	BX936449	BX936449 Danio rer
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69	433.5	18.3	178723	2	CR450794	CR450794 Danio rer
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75	428	18.1	110000	1	BX571965_10	Continuation (11 o
76	428	18.1	168607	5	BX255919	BX255919 Zebrafish
77	428	18.1	308050	1	BX248345	BX248345 Mycobacte

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79	427.5	18.1	130040	2	CR847502	CR847502 Danio rer	152	406.5	17.2	1075	6	CQ180991	CQ180991 Sequence
80	426.5	18.0	110000	8	CR382128_13	Continuation (14 o	153	406.5	17.2	1075	6	CQ205355	CQ205355 Sequence
81	426.5	18.0	166935	2	BX323830	BX323830 Danio rer	154	406.5	17.2	1075	6	CQ228754	CQ228754 Sequence
82	426	18.0	110000	1	CP000010_23	Continuation (24 o	155	406.5	17.2	1075	6	CQ266896	CQ266896 Sequence
83	426	18.0	149349	2	CR908739	CR908739 Danio rer	156	406.5	17.2	1075	6	CQ303869	CQ303869 Sequence
84	425.5	18.0	173312	5	BX324201	BX324201 Danio rer	157	406.5	17.2	1075	6	CQ341185	CQ341185 Sequence
85	424.5	18.0	161366	5	BX005382	BX005382 Zebrafish	158	406.5	17.2	162269	9	AC000097	AC000097 Homo sapi
86	423.5	17.9	19311	8	AT450929	AT450929 Chlamydom	159	406.5	17.2	167390	9	AC007263	AC007263 Homo sapi
87	423.5	17.9	103270	8	ATFIN20	ATFIN20 Arabidops	160	406	17.2	173570	2	CR457484	CR457484 Danio rer
88	423.5	17.9	196247	8	ATCHRIV56	AL161556 Arabidops	161	405.5	17.2	1403	6	CQ051669	CQ051669 Sequence
89	422.5	17.9	120185	8	AC007138	AC007138 Arabidops	162	405.5	17.2	1403	6	CQ066726	CQ066726 Sequence
90	422.5	17.9	149817	2	BX571897	BX571897 Danio rer	163	405.5	17.2	1403	6	CQ093768	CQ093768 Sequence
91	422.5	17.9	176010	1	AL935062	AL935062 Zebrafish	164	405.5	17.2	1403	6	CQ132545	CQ132545 Sequence
92	422.5	17.9	184427	14	EHVU20824	U20824 Equine herp	165	405.5	17.2	1403	6	CQ171117	CQ171117 Sequence
93	422.5	17.9	198220	8	ATCHRIV5	AL161493 Arabidops	166	405.5	17.2	1403	6	CQ200252	CQ200252 Sequence
94	422	17.9	184543	5	BX571681	BX571681 Zebrafish	167	405.5	17.2	1403	6	CQ215756	CQ215756 Sequence
95	421.5	17.8	110000	8	CR382131_06	Continuation (7 of	168	405.5	17.2	1403	6	CQ254334	CQ254334 Sequence
96	421	17.8	176142	2	CR388010	CR388010 Danio rer	169	405.5	17.2	1403	6	CQ291368	CQ291368 Sequence
97	420.5	17.8	199910	5	AL928725	AL928725 Zebrafish	170	405.5	17.2	1403	6	CQ328471	CQ328471 Sequence
98	420	17.8	211219	2	CR790363	CR790363 Danio rer	171	405.5	17.2	184929	9	AC058790	AC058790 Homo sapi
99	418	17.7	135684	2	BX784399	BX784399 Danio rer	172	405.5	17.2	189270	2	CR846096	CR846096 Danio rer
100	418	17.7	188037	5	BX545913	BX545913 Zebrafish	173	404.5	17.1	37586	6	AX191745	AX191745 Sequence
101	417.5	17.7	194481	2	CR293529	CR293529 Danio rer	174	404.5	17.1	75657	9	HSB1117C8	Continuation (25 o
102	417.5	17.7	208136	2	CR391991	CR391991 Danio rer	175	404.5	17.1	110000	1	AE000516_24	Continuation (13 o
103	416	17.6	167254	9	CNS05TDS	AL357093 Human chr	176	404.5	17.1	346186	1	BX842578	MYcobacte
104	416	17.6	216208	5	BX248122	BX248122 Zebrafish	177	404	17.1	170295	5	BX663508	Zebrafish
105	415.5	17.6	180645	2	CR376781	CR376781 Danio rer	178	403	17.1	110000	8	CR382125_12	Continuation (13 o
106	415	17.6	144093	10	AC109193	AC109193 Mus muscu	179	402.5	17.0	2580	10	AY497550	Mus muscu
107	414	17.5	146704	2	CR774192	CR774192 Danio rer	180	401.5	17.0	97839	2	AC141520	Rattus no
108	414	17.5	154153	9	AL445933	AL445933 Human DNA	181	401.5	17.0	214001	5	BX511164	Zebrafish
109	414	17.5	167376	5	BX004803	BX004803 Zebrafish	182	401	17.0	3281	2	AC143602	Macaca mu
110	413.5	17.5	239613	2	CR790367	CR790367 Danio rer	183	401	17.0	183902	5	BX323815	Zebrafish
111	413	17.5	103576	8	YUR8H12	AC000098 Arabidops	184	401	17.0	322091	2	CR381647	Danio rer
112	413	17.5	247221	2	BX470211	BX470211 Arabidops	185	400.5	16.9	145427	5	BX276112	Zebrafish
113	412.5	17.5	1452	6	AX751813	AX751813 Sequence	186	399.5	16.9	122934	9	AC092898	Homo sapi
114	412	17.4	202327	2	BX571942	BX571942 Danio rer	187	399.5	16.9	349306	1	BX842575	MYcobacte
115	411	17.4	121112	9	AC124319	AC124319 Homo sapi	188	399	16.9	7135	4	AF000949	Canis fam
116	410.5	17.4	124244	10	AL929026	AL929026 Mouse DNA	189	398	16.8	157152	10	AC114679	Mus muscu
117	409.5	17.3	110000	1	AE000516_11	Continuation (12 o	190	398	16.8	189019	5	BX465205	Zebrafish
118	409.5	17.3	215607	2	CR678456	CR678456 Danio rer	191	398	16.8	203947	2	BX324126	Danio rer
119	408.5	17.3	1635	6	CQ057625	CQ057625 Sequence	192	398	16.8	203947	2	BX248337	MYcobacte
120	408.5	17.3	1635	6	CQ076913	CQ076913 Sequence	193	397.5	16.8	327650	9	AC087455	Homo sapi
121	408.5	17.3	1635	6	CQ107909	CQ107909 Sequence	194	397.5	16.8	185644	9	AC087455	MYcobacte
122	408.5	17.3	1635	6	CQ146551	CQ146551 Sequence	195	397	16.8	327650	1	BX248337	MYcobacte
123	408.5	17.3	1635	6	CQ181991	CQ181991 Sequence	196	397	16.8	2694	3	AY566305	Agelenops
124	408.5	17.3	1635	6	CQ206364	CQ206364 Sequence	197	396	16.8	180309	10	AL590873	Mouse DNA
125	408.5	17.3	1635	6	CQ229773	CQ229773 Sequence	198	395	16.7	306550	1	BX248342	MYcobacte
126	408.5	17.3	1635	6	CQ267909	CQ267909 Sequence	199	395	16.7	110000	1	AE000516_27	Continuation (28 o
127	408.5	17.3	1635	6	CQ304933	CQ304933 Sequence	200	395	16.7	185541	5	BX649638	Zebrafish
128	408.5	17.3	1635	6	CQ342167	CQ342167 Sequence	201	395	16.7	240931	2	AC107097	Rattus no
129	408.5	17.3	1635	6	CQ052617	CQ052617 Sequence	202	394.5	16.7	346051	1	BX842580	MYcobacte
130	408.5	17.3	1635	6	CQ067689	CQ067689 Sequence	203	394	16.7	178405	5	EX005017	Zebrafish
131	408.5	17.3	19373	6	CQ094745	CQ094745 Sequence	204	393	16.6	228056	2	AC144061	Macaca mu
132	408.5	17.3	19373	6	CQ133505	CQ133505 Sequence	205	393	16.6	167830	2	CR384108	Danio rer
133	408.5	17.3	19373	6	CQ172075	CQ172075 Sequence	206	393	16.6	199378	2	AC108256	Rattus no
134	408.5	17.3	19373	6	CQ201223	CQ201223 Sequence	207	392.5	16.6	308050	1	BX248345	MYcobacte
135	408.5	17.3	19373	6	CQ216736	CQ216736 Sequence	208	392.5	16.6	110000	1	AE000516_10	Continuation (11 o
136	408.5	17.3	19373	6	CQ255305	CQ255305 Sequence	209	392.5	16.6	125402	9	AC114815	Homo sapi
137	408.5	17.3	19373	6	CQ292390	CQ292390 Sequence	210	392	16.6	110000	3	AF226688	Bombyx mo
138	408.5	17.3	19373	6	CQ329411	CQ329411 Sequence	211	392	16.6	80009	3	AF226688	Continuation (17 o
139	408.5	17.3	168239	9	AC007663	AC007663 Homo sapi	212	392	16.6	110000	1	AE000516_37	Continuation (38 o
140	408.5	17.3	174840	9	AC006549	AC006549 Homo sapi	213	392	16.6	187126	10	AC113315	Mus muscu
141	408.5	17.3	179269	9	AC006547	AC006547 Homo sapi	214	392	16.6	348264	1	BX842576	MYcobacte
142	408.5	17.3	190374	5	BX088726	BX088726 Zebrafish	215	392	16.6	349563	1	BX842582	MYcobacte
143	408.5	17.3	223311	2	AC094165	AC094165 Rattus no	216	391.5	16.6	155665	5	BX247944	Zebrafish
144	408	17.3	200574	10	BX005304	BX005304 Mouse DNA	217	391.5	16.6	197771	2	CR847901	Danio rer
145	407.5	17.2	110000	2	CR381548_1	Continuation (2 of	218	391	16.5	110000	2	BX649395_0	Danio rer
146	407.5	17.2	168393	2	CR383673	CR383673 Danio rer	219	390.5	16.5	110000	2	AE000516_12	Continuation (13 o
147	407.5	17.2	200867	5	BX470244	BX470244 Zebrafish	220	389.5	16.5	110000	2	AC120236_0	Rattus no
148	407.5	17.2	1075	6	CQ056637	CQ056637 Zebrafish	221	389.5	16.5	167395	9	AC120236_0	Continuation (13 o
149	406.5	17.2	1075	6	CQ075914	CQ075914 Sequence	222	389.5	16.5	300050	1	BX248339	MYcobacte
150	406.5	17.2	1075	6	CQ106891	CQ106891 Sequence	223	389	16.5	168354	2	AC025229	Homo sapi

c 224	389	16.5	171307	9	AC104030	AC104020 Homo sapi	297	379.5	16.1	230272	2	AC142671	AC142671 Macaca mu
c 225	388	16.4	110000	1	AE000516_29	Continuation (30 o	c 298	379	16.0	1925	8	PVGRP18	X13596 Bean DNA fo
c 226	388	16.4	194736	10	AC126271	Mus muscu	c 299	379	16.0	68651	9	AC027343	AC027343 Homo sapi
c 227	387.5	16.4	1969	14	AB037275	Cynomolgu	c 300	378.5	16.0	76941	10	BX000698	BX000698 Mouse DNA
c 228	386.5	16.4	1988	8	AK101495	Oryza sat	c 301	378.5	16.0	306050	1	BX248341	BX248341 Mycobacte
c 229	386.5	16.4	105739	5	EX571815	Zebrafish	c 302	378	16.0	1873	3	NCU37520	U37520 Nephila cla
c 230	386.5	16.4	244742	2	AC125663	Rattus no	c 303	378	16.0	152618	10	AC127583	AC127583 Mus muscu
c 231	386	16.3	145543	8	AC137071	Genomic s	c 304	377.5	16.0	197411	10	AC135961	AC135961 Mus muscu
c 232	386	16.3	167588	8	AF461424	Oryza sat	c 305	377	16.0	163321	5	AF309414	AF309414 Homo sapi
c 233	386	16.3	195690	10	AC098726	Mus muscu	c 306	376.5	15.9	1519	5	AF309414	AF309414 Cyprinus
c 234	386	16.3	243314	2	AC133375	Rattus no	c 307	376.5	15.9	18555	8	AV450930	AV450930 Chlamydom
c 235	386	16.3	247614	2	AC096414	Rattus no	c 308	376.5	15.9	150273	2	CR762461	CR762461 Danio rer
c 236	386	16.3	307550	1	EX248343	Mycobacte	c 309	376.5	15.9	182073	5	EX119973	EX119973 Zebrafish
c 237	384.5	16.3	254088	2	AC097865	Rattus no	c 310	376.5	15.9	186552	2	CR392001	CR392001 Danio rer
c 238	384.5	16.3	299611	2	AC113928	Rattus no	c 311	376.5	15.9	349564	1	EX842574	EX842574 Mycobacte
c 239	383.5	16.2	124576	2	AC105124	Homo sapi	c 312	376	15.9	112623	5	AX129192	AX129192 Zebrafish
c 240	383.5	16.2	185892	5	CR293514	Zebrafish	c 313	376	15.9	203157	5	AX1119314	AX1119314 Zebrafish
c 241	383.5	16.2	194387	10	AC105989	Mus muscu	c 314	375.5	15.9	253711	2	AC143308	AC143308 Macaca mu
c 242	383.5	16.2	245684	2	AC098110	Rattus no	c 315	375	15.9	9547	1	AF357166	AF357166 Mycobacte
c 243	383	16.2	1150	14	HS498113	epstein-bar	c 316	375	15.9	110000	1	AE000516_19	Continuation (20 o
c 244	383	16.2	1926	6	AR217866	Sequence	c 317	375	15.9	291050	1	EX248340	EX248340 Mycobacte
c 245	383	16.2	1926	6	AR254714	Sequence	c 318	375	15.9	347496	1	EX842577	EX842577 Mycobacte
c 246	383	16.2	1926	6	AX107940	Sequence	c 319	374.5	15.8	410	6	AX245107	AX245107 Sequence
c 247	383	16.2	2580	6	AR108994	Sequence	c 320	374.5	15.8	178620	10	AC121865	AC121865 Mus muscu
c 248	383	16.2	5452	6	AR083151	Sequence	c 321	374.5	15.8	211947	10	AC107828	AC107828 Mus muscu
c 249	383	16.2	5452	12	U02454	Cloning vec	c 322	374	15.8	3783	6	AX358421	AX358421 Sequence
c 250	383	16.2	8705	6	BD225380	Targeting	c 323	374	15.8	5658	6	AX358423	AX358423 Sequence
c 251	383	16.2	8705	6	AR349578	Sequence	c 324	374	15.8	158134	5	AL953878	AL953878 Zebrafish
c 252	383	16.2	9482	6	Q0829527	Sequence	c 325	374	15.8	343050	1	EX248334	EX248334 Mycobacte
c 253	383	16.2	9600	6	A92665	Sequence 1	c 326	373.5	15.8	37969	8	CR382137_20	Continuation (21 o
c 254	383	16.2	9600	6	AR158345	Sequence	c 327	373.5	15.8	110000	2	AE000516_40	Continuation (41 o
c 255	383	16.2	9600	6	AR241207	Sequence	c 328	373.5	15.8	165718	2	AC127508	AC127508 Homo sapi
c 256	383	16.2	10285	6	AX551315	Sequence	c 329	373.5	15.8	316050	1	EX248346	EX248346 Mycobacte
c 257	383	16.2	10285	6	AX552015	Sequence	c 330	373.5	15.8	349306	1	EX842575	EX842575 Mycobacte
c 258	383	16.2	10330	6	Q0789661	Sequence	c 331	373.5	15.8	349606	1	EX842583	EX842583 Mycobacte
c 259	383	16.2	10477	6	Q0789659	Sequence	c 332	373	15.8	686	6	BD210474	BD210474 Human gen
c 260	383	16.2	10516	6	Q0789657	Sequence	c 333	373	15.8	700	6	AX135555	AX135555 Sequence
c 261	383	16.2	10561	6	Q0789655	Sequence	c 334	373	15.8	991	9	BC011886	BC011886 Homo sapi
c 262	383	16.2	10596	6	I25041	Sequence 15	c 335	373	15.8	1579	6	AX834018	AX834018 Sequence
c 263	383	16.2	10596	6	I30503	Sequence 15	c 336	373	15.8	1579	9	AK096215	AK096215 Homo sapi
c 264	383	16.2	10615	6	Q0789682	Sequence	c 337	373	15.8	2336	3	NEPDSF	M37137 N.clavipec
c 265	383	16.2	10737	12	XXU02428	Cloning vec	c 338	373	15.8	2338	6	AR088543	AR088543 Sequence
c 266	383	16.2	10774	6	Q0789660	Sequence	c 339	373	15.8	2338	6	I92789	I92789 Sequence 1
c 267	383	16.2	10850	12	U02455	Cloning vec	c 340	373	15.8	2830	3	AF027972	AF027972 Nephila c
c 268	383	16.2	10921	6	Q0789658	Sequence	c 341	373	15.8	2830	6	AR091362	AR091362 Sequence
c 269	383	16.2	10961	6	Q0789656	Sequence	c 342	373	15.8	110000	1	AE000516_15	Continuation (16 o
c 270	383	16.2	11006	6	Q0789654	Sequence	c 343	372.5	15.8	1931	3	AY061814	AY061814 Nephila c
c 271	383	16.2	11059	6	Q0789683	Sequence	c 344	372.5	15.8	218780	2	AC115552	AC115552 Rattus no
c 272	383	16.2	16080	6	AR404205	Sequence	c 345	372	15.7	1080	8	NC0019AP	AL112229 Botrytis
c 273	383	16.2	17753	6	Q0790449	Sequence	c 346	372	15.7	205766	2	CR318620	CR318620 Danio rer
c 274	383	16.2	22960	12	AV192024	BAC cloni	c 347	372	15.7	320050	1	CR248336	CR248336 Mycobacte
c 275	383	16.2	171823	14	HHV507799	Human her	c 348	371.5	15.7	2985	6	AX358422	AX358422 Sequence
c 276	383	16.2	172381	14	EBV	Epstein-Bar	c 349	371.5	15.7	162929	5	EX323842	EX323842 Zebrafish
c 277	383	16.2	184113	14	HS48958RAJ	Epstein-Bar	c 350	371.5	15.7	190968	2	EX649269	EX649269 Danio rer
c 278	382.5	16.2	110000	2	EX649395_2	Continuation (3 of	c 351	371.5	15.7	224686	2	AC110974	AC110974 Rattus no
c 279	382.5	16.2	210220	5	EX664707	Zebrafish	c 352	371	15.7	110000	1	AE000516_03	Continuation (4 of
c 280	382	16.2	87076	9	AC005918	Homo sapi	c 353	371	15.7	125933	8	CR382132_28	Continuation (29 o
c 281	382	16.2	87734	9	AC013277	Homo sapi	c 354	371	15.7	125933	8	AP003816	AP003816 Oryza sat
c 282	381.5	16.1	38128	2	EX296528	Homo sapi	c 355	371	15.7	152928	8	AP004316	AP004316 Oryza sat
c 283	381.5	16.1	122272	2	AC143808	Macaca mu	c 356	371	15.7	307550	1	EX248343	EX248343 Mycobacte
c 284	381.5	16.1	157754	10	AC132313	Mus muscu	c 357	371	15.7	348676	1	EX842581	EX842581 Mycobacte
c 285	381	16.1	1653	8	TA2276509	Triticum	c 358	370.5	15.7	3030	8	VCA429230	AC046159 Homo sapi
c 286	381	16.1	216959	10	AC116998	Mus muscu	c 359	370.5	15.7	177883	2	AC046159	AC046159 Homo sapi
c 287	381	16.1	238892	10	AC148020	Mus muscu	c 360	370.5	15.7	178495	2	EX510329	EX510329 Danio rer
c 288	380.5	16.1	110000	1	AE000516_09	Continuation (10 o	c 361	370	15.7	2008	3	S74439	S74439 silk fibroi
c 289	380.5	16.1	238543	2	CR456635	Danio rer	c 362	370	15.7	82400	10	AC090495	AC090495 Genomic s
c 290	380.5	16.1	341957	1	EX842572	Mycobacte	c 363	370	15.7	116887	10	AL929153	AL929153 Mouse DNA
c 291	380	16.1	110000	8	CR382123_15	Continuation (16 o	c 364	370	15.7	181676	10	AC124194	AC124194 Mus muscu
c 292	380	16.1	120889	8	AC119416	Medicago	c 365	369.5	15.6	4439	3	AF023459	AF023459 Haliotis
c 293	379.5	16.1	110000	8	CR380955_09	Continuation (10 o	c 366	369.5	15.6	217069	2	AC110987	AC110987 Rattus no
c 294	379.5	16.1	169585	2	AC078821	Homo sapi	c 367	369.5	15.6	250391	2	AC096453	AC096453 Rattus no
c 295	379.5	16.1	178495	2	EX510329	Danio rer	c 368	369.5	15.6	256807	2	AC105547	AC105547 Rattus no
c 296	379.5	16.1	200352	5	AL954657	Zebrafish	c 369	369	15.6	3000	10	AF189262	AF189262 Rattus no

C 370	369	15.6	3978	10	AF255385	AF255385 Rattus no	C 443	359.5	15.2	110000	1	AE000516_18	Continuation (19 o
C 371	369	15.6	110000	8	CR382135_03	Continuation (4 of	C 444	359.5	15.2	110000	1	CP000001_04	Continuation (5 of
C 372	369	15.6	257510	8	AC112464	Rattus no	C 445	359	15.2	2565	3	AF350269_	AF350269 Dolomedes
C 373	368.5	15.6	181179	9	AL161725	Human DNA	C 446	359	15.2	40740	9	AC027349	AC027349 Homo sapi
C 374	368	15.6	179206	2	AC124108	Mus muscu	C 447	359	15.2	106209	1	D90903	D90903 Synchocyst
C 375	368	15.6	340493	10	BX883044	Rattus no	C 448	359	15.2	205054	10	AC098712	AC098712 Mus muscu
C 376	367.5	15.6	34727	3	CEP11A6	BX1498 Caenorhabdi	C 449	359	15.2	231332	10	AC096070	AC096070 Rattus no
C 377	367.5	15.6	324050	1	BX248335	Mycobacte	C 450	358.5	15.2	3060	3	AF027735	AF027735 Nephila c
C 378	367	15.5	152081	1	EX842731	AC007381 Homo sapi	C 451	358.5	15.2	128525	8	AP003118	AP003118 Oryza sat
C 379	367	15.5	342416	1	EX842573	MYcobacte	C 452	358.5	15.2	141983	8	AP003047	AP003047 Oryza sat
C 380	366.5	15.5	91040	5	BX248094	BX248094 Zebrafish	C 453	358.5	15.2	178501	10	AC121862	AC121862 Mus muscu
C 381	366.5	15.5	186248	2	AC026021	Homo sapi	C 454	358.5	15.2	214325	2	BX530020	BX530020 Danio rer
C 382	366.5	15.5	196950	2	CR589874	CR589874 Danio rer	C 455	358	15.2	2457	6	AR381691	AR381691 Sequence
C 383	366	15.5	1389	8	VURNAGR	Q67948 V.unguicula	C 456	358	15.2	2457	6	AR395204	AR395204 Sequence
C 384	366	15.5	1833	6	CO602721	CO602721 Dolomedes	C 457	358	15.2	4881	6	AR381692	AR381692 Sequence
C 385	366	15.5	2078	3	AF350270	AF350270 Dolomedes	C 458	358	15.2	4881	6	AR395206	AR395206 Sequence
C 386	365.5	15.5	1908	6	AF358426	AX358426 Sequence	C 459	358	15.2	168354	8	AP005185	AP005185 Oryza sat
C 387	365.5	15.5	110000	1	AE000516_01	Continuation (2 of	C 460	358	15.2	174673	8	AP005196	AP005196 Oryza sat
C 388	365.5	15.5	110000	1	AE000516_08	Continuation (9 of	C 461	357.5	15.1	187287	10	AL928735	AL928735 Mouse DNA
C 389	365.5	15.5	176576	2	CR385090	CR385090 Danio rer	C 462	357.5	15.1	235310	2	AC094274	AC094274 Rattus no
C 390	365.5	15.5	272563	2	AC095459	AC095459 Rattus no	C 463	357	15.1	2279	3	AY5711308	AY5711308 Kukulcani
C 391	365.5	15.5	341957	1	EX842572	EX842572 Mycobacte	C 464	357	15.1	110000	8	CR382122_12	Continuation (13 o
C 392	365.5	15.5	343050	1	BX248334	BX248334 Mycobacte	C 465	356.5	15.1	936	8	CNS01AYK	AL113536 Botrytis
C 393	365	15.4	110000	1	AE000516_31	Continuation (32 o	C 466	356.5	15.1	110000	1	AE000516_28	Continuation (29 o
C 394	364.5	15.4	1744	3	AY174110	AY174110 Araneus v	C 467	356.5	15.1	171570	10	AL807807	AL807807 Mouse DNA
C 395	364.5	15.4	2824	6	AR091363	AR091363 Sequence	C 468	356.5	15.1	243709	5	BX005367	BX005367 Zebrafish
C 396	364.5	15.4	2829	3	AF027973	AF027973 Nephila c	C 469	356	15.1	111678	8	AC149575	AC149575 Populus b
C 397	364	15.4	110000	1	AE000516_09	Continuation (10 o	C 470	356	15.1	168241	2	CR759822	CR759822 Danio rer
C 398	364	15.4	149448	2	CR382129	CR382129 Danio rer	C 471	356	15.1	168122	2	AC146997	AC146997 Arabacia p
C 399	364	15.4	191972	2	BX511207	BX511207 Danio rer	C 472	356	15.1	170012	2	CR352253	CR352253 Danio rer
C 400	364	15.4	200627	2	AC019225	AC019225 Homo sapi	C 473	356	15.1	210077	2	CR450750	CR450750 Danio rer
C 401	364	15.4	228433	10	AC097023	AC097023 Rattus no	C 474	355.5	15.0	1231	6	AX647501	AX647501 Sequence
C 402	364	15.4	349564	1	EX842574	EX842574 Mycobacte	C 475	355.5	15.0	110000	8	CR382136	CR382136 Debaryomy
C 403	363.5	15.4	197730	5	AL935334	AL935334 Mouse loric	C 476	355.5	15.0	158063	9	AP001046	AP001046 Homo sapi
C 404	363	15.4	1751	10	MUSLRCA	M34398 Zebrafish	C 477	355.5	15.0	340000	9	AP0011751	AP0011751 Homo sapi
C 405	363	15.4	6530	6	AR076241	AR076241 Sequence	C 478	355	15.0	1158	8	BNGRP22G	Z15045 B.napus GRP
C 406	363	15.4	6530	10	MMU09189	U09189 Mus muscu	C 479	355	15.0	152435	10	AC121566	AC121566 Mus muscu
C 407	363	15.4	110000	8	AE000516_20	Continuation (21 o	C 480	354.5	15.0	1280	9	BC034690	BC034690 Homo sapi
C 408	363	15.4	110000	8	CR382129_15	Continuation (16 o	C 481	354.5	15.0	172148	3	LMFP696	AL512293 Leishmani
C 409	363	15.4	166143	9	AC013447	AC013447 Homo sapi	C 482	354.5	15.0	201302	2	AC120896	AC120896 Rattus no
C 410	362.5	15.3	404	6	AX245405	AX245405 Sequence	C 483	354.5	15.0	301056	2	AE016999	AE016999 Bacillus
C 411	362.5	15.3	143406	6	AC092857	AC092857 Rattus no	C 484	354	15.0	250073	2	AC098913	AC098913 Rattus no
C 412	362.5	15.3	151578	9	AL589986	AL589986 Human DNA	C 485	353.5	15.0	111785	2	BX546471	BX546471 Danio rer
C 413	362.5	15.3	207556	10	AC128353	AC128353 Rattus no	C 486	353.5	15.0	181713	2	CR847903	CR847903 Danio rer
C 414	362	15.3	1804	10	BC026781	BC026781 Mus muscu	C 487	353.5	15.0	209550	10	AC094253	AC094253 Rattus no
C 415	362	15.3	1810	10	BC058223	BC058223 Mus muscu	C 488	353	14.9	2259	14	AB037276	AB037276 Cynomolgu
C 416	362	15.3	37000	14	BHTIUL	Z78205 Bovine herp	C 489	353	14.9	3946	1	AF071081	AF071081 Mycobacte
C 417	362	15.3	135301	14	BHV1CGEN	AJ004801 Bovine he	C 490	353	14.9	3946	6	A93410	A93410 Sequence 6
C 418	362	15.3	137828	2	CR354549	CR354549 Danio rer	C 491	353	14.9	93456	2	AC135413	AC135413 Medicago
C 419	362	15.3	146695	8	AP005451	AP005451 Oryza sat	C 492	353	14.9	100511	2	AC010774	AC010774 Homo sapi
C 420	362	15.3	159802	8	AP005447	AP005447 Oryza sat	C 493	353	14.9	178343	2	AC024049	AC024049 Homo sapi
C 421	362	15.3	204308	2	AC138676	AC138676 Mus muscu	C 494	353	14.9	291050	1	BX248340	BX248340 Mycobacte
C 422	362	15.3	210358	2	AC148095	AC148095 Mus muscu	C 495	352.5	14.9	1934	8	PHGCR1	X04335 Petunia grp
C 423	362	15.3	231001	2	AC130981	AC130981 Rattus no	C 496	352.5	14.9	157630	9	AC135012	AC135012 Homo sapi
C 424	362	15.3	258319	2	AC127770	AD000019 Mycobacte	C 497	352	14.9	180233	9	AC011767	AC011767 Homo sapi
C 425	361.5	15.3	42061	1	MSGV223	BX248338 Mycobacte	C 498	351.5	14.9	110000	8	CR380956_02	Continuation (3 of
C 426	361.5	15.3	299450	1	BX248338	BD205923 Compounds	C 499	351.5	14.9	181685	2	CR847515	CR847515 Danio rer
C 427	361	15.3	2367	6	BD205923	AR194931 Sequence	C 500	351.5	14.9	247017	2	AC105601	AC105601 Rattus no
C 428	361	15.3	2367	6	AR233203	AR233203 Sequence	C 501	351.5	14.9	347368	2	AC096620	AC096620 Rattus no
C 429	361	15.3	2367	6	AR233203	BD006431 Compounds	C 502	351	14.9	951	9	CR536555	CR536555 Homo sapi
C 430	361	15.3	2367	6	AR233203	BD006431 Compounds	C 503	351	14.9	160701	5	AL845351	AL845351 Zebrafish
C 431	361	15.3	2367	6	BD006431	BD006431 Compounds	C 504	350.5	14.8	164447	9	AC016204	AC016204 Homo sapi
C 432	361	15.3	2367	6	BD006431	Continuation (4 of	C 505	350.5	14.8	166340	2	BX511109	BX511109 Danio rer
C 433	361	15.3	110000	1	AE000516_03	AC003950 Homo sapi	C 506	350.5	14.8	265517	2	AC107094	AC107094 Rattus no
C 434	361	15.3	117621	9	AC003950	AC097628 Takifugu	C 507	350	14.8	1218	9	HUMLOR1	M61120 Human loric
C 435	360.5	15.3	88203	5	AC0097628	Continuation (5 of	C 508	350	14.8	3321	9	HUMLOR1	M94077 Human loric
C 436	360.5	15.3	110000	1	AE017355_04	AC117629 Mus muscu	C 509	350	14.8	178757	10	AC122509	AC122509 Mus muscu
C 437	360.5	15.3	248718	10	AE017355_02	AX704275 Sequence	C 510	349.5	14.8	2365	1	MBHRD	X70687 M.bovis hig
C 438	360	15.2	75216	6	AX704275	Continuation (14 o	C 511	349.5	14.8	3258	8	AF309494	AF309494 Chlamydom
C 439	360	15.2	110000	1	AE000516_13	AC117333 Rattus no	C 512	349	14.8	1854	6	AR456094	AR456094 Sequence
C 440	360	15.2	138366	10	AC111733	AC122020 Mus muscu	C 513	349	14.8	120487	10	AC103637	AC103637 Mus muscu
C 441	360	15.2	165592	10	AC122020	AC112612 Rattus no	C 514	349	14.8	347496	1	BX842577	BX842577 Mycobacte
C 442	360	15.2	268428	2	AC112612		C 515	348.5	14.7	171593	10	AC122052	AC122052 Mus muscu

c 516	348	14.7	228155	2	CR812941	CR812941	Danio rer	589	339	14.3	4764	8	CAHYRIGN	Z50123	Candida alb
c 517	348	14.7	260625	2	AC096018	AC096018	Rattus no	c 590	339	14.3	37482	3	AP024790	AP024790	Caenorhab
c 518	347.5	14.7	1588	6	AR399839	AR399839	Sequence	c 591	339	14.3	73391	8	AP02057	AP02057	Arabidops
c 519	347.5	14.7	1726	3	NCU20329	U20329	Nephila cia	592	339	14.3	131830	5	BX322605	BX322605	Zebrafish
c 520	347.5	14.7	67555	2	AC101189	AC101189	Mus muscu	593	338.5	14.3	1379	8	AK063970	AK063970	Oryza sat
c 521	347.5	14.7	112201	2	AC137670	AC137670	Medicago	594	338.5	14.3	87201	9	AC007623	AC007623	Homo sapi
c 522	347.5	14.7	148045	9	AC021860	AC021860	Homo sapi	595	338.5	14.3	197236	9	AC018710	AC018710	Homo sapi
c 523	347.5	14.7	177822	2	BX950199	BX950199	Danio rer	596	338.5	14.3	215745	10	AC117585	AC117585	Mus muscu
c 524	347	14.7	110000	14	AE000516	Continuati	(15 o	597	338	14.3	1408	3	AY177203	AY177203	Araneus v
c 525	347	14.7	137712	9	AL161636	AL161636	Human DNA	c 598	338	14.3	175252	5	BX005365	BX005365	Zebrafish
c 526	347	14.7	164520	2	AC020738	AC020738	Homo sapi	c 599	338	14.3	197858	2	AC143886	AC143886	Macaca mu
c 527	347	14.7	211239	2	CR3888209	CR3888209	Danio rer	c 600	338	14.3	252689	2	AC079433	AC079433	Mus muscu
c 528	347	14.7	231764	5	BX005426	BX005426	Zebrafish	c 601	338	14.3	325482	2	BX004858	BX004858	Danio rer
c 529	346.5	14.7	172718	2	AC141959	AC141959	Rattus no	c 602	338	14.3	335259	2	AC015834	AC015834	Homo sapi
c 530	346	14.6	1947	3	AF350266	AF350266	Argiope t	c 603	337.5	14.3	190752	2	AC114805	AC114805	Homo sapi
c 531	346	14.6	151800	9	AC138649	AC138649	Homo sapi	c 604	337.5	14.3	237814	10	AC091464	AC091464	Mus muscu
c 532	346	14.6	191753	10	AC125235	AC125235	Mus muscu	c 605	337	14.3	812	8	AJ630502	AJ630502	Arabidops
c 533	345.5	14.6	116678	8	AC148237	AC148237	Medicago	c 606	337	14.3	2978	3	AB073617	AB073617	Patinopec
c 534	345.5	14.6	143073	8	AC130603	AC130603	Oryza sat	c 607	337	14.3	3008	3	AF350265	AF350265	Argiope t
c 535	345.5	14.6	208880	10	AC123837	AC123837	Mus muscu	c 608	337	14.3	89437	2	AC095424	Continuati	(4 of
c 536	345.5	14.6	230329	2	AC142070	AC142070	Rattus no	c 609	337	14.3	211580	2	AC11089	AC11089	Mus muscu
c 537	345.5	14.6	261474	2	AC094196	AC094196	Rattus no	c 610	336	14.2	964	8	AK109396	AK109396	Oryza sat
c 538	345	14.6	590	6	AX985624	AX985624	Sequence	c 611	336	14.2	153111	8	CNS08CAN	AL831810	Oryza sat
c 539	345	14.6	2465	6	BD025234	BD025234	Sequence	c 612	336	14.2	178502	9	AC008674	AC008674	Homo sapi
c 540	345	14.6	2465	6	A31598	A31598	M.musculus	c 613	336	14.2	189825	9	AL683807	AL683807	Homo DNA
c 541	345	14.6	2465	10	NMURPERR	X02966	Mus muscu	c 614	336	14.2	222331	2	AC096794	AC096794	Rattus no
c 542	345	14.6	3530	5	FSAP18AA	M30123	Petromyzon	c 615	336	14.2	233411	2	AC109951	AC109951	Rattus no
c 543	345	14.6	136002	9	AC120024	AC120024	Homo sapi	c 616	336	14.2	234888	2	AC102097	AC102097	Mus muscu
c 544	345	14.6	219054	5	AL844192	AL844192	Zebrafish	c 617	336	14.2	291481	2	AC112086	AC112086	Rattus no
c 545	345	14.6	227856	10	AC135884	AC135884	Mus muscu	c 618	336	14.2	293771	2	AC127156	AC127156	Rattus no
c 546	344.5	14.6	234169	10	MMU400878	AJ400878	Mus muscu	c 619	335.5	14.2	2793	6	AR000990	AR000990	Sequence
c 547	344.5	14.6	169003	10	AC115699	AC115699	Mus muscu	c 620	335.5	14.2	2793	6	195876	195876	Sequence 1
c 548	344	14.6	199820	5	BX294113	BF350264	Argiope t	c 621	335.5	14.2	162873	2	CR847791	CR847791	Danio rer
c 549	344	14.6	225644	2	AC102598	AX294113	Zebrafish	c 622	335.5	14.2	172464	2	CR792425	CR792425	Danio rer
c 550	344	14.6	225644	2	AC102598	AC102598	Mus muscu	c 623	335.5	14.2	199230	2	CR762470	CR762470	Danio rer
c 551	344	14.6	225827	2	AC120694	AC120694	Rattus no	c 624	335.5	14.2	284150	2	AC119130	AC119130	Rattus no
c 552	344	14.6	240681	2	AC095407	AC095407	Rattus no	c 625	335	14.2	185549	2	BX927317	BX927317	Danio rer
c 553	344	14.6	242508	2	AC121731	AC121731	Rattus no	c 626	335	14.2	278361	2	AL606502	AL606502	Homo sapi
c 554	344	14.6	346051	1	BX842580	BX842580	Mycobacte	c 627	334.5	14.2	94227	9	CNS07BFZ	AL583810	Human chr
c 555	343.5	14.5	35848	2	AC011553	AC011553	Homo sapi	c 628	334.5	14.2	110000	8	CR382133	CR382133	Debaromy
c 556	343	14.5	1076	8	BT008615	BT008615	Arabidops	c 629	334	14.1	768	6	AX506117	AX506117	Sequence
c 557	343	14.5	1485	12	AY555585	AY555585	Synthetic	c 630	334	14.1	913	8	BT000113	BT000113	Arabidops
c 558	343	14.5	1515	12	AY555584	AY555584	Synthetic	c 631	334	14.1	1030	8	AY136328	AY136328	Arabidops
c 559	343	14.5	2046	6	AR399837	AR399837	Sequence	c 632	334	14.1	1926	6	AR217867	AR217867	Sequence
c 560	343	14.5	2076	6	AR399838	AR399838	Sequence	c 633	334	14.1	1931	6	AR083152	AR083152	Sequence
c 561	343	14.5	3135	3	U60194	U60194	Caenorhabdi	c 634	334	14.1	4492	9	HSKRT9P	X75015	H.sapiens K
c 562	343	14.5	79995	8	AB016882	AB016882	Arabidops	c 635	334	14.1	31733	8	AC007135	AC007135	Arabidops
c 563	342.5	14.5	2019	3	ADU47855	U47855	Araneus dia	c 636	334	14.1	164963	2	CR361564	CR361564	Danio rer
c 564	342.5	14.5	2322	6	AX358447	AX358447	Sequence	c 637	334	14.1	236054	2	AC114393	AC114393	Rattus no
c 565	342.5	14.5	2334	6	AX358449	AX358449	Sequence	c 638	334	14.1	287860	1	AE017265	AE017265	Bacillus
c 566	342.5	14.5	2690	3	BT003322	BT003322	Drosophila	c 639	333.5	14.1	1344	3	AF350262	AF350262	Argiope a
c 567	342.5	14.5	110000	1	AE000516	Continuati	(20 o	c 640	333.5	14.1	1506	1	AY708393	AY708393	Mycobacte
c 568	342.5	14.5	189844	5	BX649492	BX649492	Zebrafish	c 641	333.5	14.1	32735	9	AC006124	AC006124	Homo sapi
c 569	342.5	14.5	233933	2	AC128903	AC128903	Rattus no	c 642	333	14.1	11110	6	AX358427	AX358427	Sequence
c 570	342	14.5	1080	8	CNS01A60	AL112552	Botrytis	c 643	333	14.1	110000	1	AF006618	Continuati	(16 o
c 571	342	14.5	110000	2	AC096315	Continuati	(8 of	c 644	333	14.1	120476	2	AC130375	AC130375	Homo sapi
c 572	342	14.5	202878	2	AC137548	Continuati	(3 of	c 645	333	14.1	156441	2	AC122106	AC122106	Rattus no
c 573	341.5	14.5	840	8	CNS01BNS	AL137548	Macaca mu	c 646	333	14.1	166320	9	AC019349	AC019349	Homo sapi
c 574	341.5	14.5	5371	9	HSW807801	AL114464	Botrytis	c 647	333	14.1	171292	2	AC118493	AC118493	Rattus no
c 575	341.5	14.5	6999	3	GMFIBH1	BX647655	Homo sapi	c 648	333	14.1	173204	2	AC127524	AC127524	Homo sapi
c 576	341.5	14.5	110000	8	CR382130	AF095239	Galleria	c 649	333	14.1	178968	9	AF006274	AF006274	Papilio ham
c 577	341.5	14.5	221163	2	AX572628	BX572628	Danio rer	c 650	333	14.1	208462	9	AC130686	AC130686	Homo sapi
c 578	341.5	14.5	235357	9	AC103758	AC103758	Homo sapi	c 651	332.5	14.1	1181	3	BT011144	BT011144	Drosophila
c 579	341.5	14.5	251189	2	AC146824	AC146824	Otolemur	c 652	332.5	14.1	1181	6	CQ605886	CQ605886	Sequence
c 580	341	14.4	2335	8	AK175708	AK175708	Arabidops	c 653	332.5	14.1	1836	3	AY587193	AY587193	Araneus v
c 581	341	14.4	127188	8	AK144481	AC144481	Medicago	c 654	332.5	14.1	4049	3	BT001376	BT001376	Drosophila
c 582	341	14.4	181004	9	CNS01DITY	AL132990	Human chr	c 655	332.5	14.1	4905	6	CQ605885	CQ605885	Sequence
c 583	341	14.4	221924	2	CR388047	CR388047	Danio rer	c 656	332.5	14.1	57198	2	AC020115	AC020115	Drosophila
c 584	339.5	14.4	39200	9	AL954664	AL954664	Human DNA	c 657	332.5	14.1	110000	1	AE000516	Continuati	(24 o
c 585	339.5	14.4	195818	2	AC1384101	CR384101	Human	c 658	332.5	14.1	160695	2	CR381609	CR381609	Danio rer
c 586	339.5	14.4	222859	2	AC119799	AC119799	Pan trogl	c 659	332.5	14.1	169090	3	AC007300	AC007300	Drosophila
c 587	339	14.3	1238	9	AB013076	AB013076	Homo sapi	c 660	332.5	14.1	212028	2	CR751564	CR751564	Danio rer
c 588	339	14.3	2167	4	AY035849	AY035849	Sub scrofa	c 661	332.5	14.1	219865	5	BX469919	BX469919	Zebrafish

662	332.5	14.1	241432	10	AL589661	AL589661 Mouse DNA	735	323	13.7	185822	2	AC073554	AC073554 Homo sapi
663	332.5	14.1	252669	2	BX571678	BX571678 Danio rer	C 736	322	13.6	31760	9	AL954719	AL954719 Human DNA
664	332.5	14.1	261176	3	AE003629	AE003629 Drosophila	C 737	322	13.6	39373	3	AC006625	AC006625 Caenorhab
665	332.5	14.1	318930	2	AC073495	AC073495 Mus muscu	C 738	322	13.6	110000	8	CR382129_30	Continuation (31 o
666	332	14.0	1390	6	AX647245	AX647245 Sequence	C 739	322	13.6	203982	3	AY647854	AY647854 Homo sapi
667	332	14.0	89370	3	AC084153	AC084153 Caenorhab	C 740	321.5	13.6	1389	3	AY654290	AY654290 Nephila c
668	332	14.0	110000	2	AC084153	Continuation (2 of	741	321.5	13.6	33780	3	CET05C12	266500 Caenorhabd
669	332	14.0	211680	9	AC144302_1	AC144302 Homo sapi	742	321.5	13.6	180048	2	AC145885	AC145885 Pan trogl
670	331.5	14.0	106259	2	AC151909_3	Continuation (4 of	743	321.5	13.6	228492	10	AC132058	AC132058 Rattus no
671	331.5	14.0	110000	1	AE000516_06	Continuation (7 of	744	321.5	13.6	268597	2	AC094787	AC094787 Rattus no
672	331.5	14.0	144298	10	AC127682	AC127682 Mus muscu	745	321	13.6	28941	9	AC124902	AC124902 Homo sapi
673	331.5	14.0	207673	2	AC129709	AC129709 Rattus no	746	321	13.6	148619	2	AC151162	AC151162 Bos tauru
674	331	14.0	1280	6	AR128142	AR128142 Sequence	747	321	13.6	300425	1	AP005038	AP005038 Streptomy
675	331	14.0	3070	8	AK110196	AK110196 Oryza sat	748	320.5	13.6	5550	3	BT009991	BT009991 Drosophila
676	331	14.0	65233	2	AC105208	AC105208 Homo sapi	C 749	320.5	13.6	183008	2	AC019276	AC019276 Homo sapi
677	331	14.0	253328	2	AC130341	AC130341 Homo sapi	C 750	320.5	13.6	238108	2	BX248332	BX248332 Danio rer
678	330.5	14.0	75678	2	AC093372	AC093372 Mus muscu	751	320	13.5	1863	6	C0611535	C0611535 Sequence
679	330	14.0	1541	3	AF043636	AF043636 Plasmodi	752	320	13.5	5858	3	AF350276	AF350276 Nephila m
680	330	14.0	71203	9	AL160251	AL160251 Human DNA	C 753	320	13.5	147392	5	AL627261	AL627261 Zebrafish
681	330	14.0	152528	2	AC016063	AC016063 Homo sapi	754	320	13.5	156895	2	AC120107	AC120107 Rattus no
682	330	14.0	179883	2	AC007721	AC007721 Homo sapi	755	319.5	13.5	174428	9	AC005821	AC005821 Homo sapi
683	330	14.0	196840	2	CR626942	CR626942 Danio rer	C 756	319.5	13.5	208462	2	AC130686	AC130686 Homo sapi
684	330	14.0	206454	9	AC018737	AC018737 Homo sapi	757	319.5	13.5	233418	2	AC109128	AC109128 Homo sapi
685	329.5	13.9	981	11	CNS06K5P	AL402467 T7 end of	C 758	319	13.5	110000	2	AC114446_4	Continuation (5 of
686	329.5	13.9	1827	4	AY035847	AY035847 Sus scrof	C 759	319	13.5	146917	2	AC142043	AC142043 Rattus no
687	329.5	13.9	110000	8	CR382129_05	Continuation (6 of	C 760	319	13.5	176797	9	AC116552	AC116552 Homo sapi
688	329.5	13.9	180220	2	AC017043	AC017043 Homo sapi	761	319	13.5	233919	2	AC118760	AC118760 Rattus no
689	329.5	13.9	218381	2	AC150564	AC150564 Bos tauru	762	319	13.5	249432	2	AC103458	AC103458 Rattus no
690	329.5	13.9	266556	2	AC136868	AC136868 Rattus no	C 763	318.5	13.5	146111	10	AC132340	AC132340 Mus muscu
691	329	13.9	212493	2	AC080167	AC080167 Mus muscu	C 764	318.5	13.5	209230	10	AC121574	AC121574 Mus muscu
692	329	13.9	271929	2	AC116055	AC116055 Rattus no	C 765	318.5	13.5	272545	2	AC090533	AC090533 Mus muscu
693	328.5	13.9	170010	5	BX004804	BX004804 Zebrafish	766	318	13.5	5276	5	BC060753	BC060753 Xenopus 1
694	328	13.9	124457	2	AC115115	AC115115 Homo sapi	767	318	13.5	128658	2	AC147014	AC147014 Medicago
695	327.5	13.9	179145	2	AC137451	AC137451 Rattus no	C 768	318	13.5	175609	9	AC005243	AC005243 Homo sapi
696	327.5	13.9	179145	9	AC009785	AC009785 Homo sapi	C 769	318	13.5	210031	9	AC010538	AC010538 Homo sapi
697	327.5	13.9	270725	2	AC126948	AC126948 Rattus no	770	317.5	13.4	2287	9	HGKERAT9	Z29074 H.septens m
698	327	13.8	110352	8	AC006220	AC006220 Arabidops	771	317.5	13.4	2352	9	S69510	S69510 cytokeatin
699	327	13.8	143178	2	BX005034	BX005034 Homo sapi	772	317.5	13.4	199161	9	AC148307	AC148307 Pan trogl
700	326.5	13.8	152042	9	AL137857	AL137857 Human DNA	C 773	317	13.4	1173	8	AF331853	AF331853 Saccharum
701	326.5	13.8	188765	2	AL134501	AL134501 Canis fam	774	317	13.4	9921	3	AF325500	AF325500 Antherea
702	326.5	13.8	206258	2	AC112775	AC112775 Homo sapi	775	317	13.4	14999	3	AF21862181	AF218621 Nephila c
703	326	13.8	1230	8	VCA242540	AX242540 Volvox ca	C 776	317	13.4	157585	5	BX322664	BX322664 Zebrafish
704	326	13.8	25946	9	CNS010R3	BX511099 Human DNA	777	317	13.4	174631	3	AC101698	AC101698 Drosophila
705	326	13.8	200542	9	AC005109	AC005109 Human chr	778	317	13.4	228991	10	AC124627	AC124627 Mus muscu
706	326	13.8	218780	2	AC115552	AC115552 Rattus no	779	317	13.4	229190	10	AC127348	AC127348 Mus muscu
707	326	13.8	262798	2	AC111702	AC111702 Rattus no	C 780	317	13.4	263495	2	AC107152	AC107152 Rattus no
708	325.5	13.8	83549	9	AL356504	AL356504 Human DNA	C 781	317	13.4	276131	3	AE003543	AE003543 Drosophila
709	325.5	13.8	87487	8	AB015474	AB015474 Arabidops	C 782	316.5	13.4	1596	4	AY035848	AY035848 Sus scrof
710	325.5	13.8	119450	14	U97553	U97553 Murine herp	783	316.5	13.4	152728	10	AC118934	AC118934 Mus muscu
711	325.5	13.8	163945	2	AC116727	AC116727 Mus muscu	784	316.5	13.4	166055	2	AC116497	AC116497 Mus muscu
712	325.5	13.8	163945	2	AC108506	AC108506 Mus muscu	785	316.5	13.4	235471	10	AC124662	AC124662 Mus muscu
713	325.5	13.8	208735	2	AC108506	AC108506 Mus muscu	C 786	316.5	13.4	262814	2	BX537277	BX537277 Danio rer
714	325.5	13.8	217353	10	AC149611	AC149611 Mus muscu	C 787	316.5	13.4	267989	2	AC136564	AC136564 Rattus no
715	325.5	13.8	225644	2	AC102598	AC102598 Mus muscu	788	316	13.4	3485	3	CEU60449	CEU60449 Caenorhabd
716	325.5	13.8	264090	2	AC098014	AC098014 Rattus no	789	316	13.4	3728	3	AF21862382	AF218624 Nephila c
717	325	13.8	182272	10	AC122232	AC122232 Mus muscu	C 790	316	13.4	110000	8	CR380949	Continuation (2 of
718	325	13.8	233405	2	AC126733	AC126733 Rattus no	C 791	315.5	13.4	1125	3	AY077716	AY077716 Glossina
719	325	13.8	234778	2	AC097097	AC097097 Rattus no	C 792	315.5	13.4	9480	1	CTANCA	X67506 C.thermocol
720	324.5	13.7	2730	6	CQ740875	CQ740875 Sequence	C 793	315.5	13.4	80133	2	AC021347	AC021347 Homo sapi
721	324.5	13.7	4502	5	AB052836	AB052836 Oncorhync	794	315	13.3	1259	3	AY654291	AY654291 Nephila c
722	324.5	13.7	94058	2	AC141024	AC141024 Rattus no	795	315	13.3	2476	9	AB104446	AB104446 Homo sapi
723	324.5	13.7	137722	2	CR352240	CR352240 Danio rer	796	315	13.3	2790	3	AF218622	AF218622 Nephila c
724	324.5	13.7	172574	2	AC092667	AC092667 Homo sapi	797	315	13.3	37036	1	MSGY151	AD000018 Mycobacte
725	324.5	13.7	303091	2	AC084799	AC084799 Mus muscu	798	315	13.3	169583	9	AC080005	AC080005 Homo sapi
726	324	13.7	66208	9	AL450284	AL450284 Human DNA	C 799	315	13.3	173301	8	AP003539	AP003539 Oryza sat
727	324	13.7	190590	2	AC135045	AC135045 Homo sapi	800	315	13.3	224198	2	AC106674	AC106674 Rattus no
728	324	13.7	205047	2	BX511155	BX511155 Danio rer	801	314.5	13.3	36246	9	AC092316	AC092316 Homo sapi
729	324	13.7	229331	2	CR755914	CR755914 Danio rer	802	314.5	13.3	39470	9	AC005390	AC005390 Homo sapi
730	323.5	13.7	6178	3	AF203342	AF203342 Drosophila	C 803	314.5	13.3	78765	2	AC021584	AC021584 Homo sapi
731	323.5	13.7	14355	3	AF21862381	AF218623 Nephila m	C 804	314.5	13.3	80557	6	AX704276	AX704276 Sequence
732	323.5	13.7	129492	9	AC138466	AC138466 Homo sapi	C 805	314.5	13.3	110000	1	AE000516_29	Continuation (30 o
733	323.5	13.7	158693	9	AC015908	AC015908 Homo sapi	C 806	314.5	13.3	134940	2	AC018939	AC018939 Mus muscu
734	323	13.7	157087	2	AC142155	AC142155 Rattus no	C 807	314.5	13.3	141892	2	AC023197	AC023197 Mus muscu



C 808	314.5	13.3	222707	2	AC079425	Mus muscu	AC079425	808	308.5	13.1	191830	2	AC026332	Homo sapi
C 809	314.5	13.3	236692	2	BX510314	Danio rer	BX510314	882	308.5	13.1	196537	2	AC123389	Rattus no
C 810	314.5	13.3	237910	2	AL974309	Danio rer	AL974309	882	308.5	13.1	222295	2	CR318599	Danio rer
C 811	314	13.3	1463	6	AY321293	Lycopersi	AY321293	884	308.5	13.1	265537	10	AC087228	Mus muscu
C 812	314	13.3	5751	8	CQ584234	Sequence	CQ584234	885	308	13.0	2277	10	AV115494	Mus muscu
C 813	314	13.3	12099	2	AC014959	Drosophil	AC014959	886	308	13.0	10622	10	AY027660	Mus muscu
C 814	314	13.3	66491	2	AC006715	Caenorhab	AC006715	887	308	13.0	68003	2	BX323853	Homo sapi
C 815	314	13.3	78945	12	AY350715	Arabidops	AY350715	888	308	13.0	110000	2	AC151898_1	Continuatio
C 816	314	13.3	211585	10	AL626784	Mouse DNA	AL626784	889	308	13.0	121951	5	BX470145	Zebrafish
C 817	314	13.3	247608	2	AC120808	Rattus no	AC120808	890	308	13.0	130230	5	BX470145	Zebrafish
C 818	313.5	13.3	46877	9	AC104133	Homo sapi	AC104133	891	308	13.0	159182	2	CR392005	Danio rer
C 819	313.5	13.3	100580	9	BS000235	Pan trogl	BS000235	892	308	13.0	167830	9	AC016549	Homo sapi
C 820	312.5	13.3	108923	5	BX465908	Zebrafish	BX465908	893	308	13.0	175261	5	BX465981	Zebrafish
C 821	313.5	13.3	160456	9	BS000236	Pan trogl	BS000236	894	308	13.0	178530	9	AC018738	Homo sapi
C 822	313.5	13.3	165000	9	AC137894	Homo sapi	AC137894	895	308	13.0	221423	10	AC123859	Mus muscu
C 823	313.5	13.3	174520	9	BS000234	Pan trogl	BS000234	896	308	13.0	232869	10	AL603925	Mouse DNA
C 824	313.5	13.3	186759	9	AL645608	Human DNA	AL645608	897	308	13.0	240965	2	AC126054	Mus muscu
C 825	313.5	13.3	187160	9	AC138230	Homo sapi	AC138230	898	307.5	13.0	237422	5	BX546500	Zebrafish
C 826	313.5	13.3	193278	2	CR847951	Rattus no	CR847951	899	307.5	13.0	276289	1	AE017306	Thermus t
C 827	313.5	13.3	222722	2	AC095588	Rattus no	AC095588	900	307	13.0	1005	8	BT008624	Arabidops
C 828	313.5	13.3	327883	2	BX571684	Homo sapi	BX571684	901	307	13.0	33919	8	AY292860	Arabidops
C 829	313.5	13.3	349619	1	AF002996	Mesorhizo	AF002996	902	307	13.0	164043	9	AC113615	Homo sapi
C 830	313	13.2	4651	5	AB052835	Oncorhyn	AB052835	903	307	13.0	188057	2	AC128193	Rattus no
C 831	313	13.2	43709	9	BX649635	Human DNA	BX649635	904	307	13.0	224208	2	AC106236	Rattus no
C 832	313	13.2	110000	2	AC091341_5	Continuatio	Continuatio (6 of	905	307	13.0	237997	2	AC093989	Rattus no
C 833	313	13.2	124183	5	BX000361	Zebrafish	BX000361	906	307	13.0	265913	2	AC133620	Rattus no
C 834	312.5	13.2	888	8	NTGPRP	W74106	Ntabacum g	907	306.5	13.0	2796	3	AF043944	Mytilus e
C 835	312.5	13.2	1812	8	PVGRP10	X13595	Bean DNA fo	908	306.5	13.0	15750	6	AX821965	Sequence
C 836	312.5	13.2	176291	2	AC023583	Homo sapi	AC023583	909	306.5	13.0	15789	6	CQ730224	

c 954	303	12.8	41452	9	AL691455	AL691455 Human DNA	1027	300	12.7	179556	2	AC018734	AC018734 Homo sapi
955	303	12.8	93889	2	AC105432	AC105432 Magnaport	c1028	300	12.7	194827	2	AC018734	AC018734 Homo sapi
956	303	12.8	130176	8	AP006616	AP006616 Oryza sat	1029	300	12.7	198344	2	AC018734	AC018734 Homo sapi
957	303	12.8	159290	2	AP004813	AP004813 Oryza sat	1030	300	12.7	256172	2	AC005139	AC005139 Plasmodiu
c 958	303	12.8	174400	9	AC011603	AC011603 Homo sapi	c1031	299.5	12.7	816	8	CNS018K8	AL114336 Botrytis
959	303	12.8	205317	9	AC093856	AC093856 Homo sapi	1032	299.5	12.7	1932	10	AY128946	AY128946 Rattus no
960	303	12.8	218236	2	AC108828	AC108828 Mus muscu	c1033	299.5	12.7	84869	12	AY350714	AY350714 Olinarabi
961	302.5	12.8	2053	5	AB008374	AB008374 Oncorhync	c1034	299.5	12.7	166013	9	AP001648	AP001648 Homo sapi
962	302.5	12.8	9597	3	CBSC0L2P2A	M92041 Strongyloce	c1035	299.5	12.7	172763	9	AP0033783	AP0033783 Homo sapi
963	302.5	12.8	35766	3	BSRG47C05	AC084663 Caenorhab	1036	299	12.7	686	8	CNS01DIK	AL116868 Botrytis
c 964	302.5	12.8	181098	9	AC004216	AC084216 Homo sapi	1037	299	12.7	1033	8	AK064070	AK064070 Oryza sat
c 965	302.5	12.8	245684	2	AC098110	AC098110 Rattus no	1038	299	12.7	1118	3	AF350274	AF350274 Latrodect
966	302	12.8	6633	14	HEHSV1G3	X06461 Herpes simp	c1039	299	12.7	2210	6	AX834028	AX834028 Sequence
c 967	302	12.8	9976	1	AE003921	AE003921 Xylella f	c1040	299	12.7	2210	6	AX834028	AX834028 Sequence
c 968	302	12.8	12001	6	AR048721	AR048721 Sequence	c1041	299	12.7	98903	5	AX004777	AX004777 Zebrafish
969	302	12.8	26245	14	HSIUS	L00036 Human herpe	c1042	299	12.7	160830	5	AX511020	AX511020 Zebrafish
c 970	302	12.8	26245	14	HSIUS	L00036 Human herpe	c1043	299	12.7	300029	8	AE017100	AE017100 Oryza sat
971	302	12.8	152261	14	HEICG	X14112 Human herpe	1044	298.5	12.6	740	8	S47405	S47405 glycine-ric
c 972	302	12.8	152261	14	HEICG	X14112 Human herpe	c1045	298.5	12.6	2773	10	AF189263	AF189263 Mus muscu
c 973	302	12.8	175291	9	AC103925	AC103925 Homo sapi	1046	298.5	12.6	2870	3	AF029249	AF029249 Mytilus e
c 974	302	12.8	190050	1	AL646059	AL646059 Ralstonia	c1047	298.5	12.6	3601	8	AF159297	AF159297 Zea mays
c 975	302	12.8	198970	2	BX470255	BX470255 Danio rer	1048	298.5	12.6	99967	8	NCB22310	NCB22310 Neurospor
976	302	12.8	279388	2	AC117953	AC117953 Rattus no	c1049	298.5	12.6	106707	2	AC019314	AC019314 Homo sapi
977	302	12.8	300695	2	AC079431	AC079431 Mus muscu	1050	298.5	12.6	110000	1	RME591985	RME591985_10
c 978	301.5	12.8	61232	2	AC144635	AC144635 Xenopus t	1051	298.5	12.6	119156	5	BX004831	BX004831 Zebrafish
c 979	301.5	12.8	156899	2	AC103884	AC103884 Homo sapi	c1052	298.5	12.6	146691	2	BX927196	BX927196 Danio rer
c 980	301.5	12.8	162115	8	AP004687	AP004687 Oryza sat	c1053	298.5	12.6	156789	14	AF5333768	AF5333768 Cercopith
981	301.5	12.8	170440	2	CR388228	CR388228 Danio rer	1054	298.5	12.6	162195	2	BX957331	BX957331 Danio rer
c 982	301.5	12.8	223573	5	BX284616	BX284616 Zebrafish	c1055	298.5	12.6	178620	10	AC121865	AC121865 Mus muscu
983	301.5	12.8	231912	2	AC087566	AC087566 Mus muscu	c1056	298.5	12.6	196385	2	AC131309	AC131309 Homo sapi
984	301	12.7	1345	3	PFACSPB	J03203 Plasmodium	1057	298	12.6	642	3	AY571310	AY571310 Kukulcani
985	301	12.7	110000	8	CR382131_02	Continuation (3 of	c1058	298	12.6	2683	6	AX746557	AX746557 Sequence
c 986	301	12.7	123255	9	AC006003	AC006003 Homo sapi	c1059	298	12.6	2683	6	AX746557	AX746557 Sequence
c 987	301	12.7	135098	8	AC087549	AC087549 Oryza sat	c1060	298	12.6	10948	9	AB0803037	AB0803037 Homo sapi
988	301	12.7	154462	2	AC145149	AC145149 Homo sapi	1061	298	12.6	109783	10	AC124212	AC124212 Mus muscu
c 989	301	12.7	156276	2	CR769765	CR769765 Danio rer	1062	298	12.6	10310	10	AF131866	AF131866 Mus muscu
c 990	301	12.7	162227	2	AC024129	AC024129 Oryza sat	1063	298	12.6	192929	2	AC005505	AC005505 Plasmodiu
c 991	301	12.7	174019	8	AC087543	AC087543 Oryza sat	1064	298	12.6	199434	2	AC132982	AC132982 Rattus no
992	301	12.7	175234	5	BX547997	BX547997 Zebrafish	1065	298	12.6	207107	2	CR354437	CR354437 Danio rer
993	301	12.7	178195	2	AC145134	AC145134 Homo sapi	1066	298	12.6	218355	2	AC105572	AC105572 Rattus no
c 994	301	12.7	206522	2	CR792435	CR792435 Danio rer	1067	298	12.6	218656	10	AL163395	AL163395 Mus muscu
c 995	301	12.7	210869	9	CNS01DRE	AL117192 Human chr	1068	298	12.6	228732	2	CR391929	CR391929 Danio rer
c 996	301	12.7	304748	8	AE017101	AE017101 Oryza sat	c1069	298	12.6	234882	2	AC127871	AC127871 Rattus no
c 997	300.5	12.7	3036	3	AY245772	AY245772 Monosiga	c1070	298	12.6	245470	2	AC098775	AC098775 Rattus no
998	300.5	12.7	78220	9	AC023212	AC023212 Homo sapi	1071	298	12.6	250713	3	AE014850	AE014850 Plasmodiu
c 999	300.5	12.7	123004	9	AC087892	AC087892 Homo sapi	1072	298	12.6	322091	2	CR381647	CR381647 Danio rer
1000	300.5	12.7	124498	2	AC141194	AC141194 Rattus no	c1073	297.5	12.6	750	11	FW12B11B	AL684309 Penicilli
1001	300.5	12.7	164684	9	AL590683	AL590683 Human DNA	1074	297.5	12.6	39534	3	CEZK643	Z11126 Caenorhabdi
1002	300.5	12.7	174097	9	AC069513	AC069513 Homo sapi	c1075	297.5	12.6	89994	2	AC021263	AC021263 Homo sapi
1003	300.5	12.7	177162	2	AC068796	AC068796 Homo sapi	c1076	297.5	12.6	169206	2	CR293519	CR293519 Danio rer
1004	300.5	12.7	177431	2	BX571794	BX571794 Danio rer	1077	297.5	12.6	186884	2	AC119540	AC119540 Rattus no
c1005	300.5	12.7	188361	9	AC087880	AC087880 Homo sapi	c1078	297.5	12.6	198392	10	AL603745	AL603745 Mouse DNA
c1006	300.5	12.7	221879	2	AC096704	AC096704 Rattus no	1079	297.5	12.6	219004	2	CR759887	CR759887 Danio rer
c1007	300.5	12.7	222343	2	AC114531	AC114531 Rattus no	1080	297.5	12.6	227067	2	AC140391	AC140391 Mus muscu
1008	300.5	12.7	235407	2	AC094280	AC094280 Rattus no	1081	297.5	12.6	257936	2	AC079941	AC079941 Mus muscu
c1009	300.5	12.7	236522	2	CR376793	CR376793 Danio rer	1082	297	12.6	986	8	AC061298	AC061298 Oryza sat
c1010	300.5	12.7	246102	5	BX511270	BX511270 Zebrafish	1083	297	12.6	2811	6	CQ842751	CQ842751 Sequence
c1011	300	12.7	1766	14	HS1LS17	K01835 HSV-1 (stra	1084	297	12.6	2811	6	CQ842751	CQ842751 Sequence
1012	300	12.7	2214	6	AE093957	AE093957 Sequence	c1085	297	12.6	2811	9	AX125695	AX125695 Homo sapi
1013	300	12.7	2214	6	E15639	E15639 Pinctada fu	c1086	297	12.6	265436	2	AC133624	AC133624 Rattus no
1014	300	12.7	2579	10	MMWK2E	X74784 M.musculus	1087	296.5	12.5	267463	2	AC095626	AC095626 Rattus no
1015	300	12.7	3331	3	D86074	D86074 Pinctada fu	c1088	296.5	12.5	55528	3	AC105764	AC105764 Caenorhab
1016	300	12.7	3331	6	AR093958	AR093958 Sequence	c1089	296.5	12.5	142335	2	AC136164	AC136164 Rattus no
1017	300	12.7	3331	6	AR093959	AR093959 Sequence	c1090	296.5	12.5	152523	9	AC007009	AC007009 Homo sapi
1018	300	12.7	3331	6	E15640	E15640 Pinctada fu	1091	296.5	12.5	159064	2	AC138512	AC138512 Homo sapi
1019	300	12.7	3331	6	BD129567	BD129567 Polynucle	1092	296.5	12.5	161679	2	EX571843	EX571843 Danio rer
1020	300	12.7	3708	6	CQ722097	CQ722097 Sequence	c1093	296.5	12.5	205610	9	AC134312	AC134312 Homo sapi
1021	300	12.7	4060	5	AB075700	AB075700 Oncorhync	1094	296.5	12.5	324450	1	EX294146	EX294146 Pirellula
1022	300	12.7	111731	2	BX323063	BX323063 Homo sapi	1095	296.5	12.5	325483	1	AP005050	AP005050 Streptomy
c1023	300	12.7	117927	9	AC013416	AC013416 Homo sapi	1096	296	12.5	1637	8	AF181456	AF181456 Hordeum v
1024	300	12.7	121774	9	AC005383	AC005383 Homo sapi	1097	296	12.5	1981	3	NBPF1BPR	NBPF1BPR Nephila cla
1025	300	12.7	150715	14	AY714813	AY714813 Cercopith	1098	296	12.5	1995	6	AR088544	AR088544 Sequence
c1026	300	12.7	150715	14	AY714813	AY714813 Cercopith	1099	296	12.5	1995	6	I92790	I92790 Sequence 3

1100	296	12.5	6272	5	AB015438	AB015438 Cynops py	1173	292	12.4	2430	6	AX709983	AX709983 Sequence
1101	296	12.5	156789	14	AF533768	AF533768 Cercopithec	1174	292	12.4	2740	3	AF350281	AF350281 Plectreur
1102	295.5	12.5	1935	10	AF18926482	AF189265 Mus muscu	1175	292	12.4	3800	9	AF448438	AF448438 Homo sapi
1103	295.5	12.5	2779	6	CQ777537	CQ777537 Sequence	1176	292	12.4	3854	9	AF448439	AF448439 Homo sapi
1104	295.5	12.5	2781	3	AF448525	AF448525 Mytilus g	1177	292	12.4	3943	9	HUMINSPR	M10039 Human alpha
1105	295.5	12.5	15549	8	AF362475	AF362475 Arabidops	1178	292	12.4	75828	5	AL929329	AL929329 Zebrafish
1106	295.5	12.5	82024	2	AC023310	AC023310 Homo sapi	1179	292	12.4	100000	9	AP000055	AP000055 Homo sapi
1107	295.5	12.5	96438	2	AC150979	AC150979 Medicago	1180	292	12.4	100000	9	AP000170	AP000170 Homo sapi
1108	295.5	12.5	169510	2	AC140070	AC140070 Mus muscu	1181	292	12.4	163070	2	CR774194	CR774194 Danio rer
1109	295.5	12.5	180286	10	AL645600	AL645600 Mouse DNA	1182	292	12.4	170368	9	AP000330	AP000330 Homo sapi
1110	295.5	12.5	189230	2	AC120836	AC120836 Mus muscu	1183	292	12.4	183605	5	BR942837	BR942837 Zebrafish
1111	295.5	12.5	207372	10	AL731851	AL731851 Mouse DNA	1184	292	12.4	209491	2	CR392365	CR392365 Danio rer
1112	295	12.5	1856	8	ATGRPMR	Z11868 A.thaliana	1185	292	12.4	237549	2	AC107360	AC107360 Rattus no
1113	295	12.5	4170	5	AB075699	AB075699 Oncorhync	1186	292	12.4	245476	2	AC098496	AC098496 Rattus no
1114	295	12.5	110000	2	AC074221_0	AC074221 Mus muscu	1187	292	12.4	258174	2	AC0979429	AC0979429 Mus muscu
1115	294.5	12.5	2133	6	CQ500255	CQ500255 Sequence	1188	292	12.4	295094	2	AX649429	AX649429 Danio rer
1116	294.5	12.5	2198	6	CQ587499	CQ587499 Sequence	1189	292	12.4	340000	9	AP0011720	AP0011720 Homo sapi
1117	294.5	12.5	2255	3	AY089465	AY089465 Drosophil	1190	292	12.4	349528	2	AC096443	AC096443 Rattus no
1118	294.5	12.5	4329	6	CQ611534	CQ611534 Sequence	1191	291.5	12.3	36630	3	AC116032	AC116032 Dictyosce
1119	294.5	12.5	4750	9	AB029037	AB029037 Homo sapi	1192	291.5	12.3	168581	2	AC104862	AC104862 Mus muscu
1120	294.5	12.5	61964	3	AC004341	AC004341 Drosophil	1193	291.5	12.3	175302	2	AC020587	AC020587 Homo sapi
1121	294.5	12.5	68319	2	AX927093	AX927093 Danio rer	1194	291	12.3	14472	1	AE003928	AE003928 Xylella f
1122	294.5	12.5	95850	2	AC020063	AC020063 Drosophil	1195	291	12.3	18959	1	AE004032	AE004032 Xylella f
1123	294.5	12.5	96742	1	AY211023	AY211023 Streptomy	1196	291	12.3	20956	1	AE004082	AE004082 Xylella f
1124	294.5	12.5	144076	5	AL928677	AL928677 Zebrafish	1197	291	12.3	50709	1	AY034092	AY034092 Micrococ
1125	294.5	12.5	160338	3	AC099021	AC099021 Drosophil	1198	291	12.3	146664	9	AC010327	AC010327 Homo sapi
1126	294.5	12.5	188680	2	AC128917	AC128917 Rattus no	1199	291	12.3	153772	10	AC129304	AC129304 Mus muscu
1127	294.5	12.5	202083	2	AC023833	AC023833 Mus muscu	1200	291	12.3	189774	10	AC098709	AC098709 Mus muscu
1128	294.5	12.5	226519	2	AC095762	AC095762 Rattus no	1201	291	12.3	198115	2	AC099712	AC099712 Mus muscu
1129	294.5	12.5	233137	2	AC127758	AC127758 Rattus no	1202	291	12.3	199175	2	AC140836	AC140836 Homo sapi
1130	294.5	12.5	257817	2	AC006909	AC006909 Caenorhab	1203	290.5	12.3	1393	9	HUMINSHR	M28668 Human hyper
1131	294.5	12.5	272948	3	AE003805	AE003805 Drosophil	1204	290.5	12.3	2490	9	HSU04811	U04811 Human troph
1132	294.5	12.5	301443	1	AE012560	AE012560 Xylella f	1205	290.5	12.3	2490	11	G27220	CQ717362 Sequence
1133	294	12.4	4219	5	AB052837	AB052837 Oncorhync	1206	290.5	12.3	2494	6	CQ717362	CQ717362 Sequence
1134	294	12.4	6592	9	HSCTP1175	X90780 Homo sapien	1207	290.5	12.3	2524	6	AR027928	AR027928 Sequence
1135	294	12.4	10713	9	HSWUC5BEX	Z72496 H.sapiens M	1208	290.5	12.3	2524	6	AR071287	AR071287 Sequence
1136	294	12.4	56475	9	AL353658	AL353658 Human DNA	1209	290.5	12.3	2524	6	AR108720	AR108720 Sequence
1137	294	12.4	110000	8	CR382132_25	Continuation (26 o	1210	290.5	12.3	2524	6	I35489	I35489 Sequence 1
1138	294	12.4	112235	1	AE012561	AE012561 Xylella f	1211	290.5	12.3	2524	6	I59501	I59501 Sequence 1
1139	294	12.4	133069	2	AC026836	AC026836 Homo sapi	1212	290.5	12.3	3677	6	BD158648	BD158648 Primer fo
1140	294	12.4	138390	14	AY261359	AY261359 Bovine he	1213	290.5	12.3	3677	6	AX880884	AX880884 Sequence
1141	294	12.4	175330	2	CR352298	CR352298 Danio rer	1214	290.5	12.3	3677	6	BD012345	BD012345 Genes rel
1142	294	12.4	249235	2	AC094741	AC094741 Rattus no	1215	290.5	12.3	3677	9	CQ717180	CQ717180 Sequence
1143	294	12.4	249495	2	AC095394	AC095394 Rattus no	1216	290.5	12.3	4750	6	CQ717180	CQ717180 Sequence
1144	294	12.4	300029	1	AE012556	AE012556 Xylella f	1217	290.5	12.3	27543	9	AB126081	AB126081 Homo sapi
1145	294	12.4	300775	1	AE012557	AE012557 Xylella f	1218	290.5	12.3	81417	2	AC023265	AC023265 Homo sapi
1146	293.5	12.4	1692	3	AF350278	AF350278 Nephila m	1219	290.5	12.3	103115	9	HSDA14C6	AL049732 Human DNA
1147	293.5	12.4	2543	8	SSPPLTAND	Y09117 S.sagittifo	1220	290.5	12.3	124191	9	AC005153	AC005153 Homo sapi
1148	293.5	12.4	9619	8	ATGRPG	Z11858 A.thaliana	1221	290.5	12.3	128948	5	BX005029	BX005029 Zebrafish
1149	293.5	12.4	14946	8	AF362474	AF362474 Arabidops	1222	290.5	12.3	176120	8	AP005521	AP005521 Oryza sat
1150	293.5	12.4	36736	2	AC142515	AC142515 Rattus no	1223	290.5	12.3	181773	2	AC136125	AC136125 Rattus no
1151	293.5	12.4	196261	2	AC149008	AC149008 Otollemur	1224	290.5	12.3	190642	2	AC140821	AC140821 Homo sapi
1152	293.5	12.4	223878	2	AC130000	AC130000 Rattus no	1225	290.5	12.3	245976	2	AC112593	AC112593 Rattus no
1153	293.5	12.4	227897	2	AC111962	AC111962 Rattus no	1226	290.5	12.3	254172	2	CR392035	CR392035 Danio rer
1154	293	12.4	2508	9	ORAINVOL	M25312 Orang-utan	1227	290.5	12.3	265924	2	AC095740	AC095740 Rattus no
1155	293	12.4	14859	6	AX823282	AX823282 Sequence	1228	290.5	12.3	265251	2	AC106085	AC106085 Rattus no
1156	293	12.4	14874	6	AF010404	AF010404 Homo sapi	1229	290	12.3	985	6	BD205914	BD205914 Compounds
1157	293	12.4	15645	6	AX921118	AX921118 Sequence	1230	290	12.3	985	6	AR194922	AR194922 Sequence
1158	293	12.4	110000	1	AE017334_04	Continuation (5 of	1231	290	12.3	985	6	AR233194	AR233194 Sequence
1159	293	12.4	133719	14	AF083501	AF083501 Macaca mu	1232	290	12.3	985	6	AR353399	AR353399 Sequence
1160	293	12.4	144689	5	BX001033	BX001033 Zebrafish	1233	290	12.3	985	6	BD006422	BD006422 Compounds
1161	293	12.4	181079	2	AC016667	AC016667 Homo sapi	1234	290	12.3	985	6	BD006542	BD006542 Compounds
1162	293	12.4	184211	2	AC146112	AC146112 Pan trogl	1235	290	12.3	2272	10	BC016444	BC016444 Mus muscu
1163	293	12.4	219973	10	AL670227	AL670227 Mouse DNA	1236	290	12.3	2682	10	BC057987	BC057987 Mus muscu
1164	293	12.4	232885	2	AC106163	AC106163 Rattus no	1237	290	12.3	3466	10	AK128966	AK128966 Mus muscu
1165	293	12.4	290714	1	AE017025	AE017025 Bacillus	1238	290	12.3	7564	14	GFL309022	AFJ09022 Grapevine
1166	292.5	12.4	1803	1	SPY347808	AJ347808 Streptoco	1239	290	12.3	14835	6	AX281704	AX281704 Sequence
1167	292.5	12.4	36229	9	AC004799	AC004799 Homo sapi	1240	290	12.3	59113	2	AC136784	AC136784 Homo sapi
1168	292.5	12.4	199954	10	AL591208	AL591208 Mouse DNA	1241	290	12.3	98398	9	AL731533	AL731533 Human DNA
1169	292.5	12.4	216567	2	BX927074	BX927074 Danio rer	1242	290	12.3	110000	2	AC151895	AC151895 Mus muscu
1170	292.5	12.4	289751	10	AC091458	AC091458 Mus muscu	1243	290	12.3	110000	2	AC006484_3	Continuation (4 of
1171	292	12.4	1177	3	PCSEPT	X74358 P.carnea Po	1244	290	12.3	128361	9	AC004877	AC004877 Homo sapi
1172	292	12.4	2091	6	AX921763	AX921763 Sequence	1245	290	12.3	161593	9	HSBA49G10	AL121901 Human DNA

c1246	290	12.3	168423	2	AC123530	AC123530 Mus muscu	1319	287	12.1	8401	3	AJ601384	AJ601384 Paracentr
1247	290	12.3	179035	10	AL772131	AL772131 Mouse DNA	1320	287	12.1	40106	4	AF005273	AF005273 Sus scrof
1248	290	12.3	186030	8	CNS080C7W	CNS080C7W Oryza sat	1321	287	12.1	77521	8	F7H2	AC034256 Sequence
c1249	290	12.3	190711	9	AF254983	AF254983 Homo sapi	c1322	287	12.1	223352	2	BX601645	BX601645 Danio rer
c1250	290	12.3	192237	2	CR7622383	CR7622383 Danio rer	1323	287	12.1	310779	2	AC005140	AC005140 Plasmodiu
1251	290	12.3	252689	2	AC0079433	AC0079433 Mus muscu	c1324	286.5	12.1	857	11	PM7B12G	AL685079 Penicilli
c1252	290	12.3	309050	1	SC0939117	AF3939117 Streptomy	1325	286.5	12.1	2854	5	AB008372	AB008372 Oncorhyn
1253	289.5	12.3	1094	5	AF309416	AF309416 Cyprinusu	1326	286.5	12.1	16270	10	AF331848	AF331848 Mus muscu
1254	289.5	12.3	6825	6	CQ740874	CQ740874 Sequence	c1327	286.5	12.1	66882	9	BX649553	BX649553 Human DNA
c1255	289.5	12.3	37892	9	BX649333	BX649333 Human DNA	c1328	286.5	12.1	99497	9	HS29316	AL049749 Human DNA
1256	289.5	12.3	106873	14	AB096160	AB096160 Cercopith	c1329	286.5	12.1	154448	5	BX511105	BX511105 Zebrafish
1257	289.5	12.3	131423	9	AC116609	AC116609 Homo sapi	1330	286.5	12.1	174463	5	BX511007	BX511007 Zebrafish
c1258	289.5	12.3	160487	5	BX005126	BX005126 Zebrafish	c1331	286.5	12.1	196140	10	AL672150	AL672150 Mouse DNA
1259	289.5	12.3	170765	2	CR405701	CR405701 Danio rer	c1332	286.5	12.1	202863	2	BX927344	BX927344 Danio rer
c1260	289.5	12.3	174888	9	AC037459	AC037459 Homo sapi	1333	286.5	12.1	220469	2	AC074307	AC074307 Mus muscu
1261	289.5	12.3	203401	9	AC015936	AC015936 Homo sapi	1334	286	12.1	1632	5	BC045260	BC045260 Xenopus 1
c1262	289.5	12.3	206464	2	CR847516	CR847516 Danio rer	1335	286	12.1	6353	6	CQ580242	CQ580242 Sequence
1263	289.5	12.3	207661	9	AC015884	AC015884 Homo sapi	1336	286	12.1	8429	6	CQ580241	CQ580241 Sequence
c1264	289.5	12.3	344249	1	BX842654	BX842654 Bdellovib	c1337	286	12.1	13443	2	AC013070	AC013070 Drosophill
1265	289	12.2	1164	6	BD274031	BD274031 Sequences	1338	286	12.1	14626	9	AY480045	AY480045 Homo sapi
1266	289	12.2	1164	6	AX005782	AX005782 Sequences	1339	286	12.1	14646	9	AY480048	AY480048 Homo sapi
1267	289	12.2	1165	6	BD274030	BD274030 Sequences	1340	286	12.1	14675	9	AY480049	AY480049 Homo sapi
1268	289	12.2	1165	6	AX005776	AX005776 Sequences	1341	286	12.1	14689	9	AY480050	AY480050 Homo sapi
1269	289	12.2	1166	6	BD274029	BD274029 Sequences	1342	286	12.1	14755	9	AY480046	AY480046 Homo sapi
1270	289	12.2	1166	6	AX005768	AX005768 Sequences	1343	286	12.1	14755	9	AY480044	AY480044 Homo sapi
c1271	289	12.2	2828	8	AK110069	AK110069 Oryza sat	1344	286	12.1	14797	9	AY480051	AY480051 Homo sapi
1272	289	12.2	4245	3	SUSALICOL	M92040 Strongyloce	1345	286	12.1	15249	9	AY480047	AY480047 Homo sapi
c1273	289	12.2	106769	9	AL357079	AL357079 Human DNA	c1346	286	12.1	34877	9	AC010641	AC010641 Homo sapi
1274	289	12.2	119045	2	CR388374	CR388374 Danio rer	1347	286	12.1	110000	2	AL429122_5	Continuation (6 of
c1275	289	12.2	124795	10	AL840624	AL840624 Mouse DNA	1348	286	12.1	146733	2	CR788242	CR788242 Danio rer
1276	289	12.2	124795	9	AC138696	AC138696 Homo sapi	c1349	286	12.1	172674	3	AC007807	AC007807 Drosophill
1277	289	12.2	165019	2	BX005333	BX005333 Danio rer	1350	286	12.1	174906	2	CR788284	CR788284 Danio rer
1278	289	12.2	174474	9	AL591408	AL591408 Human DNA	1351	286	12.1	175527	9	AC100863	AC100863 Homo sapi
c1279	289	12.2	206525	2	BX004857	BX004857 Danio rer	1352	286	12.1	173386	3	AC104515	AC104515 Drosophill
1280	289	12.2	228492	10	AC132058	AC132058 Rattus no	1353	286	12.1	182003	9	AL355987	AL355987 Human DNA
c1281	289	12.2	290510	1	AE017130	AE017130 Yersinia	c1354	286	12.1	190866	3	AC007824	AC007824 Drosophill
1282	288.5	12.2	1583	9	CR382132_13	U36561 Human finis-1	c1355	286	12.1	199285	9	AC096709	AC096709 Homo sapi
1283	288.5	12.2	110000	8	CR382132_14	Continuation (14 o	1356	286	12.1	205350	2	AC078946	AC078946 Mus muscu
1284	288.5	12.2	110000	8	CR382132_2	Continuation (15 o	1357	286	12.1	215342	9	AC109322	AC109322 Homo sapi
c1285	288.5	12.2	124104	9	AC061979	AC061979 Homo sapi	c1358	286	12.1	220035	3	AE003716	AE003716 Drosophill
1286	288.5	12.2	204804	2	CR354372	CR354372 Danio rer	c1359	286	12.1	273948	3	AE003574	AE003574 Drosophill
c1287	288.5	12.2	204804	9	CR354372	M24151 Mus musculu	285.5	12.1	14447	14	AB074432	AB074432 Cercopith	
1288	288	12.2	1105	10	HSKPER	U72849 Homo sapien	c1360	285.5	12.1	62649	2	AC022552	AC022552 Homo sapi
1289	288	12.2	4513	9	MSAPEVPL7	Q729672 Sequence	c1361	285.5	12.1	73948	2	AC022556	AC022556 Homo sapi
1290	288	12.2	6457	6	CQ729672	CQ729672 Sequence	c1362	285.5	12.1	209812	2	CR790388	CR790388 Danio rer
1291	288	12.2	6457	6	CQ776730	AX4170730 Sequence	c1363	285.5	12.1	253921	2	AC098930	AC098930 Rattus no
1292	288	12.2	6457	6	AC110743	AX4170730 Sequence	c1364	285.5	12.1	253921	2	AC098930	AC098930 Rattus no
c1293	288	12.2	6457	9	HSU53786	U53786 Homo sapien	1365	285.5	12.1	153431	8	AT72111	AL34235 Oryza sat
1294	288	12.2	117240	2	AP003927	AP003927 Oryza sat	c1366	285.5	12.1	157092	10	AL805911	AL805911 Mouse DNA
1295	288	12.2	130913	2	AP006869	AP006869 Rattus no	1367	285.5	12.1	202472	5	AL953892	AL953892 Zebrafish
1296	288	12.2	137364	8	AP004275	AP004275 Oryza sat	1368	285.5	12.1	209812	2	CR790388	CR790388 Danio rer
1297	288	12.2	139484	9	AC040980	AC040980 Homo sapi	c1369	285.5	12.1	253921	2	AC098930	AC098930 Rattus no
1298	288	12.2	156006	2	AC141569	AC141569 Rattus no	1370	285.5	12.1	265985	2	AC087226	AC087226 Mus muscu
1299	288	12.2	176179	2	CR385031	CR385031 Danio rer	1371	285	12.1	1038	8	AK10520	AK10520 Oryza sat
1300	288	12.2	184393	9	AC018665	AC018665 Homo sapi	1372	285	12.1	1170	5	AF309415	AF309415 Cyprinusu
1301	288	12.2	197530	10	AC099174	AC099174 Rattus no	1373	285	12.1	2620	3	DDU48298	DDU48298 Dictyostell
c1302	288	12.2	218639	2	AC130753	AC099174 Rattus no	1374	285	12.1	3222	14	HPU23857	U23857 Herpesviru
1303	288	12.2	239130	2	AC079420	AC130753 Rattus no	c1375	285	12.1	39733	3	CEP10F2	Z35598 Caenorhabdi
1304	288	12.2	245697	5	AL831726	AL831726 Zebrafish	c1376	285	12.1	76052	2	AC023262	AC023262 Homo sapi
1305	288	12.2	303091	2	AC084799	AL831726 Zebrafish	c1377	285	12.1	104295	2	AP003890	AP003890 Oryza sat
1306	288	12.2	306250	1	SME591788	AC084799 Mus muscu	c1378	285	12.1	170523	8	AF004764	AF004764 Oryza sat
1307	287.5	12.2	555	3	AY571309	AL591788 Sinorhizo	c1379	285	12.1	230682	2	BX510307	BX510307 Danio rer
c1308	287.5	12.2	110000	1	CR522870_23	AY571309 Kukulcani	1380	284.5	12.0	3850	3	AK173690	AK173690 Giona int
1309	287.5	12.2	164520	2	AC020738	Continuation (24 o	c1381	284.5	12.0	34821	9	BX640545	BX640545 Human DNA
c1310	287.5	12.2	167929	2	CR847883	AC020738 Homo sapi	c1382	284.5	12.0	45978	5	BX649274	BX649274 Zebrafish
1311	287.5	12.2	188711	9	AC093336	CR847883 Danio rer	c1383	284.5	12.0	139517	9	AC105446	AC105446 Homo sapi
1312	287.5	12.2	190744	9	AC050338	CR847883 Danio rer	1384	284.5	12.0	173351	10	AL732502	AL732502 Mouse DNA
1313	287.5	12.2	193470	5	AL929321	AC093336 Homo sapi	c1385	284.5	12.0	177617	5	AL840638	AL840638 Zebrafish
c1314	287.5	12.2	193686	10	AC113052	AC050338 Homo sapi	c1386	284.5	12.0	189940	9	AC147062	AC147062 Pan trogl
1315	287.5	12.2	203115	2	AC102574	AL929321 Zebrafish	c1387	284.5	12.0	217690	10	AC126722	AC126722 Rattus no
c1316	287.5	12.2	241200	2	CR450844	AC113052 Mus muscu	1388	284.5	12.0	222895	2	AC084065	AC084065 Mus muscu
1317	287	12.1	1818	8	AF362483	AC102574 Mus muscu	1389	284	12.0	831	6	AX358428	AX358428 Sequence
1318	287	12.1	2894	3	AY498693	CR450844 Danio rer	c1390	284	12.0	2812	8	AK120222	AK120222 Oryza sat
						AY498693 Dinocampu	c1391	284	12.0	16098	6	AX680082	AX680082 Sequence

c1392	284	12.0	37026	9	CNSG00YVF	AL096808 Homo sapi	c1465	282	11.9	226464	2	AC099442	AC099442 Rattus no
c1393	284	12.0	75628	2	AC021793	AC021793 Homo sapi	1466	282	11.9	231853	2	AC093352	AC093352 Mus muscu
c1394	284	12.0	99661	2	AC137530	AC137530 Takifugu	1467	282	11.9	272563	2	AC095469	AC095469 Rattus no
c1395	284	12.0	149020	10	AC132336	AC132336 Mus muscu	1468	281.5	11.9	787	8	AK064065	AK064065 Oryza sat
c1396	284	12.0	152420	2	BX927200	BX927200 Danio rer	1469	281.5	11.9	844	8	AK119244	AK119244 Oryza sat
c1397	284	12.0	173143	2	BX649466	BX649466 Danio rer	1470	281.5	11.9	1065	8	AK064310	AK064310 Oryza sat
c1398	284	12.0	179618	10	AC124776	AC124776 Mus muscu	1471	281.5	11.9	1336	3	AF350267	AF350267 Argiope t
c1399	284	12.0	188297	2	CR759843	CR759843 Danio rer	1472	281.5	11.9	2714	6	CQ602057	CQ602057 Sequence
c1400	284	12.0	221079	2	AC149586	AC149586 Mus muscu	1473	281.5	11.9	9359	2	AC018248	AC018248 Drosophil
c1401	284	12.0	233786	2	AC113755	AC113755 Rattus no	1474	281.5	11.9	140327	2	AP003938	AP003938 Oryza sat
c1402	284	12.0	242531	10	AC108805	AC108805 Mus muscu	1475	281.5	11.9	150891	2	AC069098	AC069098 Homo sapi
c1403	284	12.0	261953	2	BX465201	BX465201 Danio rer	1476	281.5	11.9	165866	2	AC073202	AC073202 Homo sapi
c1404	284	12.0	340000	9	AP001712	AP001712 Homo sapi	1477	281.5	11.9	173153	9	AC008119	AC008119 Homo sapi
c1405	283.5	12.0	1243	3	AY654292	AY654292 Nephila c	1478	281.5	11.9	215895	2	AC121688	AC121688 Rattus no
c1406	283.5	12.0	2948	5	BC059189	BC059189 Danio rer	1479	281.5	11.9	219817	5	BX088693	BX088693 Zebrafish
c1407	283.5	12.0	152195	2	AC016331	AC016331 Homo sapi	1480	281.5	11.9	224703	2	AC115510	AC115510 Rattus no
c1408	283.5	12.0	159691	9	AC025160	AC025160 Homo sapi	1481	281.5	11.9	264103	2	AC126651	AC126651 Rattus no
c1409	283.5	12.0	165315	5	CR354380	CR354380 Zebrafish	1482	281.5	11.9	276741	2	AC096301	AC096301 Rattus no
c1410	283.5	12.0	166305	5	AL929389	AL929389 Zebrafish	1483	281.5	11.9	287765	1	AE017276	AE017276 Bacillus
c1411	283.5	12.0	182255	2	AC140810	AC140810 Homo sapi	1484	281	11.9	1511	4	PIGAPMUC	M21174 Pig apomuci
c1412	283.5	12.0	194869	5	AL954136	AL954136 Zebrafish	1485	281	11.9	3643	4	AB017601	AB017601 Sus scrofa
c1413	283.5	12.0	195319	2	CR388410	CR388410 Danio rer	1486	281	11.9	4954	3	AB017601	AB017601 Haliotis
c1414	283.5	12.0	201371	2	AC073786	AC073786 Mus muscu	1487	281	11.9	34828	9	BX537318	BX537318 Human DNA
c1415	283.5	12.0	209068	10	AL603868	AL603868 Mouse DNA	1488	281	11.9	36823	9	HSU209G1	Z68873 Human DNA
c1416	283.5	12.0	244034	2	AC122336	AC122336 Mus muscu	1489	281	11.9	137155	4	BX295537	BX295537 Platypus
c1417	283.5	12.0	267206	2	AC131871	AC131871 Rattus no	1490	281	11.9	162776	8	AP003237	AP003237 Oryza sat
c1418	283.5	12.0	269285	2	AC120096	AC120096 Rattus no	1491	281	11.9	175492	5	BX649296	BX649296 Zebrafish
c1419	283	12.0	2130	6	CQ842651	CQ842651 Sequence	1492	281	11.9	198614	2	AC073293	AC073293 Mus muscu
c1420	283	12.0	3156	3	PAUCOL2	PAUCOL2	1493	281	11.9	218178	5	BX248304	BX248304 Zebrafish
c1421	283	12.0	2130	6	AK124003	AK124003 Homo sapi	1494	281	11.9	218292	2	CR751234	CR751234 Danio rer
c1422	283	12.0	3483	10	MUSTROP	MUSTROP	1495	280.5	11.9	5560	1	AE012559	AE012559 Xylella f
c1423	283	12.0	3483	10	AX924134	AX924134 Sequence	1496	280.5	11.9	106702	8	ATP7K2	AL033545 Arabidops
c1424	283	12.0	4071	6	AC053018	AC053018 Mus muscu	1497	280.5	11.9	132348	10	CNS07Y0Z	AL713882 Mus muscu
c1425	283	12.0	4190	10	BC053018	BC053018 Mus muscu	1498	280.5	11.9	143733	2	AC142786	AC142786 Macaca mu
c1426	283	12.0	4428	5	BC049287	BC049287 Xenopus l	1499	280.5	11.9	151598	5	BX088542	BX088542 Zebrafish
c1427	283	12.0	5002	9	HUNAZCDI	HUNAZCDI	1500						
c1428	283	12.0	5254	8	AK120962	AK120962 Oryza sat							
c1429	283	12.0	5254	8	AK120962	AK120962 Oryza sat							
c1430	283	12.0	5343	10	AF319977	AF319977 Mus muscu							
c1431	283	12.0	5964	10	AF319977	AF319977 Mus muscu							
c1432	283	12.0	6177	10	AF241244	AF241244 Mus muscu							
c1433	283	12.0	6637	10	BC075630	BC075630 Mus muscu							
c1434	283	12.0	51855	1	ML1557546	ML1557546 Helitang							
c1435	283	12.0	83521	9	AC129510	AC129510 Homo sapi							
c1436	283	12.0	110000	2	AP006618	AP006618 43 o							
c1437	283	12.0	110000	2	CR381548	CR381548 Danio rer							
c1438	283	12.0	123260	10	AC087041	AC087041 Rattus no							
c1439	283	12.0	147452	8	AC026815	AC026815 Oryza sat							
c1440	283	12.0	153960	2	BX950200	BX950200 Danio rer							
c1441	283	12.0	199656	9	AC032044	AC032044 Homo sapi							
c1442	283	12.0	236354	2	AC110644	AC110644 Rattus no							
c1443	283	12.0	282681	2	AC106358	AC106358 Rattus no							
c1444	283	12.0	300929	8	AE017104	AE017104 Oryza sat							
c1445	282.5	12.0	713	11	PM12BI0B	PM12BI0B							
c1446	282.5	12.0	1818	8	AF362482	AF362482 Arabidops							
c1447	282.5	12.0	5775	5	AB034701	AB034701 Xenopus l							
c1448	282.5	12.0	72377	5	BX640520	BX640520 Zebrafish							
c1449	282.5	12.0	146798	2	AC116022	AC116022 Homo sapi							
c1450	282.5	12.0	156685	5	AL627167	AL627167 Zebrafish							
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c1452	282.5	12.0	185908	9	AC136297	AC136297 Homo sapi							
c1453	282	11.9	13095	9	HSFGFR4G	HSFGFR4G							
c1454	282	11.9	111061	9	AC078942	AC078942 Homo sapi							
c1455	282	11.9	121914	9	AC124944	AC124944 Homo sapi							
c1456	282	11.9	134752	5	BX000985	BX000985 Zebrafish							
c1457	282	11.9	149454	2	AC013648	AC013648 Homo sapi							
c1458	282	11.9	160892	2	BX248386	BX248386 Danio rer							
c1459	282	11.9	163057	10	AL928891	AL928891 Mouse DNA							
c1460	282	11.9	163736	2	AC022503	AC022503 Homo sapi							
c1461	282	11.9	169870	2	AC025977	AC025977 Homo sapi							
c1462	282	11.9	190936	5	BX548158	BX548158 Zebrafish							
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## ALIGNMENTS

RESULT 1	AX092320	Sequence 51 from Patent WO0116318.	1734 bp	DNA	linear	PAT 21-MAR-2001
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DEFINITION	AX092320	AX092320				
ACCESSION	AX092320.1	GI:13444474				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Alignment Scores:						
Pred. No.:						
Score:						
Percent Similarity:						
Best Local Similarity:						
Query Match:						
DB:						

US-10-063-699-52 (1-440) x AX092320 (1-1734)	
QY	1 MetLysPheGlnGlyProLeuAlaCysLeuLeuLeuAlaLeuCysLeuGlySerGlyGlu 20
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QY	21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyGluAlaLeuGly 40
Db	244 GCTGGCCCCCTGCAGAGCGAGAGGAAGACATGGGACAAATATTGGGAGAGGCCCTTGA 303
QY	41 HisGlyLeuGlyAspAlaLeuSerGlyValGlyLysAlaIleGlyLysGluAlaGly 60
Db	304 CATGGCTGGGACGCCCTGAGCGAGGAGTGGGAAGGCCCTTGGCAAGAGGCCGGA 363
QY	61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80
Db	364 GGGGACAGTGGCTCTAAAGTCAGTCAGGCCCTTGGCAAGGACCAGAGCAGTTGGC 423
QY	81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100
Db	424 ACTGGAGTCAGCGAGTTCAGGCTTCCAGGCTTTGGCGCAGAGATGCTTCGCATCCCG 1503
RESULT 2	
QY	AX358902 1734 bp DNA linear PAT 13-PBB-2002
Db	Sequence 155 from Patent WO0193983.
QY	AX358902
Db	AX358902.1 GI:18675352
QY	Homo sapiens (human)
Db	Homo sapiens
QY	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
QY	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Db	Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
QY	Watanabe, C.K. and Wood, W.I.
Db	Secreted and transmembrane polypeptides and nucleic acids encoding
QY	the same
Db	Patent: WO 0193983-A 155 13-DEC-2001;
QY	Genentech Inc. (US)
Db	Location/Qualifiers
QY	1..1734
Db	/organism="Homo sapiens"
QY	/mol_type="unassigned DNA"
Db	/db_xref="taxon:9606"
ORIGIN	
Alignment Scores:	
Pred. No.:	7,18e-63 Length: 1734
Score:	2363.00 Matches: 440
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	6 Gaps: 0
US-10-063-699-52 (1-440) x AX358902 (1-1734)	
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QY	21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyGluAlaLeuGly 40
Db	244 GCTGGCCCCCTGCAGAGCGGAGAGGAAGACATGGGACAAATATTGGGAGAGGCCCTTGA 303
QY	41 HisGlyLeuGlyAspAlaLeuSerGlyValGlyLysAlaIleGlyLysGluAlaGly 60
Db	304 CATGGCTGGGAGAGGCCCTGAGCGAGGAGTGGGAAGGCCCTTGGCAAGAGGCCGGA 363
QY	61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80
Db	364 GGGGACAGTGGCTCTAAAGTCAGTCAGGCCCTTGGCAAGGACCAGAGCAGTTGGC 423
QY	81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100
Db	424 ACTGGAGTCAGCGAGTTCAGGCTTCCAGGCTTTGGCGCAGAGATGCTTCGCATCCCG 483











QY 421 LysLeuGlyPheIleAsnTrpAspAlaIleAsnLysAspGlnArgSerSerArgIlePro 440  
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Db 1444 AGCTGGGTTTCATCACTGGGATGCCATTAACACAGGACAGAGAGCTCTGCATCCG 1503

RESULT 6  
AX454564  
LOCUS AX454564 1734 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 149 from Patent WO0208284.  
ACCESSION AX454564  
VERSION AX454564.1 GI:21713906  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.B., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 149 31-JAN-2002;  
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone  
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,  
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);  
Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);  
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);  
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William  
I. (US)

FEATURES  
Source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 7,18e-63 Length: 1734  
Score: 2363.00 Matches: 440  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-699-52 (1-440) x AX454564 (1-1734)

QY 1 MetLysPheGlnGlyProLeuAlaCysLeuLeuAlaLeuCysLeuGlySerGlyGlu 20  
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Db 184 ATGAAGTTCAGGGGCCCCCTGGCTGCTCTCTGCTGGCCCTCTGCTGGGAGTGGGAG 243

QY 21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyAlaLeuGly 40  
|||||  
Db 244 GCTGGCCCCCTGCAGACGGGAGGAGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGG 303

QY 41 HisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGlyLysGluAlaGly 60  
|||||  
Db 304 CATGGCTGGGAGACCCCTTGAGCGAGGGGGTGGAAAGCCATTGGCAAGAGGCCGGA 363

QY 61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80  
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Db 364 GGGGAGCTGGCTCTAAAGTCAGTAGGAGCCCTTGGCCAAAGGACACAGAGAGTGGC 423

QY 81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100  
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QY 101 GluAlaAlaHisAlaLeuGlyAsnThrGlyHisGluIleGlyArgGlnAlaGluAspVal 120  
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Db 484 GAAGCAGCCCATGCTCTGGGAAACACTGGGACAGATTGGCAGACAGCAGAGATGTC 543

QY 121 IleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGly 140  
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Db 544 ATTTCACACGAGCAGATGCTGCTCCGCGCTCTCTGGCAGGGGGTGCCTGGCCACAGTGGT 603  
QY 141 AlaTrpGluThrSerGlyGlyHisGlyIlePheGlySerGlnGlyGlyLeuGlyGlyGln 160  
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Db 604 GCTTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGGCTTGGAGGCCAG 663

QY 161 GlyGlnGlyAsnProGlyGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSer 180  
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Db 664 GGCAGGGCAATCTCTGGAGGCTCTGGGACTCGTGGGTCCAGGGATACCCCGGAATCA 723

QY 181 AlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyGlyAsnGlyGly 200  
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Db 784 CCACCAAACTTTGGGACCAACACTCAGGAGCTGTGGGCCAGCCCTGGCTATGTTTCAGTG 843

QY 221 ArgAlaSerAsnGlnAsnGluGlyCysThrAsnProProProSerGlySerGlyGly 240  
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Db 844 AGAGCCAGCAACCAGAAATGAAGGTGCACGAATCCCCCACCATCTGGCTCAGTGGAGGC 903

QY 241 SerSerAsnSerGlyGlyGlySerGlySerGlnSerGlySerSerGlySerGlySerAsn 260  
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Db 904 TCCAGCAACTCTTGGGGAGGAGCGGCTCACAGTCCGGCAGCAGTGGCAGTGGCAGCAAT 963

QY 261 GlyAspAsnAsnAsnGlySerSerSerGlyGlySerSerGlySerSerGlySerSer 280  
|||||  
Db 964 GGTGACACACAAATGGCAGCAGTGGTGACAGCAGTGGCAGCAGTGGCAGCAGTGGCAGC 1023

QY 281 SerSerGlyGlySerSerGlyGlySerSerGlyGlySerSerGlyGlySerGlyGlySer 300  
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Db 1024 AGCAGTGGCGCAGCAGTGGCGCAGCAGTGGTGACAGCAGTGGCAACAGTGGTGGCAGC 1083

QY 301 ArgGlyAspSerGlySerGluSerSerTrpGlySerSerThrGlySerSerSerGlyAsn 320  
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Db 1084 AGAGGTGACAGCGGCAGTGAAGTCTCTCTGGGGATCCAGCAGCCGCTCTCTCCCGCAAC 1143

QY 321 HisGlyGlySerGlyGlyGlyAsnGlyHisLysProGlyCysGluLysProGlyAsnGlu 340  
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Db 1144 CACGGTGGGAGCGCGGAGGAAATGGACATAAACCCGGGTGTGAAGCCAGGGGAATGAA 1203

QY 341 AlaArgGlySerGlyGluSerGlyIleGlnGlyPheArgGlyGlnGlyValSerSerAsn 360  
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Db 1204 GCCCGCGGAGCGGGGAATCTGGGATTCAGGGCTTCAGAGGACAGGGAGTTTCCAGCAAC 1263

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Db 1264 ATGAGGAAATAAGCAAGAGGGCAATCGCCTCTCTTGGAGGCTCTGGAGACAAATTTATCGG 1323

QY 381 GlyGlnGlySerSerTrpGlySerGlyGlyAspAlaValGlyValAsnThrVal 400  
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Db 1324 GGGCAAGGGTTCAGCTGGGGCAGTGGAGAGTGAACGCTGTGTGGTGGAGTCAATACTGTG 1383

QY 401 AsnSerGluThrSerProGlyMetPheAsnPheAspThrPheTrpLysAsnPhelysSer 420  
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Db 1384 AACTCTGAGACGCTCTCTGGGATGTTTAACCTTGACACTTCTCGAAGAAATTTTAATCC 1443

QY 421 LysLeuGlyPheIleAsnTrpAspAlaIleAsnLysAspGlnArgSerSerArgIlePro 440  
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RESULT 7  
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LOCUS AX491042 1734 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 149 from Patent WO0200690.  
ACCESSION AX491042  
VERSION AX491042.1 GI:22323858  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]



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## ORIGIN

## Alignment Scores:

Pred. No.: 7,186-63 Length: 1734  
Score: 2363.00 Matches: 440  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-063-699-52 (1-440) x AY358412 (1-1734)

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DB 244 GCTGGCCCTCTCAGAGCGGAGAGAAACACTGGGACAAATATTGGGGAGGCCCTTGGGA 303  
QY 41 HisGlyLeuGlyAspAlaLeuSerGlyGlyValGlyLysAlaIleGlyLysGluAlaGly 60  
DB 304 CATGGCCTGGGAGACGCCCTGAGCGGAAGGGGTGGGAAAGGCCATTGGCAAGAGGCCGA 363  
QY 61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80  
DB 364 GGGGAGCTGGCTCTAAAGTCAAGTGGGCGCTTGGCCAGGGACCCAGAGACAGTTGGC 423  
QY 81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100  
DB 424 ACTGGAGTCAGCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGCTCGGG 483  
QY 101 GluAlaAlaHisGlnLeuGlyAsnThrGlyHisGlyLysGlnAlaGluAspVal 120  
DB 484 GAAGCAGCCCATGCTCTGGGAAACACTGGGCAAGATTGGCAGACAGCAGAGATGTC 543  
QY 121 IleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGly 140  
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QY 141 AlaTrpGluThrSerGlyHisGlyIlePheGlySerGlnGlyLeuGlyGln 160  
DB 604 GCTTGGGAACTCTCGAGGCCATGCACTTTGGCTCTCAAGGTGGCTTGGAGCCAG 663  
QY 161 GlyGlnGlyAsnProGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSer 180  
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QY 181 AlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyAsnGlyGly 200  
DB 724 GCAGGCGAGTTTGGATGATCTCAGGAGAGCTCCCTGGGGTCAAGAGGCAATGGAGGG 783  
QY 201 ProProAsnPheGlyThrAsnThrGlnGlyAlaValAlaGlnProGlyTyrGlySerVal 220  
DB 784 CCACCAAACTTTGGGACCAACACTCAGGAGAGCTGTGGCCAGCCTGGCTATGTTCAAGTG 843  
QY 221 ArgAlaSerAsnGlnAsnGlnGlyCysThrAsnProProProSerGlySerGlyGly 240  
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QY 241 SerSerAsnSerGlyGlySerGlySerGlnSerGlySerSerGlySerGlySerAsn 260  
DB 904 TCAGGCACTCTGGGGGAGGAGCGGCTCACAGTCGGGAGCAGAGTGGCAGTGGCAGCAAT 963  
QY 261 GlyAspAsnAsnAsnGlySerSerGlyGlySerSerGlySerSerGlySerGlySer 280  
DB 964 GGTGCAACAACAATGGCAGCAGCAGTGTGTGGCAGCAGCAGTGGCAGCAGTGGCAGC 1023  
QY 281 SerSerGlyGlySerSerGlyGlySerSerGlyGlySerSerGlyGlySerGlySer 300  
DB 1024 AGCAGTGGCGGAGCAGTGGCGGAGCAGTGGTGGCAGCAGTGGCAGCAGTGGTGGCAGC 1083

QY 301 ArgGlyAspSerGlySerGlySerSerTrpGlySerSerThrGlySerSerSerGlyAsn 320  
DB 1084 AGAGGTGACAGCGGCAGTGAGTCTCTCTGGGATCCAGCACCGGCTCTCTCTCCGCAAC 1143  
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DB 1384 AACTCTGAGAGCTCTCTGGGATGTTTAACTTTTGACACTTTCTGGAGAAATTTTAAATCC 1443  
QY 421 LysLeuGlyPheIleAsnTrpAspAlaIleAsnLysAspGlnArgSerSerArgIlePro 440  
DB 1444 AAGCTGGGTTTCATCACTCACTGGGATGCCATAAACAGGACAGAGAAGCTCTCGCATCCG 1503

## RESULT 10

BD275935 1441 bp DNA linear PAT 17-JUL-2003  
LOCUS BD275935  
DEFINITION BD275935  
ACCESSION BD275935  
VERSION BD275935.1 GI:33085703  
KEYWORDS JP 2002543771-A/13.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1441)  
AUTHORS Birse,C.E., Moutet,P.A., Florence,K.A., Ruben,S.M.,  
Komatsoulis,G.A., Ni,J., Ebner,R., W.D., Lafleur, Olsen,H.S.,  
Shi,Y., Soppet,D.R., Rosen,C.A. and Young,P.E.  
TITLE 62 Human secreted proteins  
JOURNAL Patent: JP 2002543771-A 13 24-DEC-2002;  
Human Genome Sciences Inc  
COMMENT OS Homo sapiens  
PN JP 2002543771-A/13  
PD 24-DEC-2002  
PF 06-APR-2000 JP 2000611564  
PR 09-APR-1999 US 60/128693,26-APR-1999 US 60/130991 PI  
Charles e birse,paul a moutet,kimberly a florence,steven m pi  
ruben,  
PI George a komatsoulis,jian ni,reinhard ebner,david w pi  
lafleur,henrik s olsen,  
PI yanggu shi,daniel r soppet,craig a rosen,paul e young CC  
FH Key Location/Qualifiers  
FT SITE (1436)  
FT SITE /note='n equals a,t,g, or c'  
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FEATURES  
source

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## ORIGIN

Alignment Scores:  
Pred. No.: 5,248-53 Length: 1441  
Score: 2030.00 Matches: 385  
Percent Similarity: 87.73% Conservative: 1



Percent Similarity:	87.56%	Conservative:	2
Best Local Similarity:	87.10%	Mismatches:	0
Query Match:	84.47%	Indels:	54
DB:	9	Gaps:	2
US-10-063-699-52 (1-440) x AY622965 (1-1431)			
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QY	21	AlaGlyProLeuGlnSerGlyGluGlnSerThrGlyThrAsnIleGlyGluAlaLeuGly	40
DB	61	GCTGGCCCCCTCCAGAGCGGAGGAAAGCATGGGACAAATATTGGGAGGCCCTTGG	120
QY	41	HisGlyLeuGlyAspAlaLeuSerGluGlyValGlyLysAlaIleGlyLysGluAlaGly	60
DB	121	CATGGCCCTGGGAGAGCCCTGAGCGAGGGGTGGGAAAGGCCATTGGCAAGAGGCCCG	180
QY	61	GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly	80
DB	181	GGGGCAGCTGGCTCTAAAGTCAGTGGGCCCTTGGCCAGGGACCCAGAGCAGTGGC	240
QY	81	ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly	100
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QY	121	IleArgHisGlyAlaAspAlaValArgGlySerTrpGlnGlyValProGlyHisSerGly	140
DB	361	ATTGACACGGAGCAGATGCTCTCCGGCTCTCTGGCAGGGGTGCTGGCCACAAATGGT	420
QY	141	AlaTrpGluThrSerGlyHisGlyIlePheGlySerGlnGlyLeuGlyGlyGln	160
DB	421	GCTTGGGAAACTCTGGAGGCGCATGCTCTTGGCTCTCAAGGTGGCTTGGAGGCCAG	480
QY	161	GlyGlnGlyAsnProGlyLeuGlyThrProTrpValHisGlyTyrProGlyAsnSer	180
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QY	181	AlaGlySerPheGlyMetAsnProGlnGlyAlaProTrpGlyGlnGlyAsnGlyGly	200
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QY	221	ArgAlaSerAsnGlnAsnGluGlyCysThrAsnProProSerGlySerGlyGlyGly	240
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QY	241	SerSerAsnSerGlyGlySerGlySerGlnSerGlySerSerGlySerGlySerAsn	260
DB	721	TCCAGCAACTCTGGGGAGCGAGCGCTCACAGTCGGGCGAGTCAGTGGCAGCAAT	780
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QY	281	SerSerGlyGlySerSerGlySerGlySerGlySerGlySerGlySerGlySer	300
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QY	301	ArgGlyAspSerGlySerGluSerSerTrpGlySerSerThrGlySerSerSerGlyAsn	320
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DB	1038	-----	1038
QY	381	GlyGlnGlySerSerTrpGlySerGlyGlyAspAlaValGlyGlyValAsnThrVal	400
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QY	401	AsnSerGluThrSerProGlyMetPheAsnPheAspThrPheTrpLysAsnPhelysSer	420
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QY	421	LysLeuGlyPheIleAsnTrpAspAlaIleAsnLysAspGln	434
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RESULT 12			
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LOCUS	Homo sapiens dermokine, mRNA (cdna clone MGC:21664 IMAGE:4752921),		PRI 12-OCT-2004
DEFINITION	complete cds.		
ACCESSION	BC035311		
VERSION	BC035311.1	GI:23240833	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1982)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulligh, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1982)		
AUTHORS	Director MGC Project.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC		



Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavatti,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 28 Row: O Column: 20.

## FEATURES

## source

Location/Qualifiers  
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## ORIGIN

## Alignment Scores:

Pred. No.: 6,79e-52 Length: 1982  
 Score: 1996.00 Matches: 378  
 Percent Similarity: 87.56% Conservative: 2  
 Best Local Similarity: 87.10% Mismatches: 0  
 Query Match: 84.47% Indels: 54  
 DB: 9 Gaps: 2

US-10-063-699-52 (1-440) x BC035311 (1-1982)

QY 1 MetLysPheGlnGlyProLeuAlaCysLeuLeuLeuAlaLeuCysLeuGlySerGlyGlu 20  
 DB 178 ATGAAGTTCAGGGGCCCTGGCCCTCCCTGCTGGCCCTCTGCTGGCCAGTGGGGAG 237  
 QY 21 AlaGlyProLeuGlnSerGlyGluGluSerThrGlyThrAsnIleGlyGluAlaLeuGly 40  
 DB 238 GTTGGCCCCCTGCAGAGCGGAGGAGGAGACATGGGACAAATATTGGGAGGCCCTTGA 297  
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 DB 298 CATGGCCCTGGAGACGCCCTGAGCGAAGGGGTGGGAAGGCCATTGGCAAGAGGCCGA 357  
 QY 61 GlyAlaAlaGlySerLysValSerGluAlaLeuGlyGlnGlyThrArgGluAlaValGly 80  
 DB 358 GGGGCGAGCTGGCTCTAAAGTCAGTAGAGGCCCTTGGCCAAAGGGACCAAGACAGTTGGC 417  
 QY 81 ThrGlyValArgGlnValProGlyPheGlyAlaAlaAspAlaLeuGlyAsnArgValGly 100  
 DB 418 ACTGGAGTCAGCAGAGTTCCAGGCTTTGGCAGCAGATGCTTTGGCAGAGGTCGGG 477  
 QY 101 GluAlaAlaHisAlaLeuGlyAsnThrGlyHisGlyIleGlyArgGlnAlaGluAspVal 120

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 QY 401 AsnSerGluThrSerProGlyMetPheAsnPheAspThrPheTrpLysAsnPhelysSer 420  
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 QY 421 LysLeuGlyPheIleAsnTrpAspAlaIleAsnLysAspGln 434  
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## RESULT 13

AC138125/c  
 LOCUS AC138125 11311 bp DNA linear PRI 17-DEC-2002  
 DEFINITION Homo sapiens chromosome 19 clone LLNLR-228H6, complete sequence.  
 ACCESSION AC138125  
 VERSION AC138125.1 GI:27151356  
 KEYWORDS HTG.













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